E value

3.0e-65

```
Method
                     BLASTX
  NCBI GI
                     g4741960
  BLAST score
                     574
  E value
                     2.0e-59
  Match length
                     128
  % identity
  NCBI Description
                    (AF134130) Lhcb6 protein [Arabidopsis thaliana]
  Seq. No.
                    163411
  Seq. ID
                    LIB3177-062-P1-K1-F5
  Method
                    BLASTN
  NCBI GI
                    g4249393
  BLAST score
                    103
  E value
                    6.0e-51
  Match length
                    131
  % identity
  NCBI Description
                    Arabidopsis thaliana chromosome II BAC T9J23 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    163412
 Seq. ID
                    LIB3177-062-P1-K1-F6
 Method
                    BLASTX
 NCBI GI
                    g2104957
 BLAST score
                    584
 E value
                    2.0e-60
 Match length
                    107
 % identity
                    100
 NCBI Description (U96924) immunophilin [Arabidopsis thaliana]
 Seq. No.
                   163413
 Seq. ID
                   LIB3177-062-P1-K1-F7
 Method
                   BLASTX
 NCBI GI
                   g3413714
 BLAST score
                   364
E value
                   7.0e-35
Match length
                   105
 % identity
                   22
NCBI Description
                   (AC004747) putative myrosinase-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   163414
Seq. ID
                   LIB3177-062-P1-K1-F8
Method
                   BLASTN
NCBI GI
                   g3985958
BLAST score
                   286
E value
                   1.0e-160
Match length
                   419
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163415
Seq. ID
                  LIB3177-062-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g2760167
BLAST score
                  127
```

```
Match length
                     246
  % identity
                     100
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                    MCO15, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    163416
  Seq. ID
                    LIB3177-062-P1-K1-G1
  Method
                    BLASTX
  NCBI GI
                    g2088662
  BLAST score
                    605
  E value
                    6.0e-63
 Match length
                    140
  % identity
                    85
  NCBI Description
                    (AF002109) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    163417
 Seq. ID
                    LIB3177-062-P1-K1-G10
 Method
                    BLASTN
 NCBI GI
                    g4220632
 BLAST score
                    164
 E value
                    4.0e-87
 Match length
                    429
 % identity
                    98
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K6M13, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    163418
 Seq. ID
                   LIB3177-062-P1-K1-G12
 Method
                   BLASTX
 NCBI GI
                   q2500378
 BLAST score
                   464
 E value
                   2.0e-46
Match length
                   95
 % identity
                   92
NCBI Description
                  60S RIBOSOMAL PROTEIN L37
Seq. No.
                   163419
Seq. ID
                   LIB3177-062-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g3286693
BLAST score
                   450
E value
                   4.0e-58
Match length
                   125
% identity
NCBI Description
                   (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                   (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                   163420
Seq. ID
                  LIB3177-062-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  g4090568
BLAST score
                  114
E value
                  1.0e-57
Match length
                  186
% identity
                  97
NCBI Description
                  Arabidopsis thaliana Myb-related transcription factor CCA1
                  gene, complete cds
```

```
Seq. No.
                   163421
 Seq. ID
                   LIB3177-062-P1-K1-G4
 Method
                   BLASTX
 NCBI GI
                   g2500497
 BLAST score
                   314
 E value
                   7.0e-29
 Match length
                   72
 % identity
                   78
                   40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225.1_
 NCBI Description
                   (X98656) ribosomal protein S21 [Zea mays]
 Seq. No.
                   163422
 Seq. ID
                   LIB3177-062-P1-K1-G5
 Method
                   BLASTX
 NCBI GI
                   g115385
 BLAST score
                   62
 E value
                   6.0e-67
Match length
                   132
 % identity
                   99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
~Seq. No.
                   163423
Seq. ID
                   LIB3177-062-P1-K1-G6
Method '
                   BLASTX
NCBI GI
                   g1732570
BLAST score
                   713
E value
                   1.0e-75
Match length
                   157
% identity
                   85
NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                  163424
                  LIB3177-062-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062161
BLAST score
                  735
E value ·
                  3.0e-78
Match length
                  139
% identity
                  50
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  163425
Seq. ID
                  LIB3177-062-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3286693
BLAST score
                  611
E value
                  9.0e-64
Match length
                  125
% identity
                  98
NCBI Description
                 (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                  (OEC) in photosystem II [Arabidopsis thaliana]
```

Method

BLASTX

```
Seq. ID
                   LIB3177-062-P1-K1-G9
 Method
                   BLASTX
 NCBI GI
                   q3096931
 BLAST score
                   576
 E value ·
                   1.0e-59
 Match length
                   113
 % identity
                   99
 NCBI Description
                   (AL023094) putative ribosomal protein S16 [Arabidopsis
                   thaliana]
 Seq. No.
                   163427
Seq. ID
                   LIB3177-062-P1-K1-H10
Method
                   BLASTN
NCBI GI
                   q2281081
BLAST score
                   227
E value
                   1.0e-125
Match length
                   227
% identity
                   100
                   Arabidopsis thaliana chromosome II BAC F18019 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163428
Seq. ID
                   LIB3177-062-P1-K1-H11
Method
                   BLASTN
NCBI GI
                   g2351062
BLAST score
                   210
E value
                   1.0e-114
Match length
                   362
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163429
Seq. ID
                   LIB3177-062-P1-K1-H2
Method ··
                   BLASTX
NCBI GI
                   g2199574
BLAST score
                   340
E value
                   2.0e-32
Match length
                   65
% identity
                   98
NCBI Description
                  (AF004293) aquaporin [Brassica rapa]
Seq. No.
                  163430
Seq. ID
                  LIB3177-062-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3914658
BLAST score
                  294
E value
                  5.0e-27
Match length
                  74
% identity
                  80
NCBI Description
                  50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
                  >gi_1694974_emb CAA70851_ (Y09635) plastid ribosomal
                  protein [Arabidopsis thaliana]
Seq. No.
                  163431
Seq. ID
                  LIB3177-062-P1-K1-H4
```

```
NCBI GI
                    g2506443
BLAST score
                    553
E value
                    6.0e-57
Match length
                    139
% identity
                    78
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                    CHLOROPLAST >gi_2117520_pir__JQ1285
                    glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                    (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                    Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                   3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130)
                    glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                    (phosphorylating) [Arabidopsis thaliana]
Seq. No.
                   163432
Seq. ID
                   LIB3177-062-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g113026
BLAST score
                   372
E value
                   9.0e-63
Match length
                   135
                   87
% identity
                   ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                   >gi_68211_pir__WZRPI_isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
                   S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
                   napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
                   isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A
                   isocitrate lyase [Brassica napus]
                   163433
Seq. No.
Seq. ID
                   LIB3177-062-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g4741952
BLAST score
                   98
                   8.0e-66
E value
Match length
                   125
% identity
                   60
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                   163434
Seq. ID
                   LIB3177-062-P1-K1-H7
                   BLASTX
Method
NCBI GI
                   g132090
BLAST score
                   618
E value
                   2.0e-64
Match length
                   113
% identity
                   99
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   Bl precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana
```

```
Seq. ID
                   LIB3177-062-P1-K1-H9
Method
                   BLASTN
NCBI GI
                   g4587641
BLAST score
                   165
E value
                   1.0e-87
Match length
                   286
 % identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F20D21 genomic
                   sequence, complete sequence
Seq. No.
                   163436
Seq. ID
                   LIB3177-063-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   g3047100
BLAST score
                   90
                   2.0e-43
E value
Match length
                   122
% identity
                   94
NCBI Description Arabidopsis thaliana BAC F6N23
Seq. No.
                   163437
Seq. ID
                   LIB3177-063-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   g4756963
BLAST score
                   280
E value
                   1.0e-156
Match length
                   326
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                   163438
Seq. ID
                   LIB3177-063-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   q2661422
BLAST score
                   442
E value
                   3.0e-57
Match length
                   122
% identity
                   94
                   (AJ001342) Putative S-phase-specific ribosomal protein
NCBI Description
                   [Arabidopsis thaliana] >gi_3096936 emb CAA18846.1
                   (AL023094) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana]
Seq. No.
                   163439
Seq. ID
                  LIB3177-063-P1-K1-A5
Method
                   BLASTX
NCBI GI
                  g3157947
BLAST score
                   361
E value
                  7.0e-35
Match length
                  74
% identity
NCBI Description
                  (ACO02131) Similar to protein gb_Z74962 from Brassica
                  oleracea which is similar to bacterial YRN1 and HEAHIO
                  proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366,
                  gb R90704, gb F155\overline{0}0 and gb \overline{F1}4353 come from this gene.
```

[Arabidopsis tha

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Seq. No.
                    163440
 Seq. ID
                    LIB3177-063-P1-K1-A6
 Method
                    BLASTX
 NCBI GI
                    g3892722
 BLAST score
                    534
 E value
                    1.0e-54
 Match length
                    120
 % identity
                    92
 NCBI Description (AL033545) putative protein [Arabidopsis thaliana]
 Seq. No.
                   163441
 Seq. ID
                   LIB3177-063-P1-K1-A7
 Method
                   BLASTX
 NCBI GI
                   g121075
 BLAST score
                   259
 E value
                   5.0e-23
 Match length
                   63
 % identity
                   84
 NCBI Description
                   GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >qi 166725
                   (M82921) H-Protein precursor [Arabidopsis thaliana]
                   >gi_861215 (U27144) glycine decarboxylase complex H-protein
                   precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                   glycine decarboxylase complex H-protein [Arabidopsis
                   thaliana] >gi_445119_prf__1908425A Gly
                   decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
Seq. No.
                   163442
Seq. ID
                   LIB3177-063-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g115385
BLAST score
                   216
E value
                   5.0e-18
Match length
                   43
% identity
                   100
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   163443
Seq. ID
                   LIB3177-063-P1-K1-B11
Method
                   BLASTN
NCBI GI
                   g4455262
BLAST score
                   97
E value
                   2.0e-47
Match length
                  .217
% identity
                  58
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                   (ESSAII project)
Seq. No.
                  163444
Seq. ID
                  LIB3177-063-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g4587564
BLAST score
                  364
E value
                  1.0e-72
Match length
                  145
```

E value

4.0e-45

```
% identity
                   100
 NCBI Description
                   (AC006550) Strong similarity to gb_X14017 photosystem I
                   reaction centre subunit II precursor (psaD) from Spinacia
                   oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,
                   gb_N65521, gb_T42498, gb_T41918, gb_N38024
 Seq. No.
                   163445
 Seq. ID
                   LIB3177-063-P1-K1-B2
 Method
                   BLASTN
 NCBI GI
                   g4757417
 BLAST score
                   236
 E value
                   1.0e-130
 Match length
                   364
 % identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   T30G6, complete sequence
 Seq. No.
                   163446
Seq. ID
                   LIB3177-063-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g1170247
BLAST score
                   324
E value
                   1.0e-30
Match length
                   64
                   89
 % identity
NCBI Description
                   HEVEIN-LIKE PROTEIN PRECURSOR >gi_407248 (U01880)
                   pre-hevein-like protein [Arabidopsis thaliana]
Seq. No.
                   163447
Seq. ID
                   LIB3177-063-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g418405
BLAST score
                   45
E value
                   1.0e-09
Match length
                   82
% identity
                   45
                   HYPOTHETICAL 55.9 KD PROTEIN IN GDA1-UTR2 INTERGENIC REGION
NCBI Description
                   >gi 320711 pir S30838 hypothetical protein YEL041w - yeast
                   (Saccharomyces cerevisiae) >gi_603638 (U18779) Yel041wp
                   [Saccharomyces cerevisiae]
Seq. No.
                  163448
                  LIB3177-063-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4056502
BLAST score
                  115
E value
                  1.0e-36
Match length
                  102
% identity
NCBI Description
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.
                  163449
Seq. ID
                  LIB3177-063-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q3236246
BLAST score
                  450
```

Match length

```
Match length
                   89
% identity
                   93
NCBI Description (AC004684) putative expansin protein [Arabidopsis thaliana]
Seq. No.
                   163450
Seq. ID
                   LIB3177-063-P1-K1-B7
Method
                   BLASTX
                   g132110
NCBI GI
BLAST score
                   343
E value
                   1.0e-32
Match length
                   69
                   97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   163451
Seq. ID
                  LIB3177-063-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q2688824
BLAST score
                  200
E value
                   4.0e-16
Match length
                  53 ~
% identity
                  72
NCBI Description
                  (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
Seq. No.
                  163452
Seq. ID
                  LIB3177-063-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g16470
BLAST score
                  107
E value
                  2.0e-53
Match length
                  159
                  92
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for rubisco activase
Seq. No.
                  163453
Seq. ID
                  LIB3177-063-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g4455248
BLAST score
                  461
                  3.0e-46
E value
Match length
                  105
% identity
                  96
NCBI Description
                  (AL035523) acyl carrier-like protein [Arabidopsis thaliana]
Seq. No.
                  163454
Seq. ID
                  LIB3177-063-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  g4757409
BLAST score
                  71
E value
                  1.0e-31
```

```
% identity
                   68
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MVC8, complete sequence
Seq. No.
                   163455
Seq. ID
                   LIB3177-063-P1-K1-C5
Method
                   BLASTN
NCBI GI
                   g4733953
BLAST score
                   138
E value
                  1.0e-71
Match length
                   285
% identity
                   94
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                  163456
Seq. ID
                  LIB3177-063-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1488604
BLAST score
                  147
E value
                  2.0e-09
Match length
                  36
% identity
                  86
NCBI Description (Z49842) ribulosebiphosphate carboxylase [Hordeum lechleri]
Seq. No.
                  163457
Seq. ID
                  LIB3177-063-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g4757405
BLAST score
                  154
E value
                  3.0e-81
Match length
                  347
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOJ10, complete sequence
Seq. No.
                  163458
                  LIB3177-063-P1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3046849
BLAST score
                  209
E value
                  1.0e-114
Match length
                  213
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163459
                  LIB3177-063-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170939
BLAST score
                  687
E value
                  1.0e-72
Match length
                  139
% identity
                  93
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
```

```
S-adenosyl-L-methionine synthetase [Lycopersicon
                   esculentum]
 Seq. No.
                   163460
 Seq. ID
                   LIB3177-063-P1-K1-D1
Method
                   BLASTN
 NCBI GI
                   g3335356
 BLAST score
                   91
E value
                   8.0e-44
Match length
                   195
                   98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163461
Seq. ID
                   LIB3177-063-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g3738340
BLAST score
                   360
E value
                  1.0e-34
Match length
                  80
% identity
                  81
NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]
Seq. No.
                  163462
Seq. ID
                  LIB3177-063-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g399013
BLAST score
                  261
E value
                  4.0e-23
Match length
                  54
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi_16175_emb CAA46518 (X65549)
                  adenylate translocator [Arabidopsis thaliana]
                  >gi_445607_prf__1909354A adenylate translocator
                  [Arabidopsis thaliana]
Seq. No.
                  163463
Seq. ID
                  LIB3177-063-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q4539415
BLAST score
                  142
E value
                  3.0e-74
Match length
                  210
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
                  project)
Seq. No.
                 163464
Seq. ID
                  LIB3177-063-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  q4584387
```

>gi_1084408_pir__S46540 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429108_emb_CAA80867 (Z24743)

Method

BLASTX

```
BLAST score
                    53
 E value
                    3.0e-21
 Match length
                    124
 % identity
                    94
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
                    (ESSA project)
 Seq. No.
                    163465
 Seq. ID
                   LIB3177-063-P1-K1-D5
 Method
                   BLASTX
 NCBI GI
                   g3834310
 BLAST score
                   644
 E value
                   1.0e-67
 Match length
                   130
 % identity
                   98
 NCBI Description
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
                   gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                   gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122
                   come from this gene. [Arabidopsis thaliana]
 Seq. No.
                   163466
 Seq. ID
                   LIB3177-063-P1-K1-D7
 Method
                   BLASTN
 NCBI GI
                   g2262135
 BLAST score
                   202
E value
                   1.0e-110
Match length
                   241
% identity
NCBI Description Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                   cM, complete sequence
Seq. No.
                   163467
Seq. ID
                   LIB3177-063-P1-K1-D8
Method
                   BLASTN
NCBI GI
                   g4741959
BLAST score
                   34
E value
                   5.0e-10
Match length
                   41
% identity
                   98
NCBI Description
                  Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
Seq. No.
                  163468
Seq. ID
                  LIB3177-063-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g135467
BLAST score
                  208
E value
                  4.0e-17
Match length
                  39
% identity
                  95
                  TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4
NCBI Description
                  - Arabidopsis thaliana >gi_16664\overline{0} (M\overline{21}415) beta-tubulin
                  [Arabidopsis thaliana]
Seq. No.
                  163469
Seq. ID
                  LIB3177-063-P1-K1-E10
```

```
NCBI GI
                     g3123745
  BLAST score
                     230
  E value
                     2.0e-19
  Match length
                     83
  % identity
                     52
  NCBI Description
                     (AB013447) aluminum-induced [Brassica napus]
  Seq. No.
                     163470
  Seq. ID
                     LIB3177-063-P1-K1-E11
  Method
                     BLASTX
  NCBI GI
                     q132110
  BLAST score
                     161
 E value
                     1.0e-11
 Match length
                     34
  % identity
                     97
 NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                    (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                     (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                     thalianal
 Seq. No.
                    163471
 Seq. ID
                    LIB3177-063-P1-K1-E12
 Method
                    BLASTX
 NCBI GI
                    g4586256
 BLAST score
                    447
 E value
                    2.0e-44
 Match length
                    129
 % identity:
                    72
 NCBI Description
                    (AL049640) probable photosystem I chain XI precursor
                    [Arabidopsis thaliana]
Seq. No.
                    163472
Seq. ID
                    LIB3177-063-P1-K1-E2
Method
                    BLASTN
NCBI GI
                    g3169309
BLAST score
                    51
E value
                    7.0e-20
Match length
                    67
% identity
                    94
NCBI Description
                   Arabidopsis thaliana nucleoside diphosphate kinase type 1
                    (NDPK1) gene, complete cds
Seq. No.
                   163473
Seq. ID
                   LIB3177-063-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g1175013
BLAST score
                   331
E value
                   2.0e-31
Match length
                   78
% identity
                   87
NCBI Description
                   PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084
                   plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                   >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
```

protein 2a [Arabidopsis thaliana]

```
Seq. No.
                   163474
 Seq. ID
                   LIB3177-063-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g1916290
BLAST score
                   215
E value .
                   2.0e-17
Match length
                   72
 % identity
                   51
NCBI Description (U89876) ALY [Mus musculus]
Seq. No.
                   163475
Seq. ID
                   LIB3177-063-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   g3702734
BLAST score
                   302
E value
                   1.0e-169
Match length
                   334
% identity
                   97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNB8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163476
Seq. ID
                  LIB3177-063-P1-K1-E9
Method
                  BLASTX.
NCBI GI
                  q1345592
BLAST score
                  381
E value
                  5.0e-37
Match length
                  83
% identity
                  95
NCBI Description 14-3-3-LIKE PROTEIN GF14 EPSILON >gi_1022778 (U36446) GF14
                  epsilon isoform [Arabidopsis thaliana]
Seq. No.
                  163477
                  LIB3177-063-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2119846
BLAST score
                  601
E value
                  3.0e-68
Match length
                  144
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  163478
Seq. ID
                  LIB3177-063-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  g3510247
BLAST score
                  209
E value
                  1.0e-114
Match length .
                  408
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F19D11 genomic
```

163483

sequence, complete sequence [Arabidopsis thaliana]

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```
Seq. No.
                    163479
 Seq. ID
                    LIB3177-063-P1-K1-F12
 Method
                    BLASTX
 NCBI GI
                    g548355
BLAST score
                    459
E value
                    4.0e-46
Match length
                    100
 % identity
                    NITRATE REDUCTASE 1 (NR1) >gi_486751_pir_S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana
NCBI Description
                    >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase [Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate
                    reductase [Arabidopsis thaliana]
Seq. No.
                    163480
Seq. ID
                    LIB3177-063-P1-K1-F2
Method
                    BLASTX
NCBI GI
                    q136636
BLAST score
                    288
E value
                    9.0e-26
Match length
                    75
% identity
                    80
NCBI Description
                    UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                    LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                    >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                    Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                    Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                    Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                    >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                    thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                    [Arabidopsis thaliana]
Seq. No.
                    163481
                    LIB3177-063-P1-K1-F3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1363489
BLAST score
                    691
E value
                    4.0e-73
Match length
                    128
% identity
                    99
                   thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                   thaliana >gi_984052 emb_CAA61592 (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   163482
Seq. ID
                   LIB3177-063-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g4678260
BLAST score
                   497
E value
                   3.0e-50
Match length
                   121
% identity
NCBI Description
                   (AL049657) putative protein [Arabidopsis thaliana]
```

Method

BLASTX

```
Seq. ID
                   LIB3177-063-P1-K1-F5
Method
                   BLASTN
NCBI GI
                   g3510247
BLAST score
                   35
E value
                   3.0e-10
Match length
                   47
% identity
                   94
                  Arabidopsis thaliana chromosome II BAC F19D11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163484
Seq. ID
                   LIB3177-063-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   g4586111
BLAST score
                   227
E value
                   1.0e-18
Match length
                  78
% identity
                   65
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]
Seq. No.
                  163485
Seq. ID
                  LIB3177-063-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  q4581084
BLAST score
                  121
E value
                  1.0e-61
Match length
                  280
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
                  sequence, complete sequence
Seq. No.
                  163486
Seq. ID
                  LIB3177-063-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g4582437
BLAST score
                  86
E value
                  6.0e-41
Match length
                  171
% identity
                  99
NCBI Description Arabidopsis thaliana chromosome II BAC F7024 genomic
                  sequence, complete sequence
Seq. No.
                  163487
                  LIB3177-063-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585935
BLAST score
                  735
E value
                  3.0e~78
Match length
                  140
% identity
NCBI Description
                  (AC007211) putative chlorophyll A/B binding protein
                  [Arabidopsis thaliana] >gi_4741946 gb AAD28770.1 AF134123 1
                  (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  163488
Seq. ID
                  LIB3177-063-P1-K1-G10
```

```
NCBI GI
                   g4454048
 BLAST score
                    61
 E value
                    4.0e-70
 Match length
                   131
 % identity
                   99
 NCBI Description
                   (AL035394) putative protein [Arabidopsis thaliana]
 Seq. No.
                   163489
 Seq. ID
                   LIB3177-063-P1-K1-G3
Method
                   BLASTX
 NCBI GI
                   q115767
BLAST score
                   531
E value
                   7.0e-65
Match length
                   129
% identity
                   98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab16\overline{5} - Arabidopsis thaliana
                   >gi_16368 emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372\_emb\_CAA27541\_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   163490
Seq. ID
                  LIB3177-063-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g1076308
BLAST score
                   428
E value
                   3.0e-42
Match length
                   123
% identity
                   72
                   RNA-binding protein cp33 precursor - Arabidopsis thaliana
NCBI Description
                   >gi_681910_dbj_BAA06522_ (D31714) cp33 [Arabidopsis
                   thaliana]
Seq. No.
                   163491
Seq. ID
                   LIB3177-063-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g4204266
BLAST score
                   323
E value
                   1.0e-53
Match length
                   128
% identity
                   93
                  (AC005223) 52263 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   163492
                   LIB3177-063-P1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   602
E value
                   9.0e-63
Match length
                  110
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
```

Al precursor - Arabidopsis thaliana

```
Seq. No.
                    163493
 Seq. ID
                    LIB3177-063-P1-K1-G9
 Method
                    BLASTN
 NCBI GI
                    g1843627
BLAST score
                    70
 E value
                    4.0e-31
 Match length
                    126
 % identity
                    89
 NCBI Description
                   Arabidopsis thaliana SNF5 homolog BSH (bsh) mRNA, complete
 Seq. No.
                    163494
 Seq. ID
                    LIB3177-063-P1-K1-H1
 Method
                   BLASTX
 NCBI GI
                   g2506496
 BLAST score
                   663
 E value
                   9.0e-70
 Match length
                   128
 % identity
                   99
                   GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI)
 NCBI Description
                   >gi_1890156_emb_CAA72413_ (Y11727) gluthatione
                   S-transferase [Arabidopsis thaliana]
 Seq. No.
                   163495
 Seq. ID
                   LIB3177-063-P1-K1-H10
Method
                   BLASTN
NCBI GI
                   q4584351
BLAST score
                   346
E value
                   0.0e + 00
Match length
                   390
% identity
                   97
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T12H3 genomic
                   sequence, complete sequence
Seq. No.
                   163496
Seq. ID
                   LIB3177-063-P1-K1-H12
Method
                   BLASTN
NCBI GI
                   g2244991
BLAST score
                   152
E value
                   5.0e-80
Match length
                   282
% identity
                   98
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                  163497
Seq. ID
                  LIB3177-063-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4539316
BLAST score
                  535
E value
                  8.0e-55
Match length
                  121
% identity
                  93
NCBI Description
                  (AL035679) putative fructose-bisphosphate aldolase
```

[Arabidopsis thaliana]

```
Seq. No.
                      163498
  Seq. ID
                      LIB3177-063-P1-K1-H3
  Method
                      BLASTX .
  NCBI GI .
                      g4337175
  BLAST score
                      591
  E value
                      2.0e-61
  Match length
                      133
  % identity
                      89
  NCBI Description
                      (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
                     gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
  Seq. No.
                      163499
  Seq. ID
                      LIB3177-063-P1-K1-H4
  Method
                      BLASTX
  NCBI GI
                      g1732570
  BLAST score
                      774
 E value
                      8.0e-83
 Match length
                     145
 % identity
                     98
 NCBI Description
                    (U72153) beta-glucosidase [Arabidopsis thaliana]
 Seq. No.
                     163500
 Seq. ID
                     LIB3177-063-P1-K1-H5
 Method
                     BLASTX
 NCBI GI
                     g2129562
 BLAST score
                     707
 E value
                     6.0e-75
 Match length
                     139
 % identity
                     96
 NCBI Description
                     class III ADH, glutathione-dependent formaldehyde
                     dehydrogenase. - Arabidopsis thaliana
                     >gi_1143388_emb_CAA57973_ (X82647) class III ADH,
                     glutathione-dependent formaldehyde dehydrogenase.
                     [Arabidopsis thaliana]
 Seq. No.
                     163501
 Seq. ID
                    LIB3177-063-P1-K1-H6
Method
                    BLASTN
NCBI GI
                    g4584351
BLAST score
                    410
E value
                    0.0e + 00
Match length
                    446
% identity
                    98
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T12H3 genomic
                    sequence, complete sequence
Seq. No.
                    163502
Seq. ID
                    LIB3177-063-P1-K1-H7
Method
                    BLASTX
NCBI GI
                    g4204274
BLAST score
                    783
E value
                    8.0e-84
Match length
                    142
% identity
                    99
NCBI Description (AC004146) ribulose bisphosphate carboxylase, small subunit
```

163508

[Arabidopsis thaliana] Seq. No. 163503 Seq. ID LIB3177-064-P1-K1-A1 Method BLASTX . NCBI GI g1769905 BLAST score 365 E value 7.0e-35 Match length 112 % identity 64 (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) NCBI Description [Arabidopsis thaliana] Seq. No. 163504 Seq. ID LIB3177-064-P1-K1-A11 Method BLASTX NCBI GI g2213884 BLAST score 439 E value 1.0e-43 Match length 119 % identity 73 NCBI Description (AF004166) 2-isopropylmalate synthase [Lycopersicon pennellii] Seq. No. 163505 Seq. ID LIB3177-064-P1-K1-A2 Method BLASTN NCBI GI g2264306 BLAST score 457 E value 0.0e+00 Match length 457 % identity Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: NCBI Description MBK5, complete sequence [Arabidopsis thaliana] Seq. No. 163506 Seq. ID LIB3177-064-P1-K1-A3 Method BLASTN NCBI GI g3540210 BLAST score 54 E value 2.0e-22 Match length 54 % identity 100 NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 163507 Seq. ID LIB3177-064-P1-K1-A4 Method BLASTX NCBI GI g3193285 BLAST score 497 E value 2.0e-50 Match length 99 % identity 99 NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana]

```
Seq. ID
                   LIB3177-064-P1-K1-A5
 Method
                   BLASTX
 NCBI GI
                   q1764100
 BLAST score
                   348
 E value
                   7.0e-33
 Match length
                   67
 % identity
                   99
 NCBI Description
                   (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
                   thalianal
 Seq. No.
                   163509
 Seq. ID
                   LIB3177-064-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q3142289
BLAST score
                   455
E value
                   2.0e-45
Match length
                   94
 % identity
                   90
NCBI Description
                   (AC002411) Strong similarity to beta-keto-Coa synthase
                   gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
Seq. No.
                   163510
Seq. ID
                   LIB3177-064-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g2492952
BLAST score
                   224
E value
                   1.0e-18
Match length
                   95
% identity
                   88
NCBI Description
                   CHORISMATE SYNTHASE 1 PRECURSOR
                   (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)
                   >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1
                   precursor - tomato >gi_410482_emb_CAA79859_ (Z21796)
                   chorismate synthase 1 [Lycopersicon esculentum]
Seq. No.
                   163511
Seq. ID
                   LIB3177-064-P1-K1-A9
Method.
                   BLASTN
NCBI GI
                   g2264307
BLAST score
                   344
E value
                   0.0e + 00
Match length
                   445
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MED24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163512
Seq. ID
                  LIB3177-064-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1710530
BLAST score
                  758
E value
                  6.0e-81
Match length
                  141
% identity
                  99
NCBI Description
                  60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir__S71256
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
```

Match length

68

L27a [Arabidopsis thaliana]

```
Seq. No.
                   163513
 Seq. ID
                   LIB3177-064-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g2499535
BLAST score
                   145
E value
                   3.0e-09 `
Match length
                   32
 % identity
                   78
NCBI Description
                   2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi 595681
                   (U13238) 2-oxoglutarate/malate translocator [Spinacia
                   oleracea)
Seq. No.
                   163514
Seq. ID
                   LIB3177-064-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g3785991
BLAST score
                   368
E value
                   2.0e-35
Match length
                  79
% identity
                  .92
NCBI Description (AC005560) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                  163515
Seq. ID
                  LIB3177-064-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g131381
BLAST score
                  355
E value
                  3.0e-34
Match length
                  69
                  97
% identity
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852
                  photosystem II oxygen-evolving complex protein 1 precursor
                  - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33
                  kDa oxygen-evolving protein [Arabidopsis thaliana]
Seq. No.
                  163516
Seq. ID
                  LIB3177-064-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2245031
BLAST score
                  408
E value
                  0.0e+00
Match length
                  431
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  163517
Seq. ID
                  LIB3177-064-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g4538963
BLAST score
                  330
                  9.0e-31
E value
```

Seq. ID

```
% identity
                    96
                   (AL049488) chlorophyll a/b-binding protein-like
 NCBI Description
                    [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                    (AF134129) Lhcb5 protein [Arabidopsis thaliana]
 Seq. No.
                   163518
 Seq. ID
                   LIB3177-064-P1-K1-B5
 Method
                   BLASTX
 NCBI GI
                   q4538963
 BLAST score
                   366
 E value
                   2.0e-58
 Match length
                   143
 % identity
                   76
 NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
 Seq. No.
 Seq. ID
                   LIB3177-064-P1-K1-B6
 Method
                   BLASTN
 NCBI GI
                   g4757405
 BLAST score
                   133
 E value
                   1.0e-68
 Match length
                   426
 % identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                  MOJ10, complete sequence
Seq. No.
                   163520
Seq. ID
                  LIB3177-064-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1168200
BLAST score
                  324
E value
                   4.0e-30
Match length
                  80
% identity
NCBI Description
                  14-3-3-LIKE PROTEIN GF14 PSI (14-3-3-LIKE PROTEIN RCI1)
                  >gi_1361988_pir__S57277 GF14 protein psi chain -
                  Arabidopsis thaliana >gi_166717 (L09110) GF14 psi chain
                  [Arabidopsis thaliana] >gi_487789 (U09375) GF14psi isoform
                  [Arabidopsis thaliana]
Seq. No.
                  163521
Seq. ID
                  LIB3177-064-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3367536
BLAST score
                  415
E value
                  2.0e-46
Match length
                  99
% identity
                  (AC004392) Contains similarity to symbiosis-related like
NCBI Description
                  protein F1N20.80 gi_2961343 from A. thaliana BAC
                  gb_AL022140. EST gb_T04695 comes from this gene.
                  [Arabidopsis thaliana].
Seq. No.
                  163522
```

LIB3177-064-P1-K1-C10

```
Method
                    BLASTX
 NCBI GI
                    q541858
 BLAST score
                    614
 E value
                    8.0e-64
 Match length
                    127
 % identity
 NCBI Description
                   endoxyloglucan transferase - Arabidopsis thaliana
                   >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
 Seq. No.
Seq. ID
                   LIB3177-064-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g136636
BLAST score
                   469
E value
                   5.0e-47
Match length
                   87
% identity
                   99
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                   Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis thaliana]
Seq. No.
                   163524
                   LIB3177-064-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2956690
BLAST score
                   433
E value
                   6.0e-43
Match length
                   116
% identity
                   58
NCBI Description
                   (AJ223306) PSBY [Arabidopsis thaliana] >gi 3414928
                   (AF079800) PsbY precursor [Arabidopsis thaliana]
Seq. No.
                   163525
Seq. ID
                   LIB3177-064-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   q2506443
BLAST score
                   279
E value
                   4.0e-25
Match length
                   87
% identity
                   69
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi 2117520 pir JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi 166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi 1402885 emb_CAA66816_ (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) [Arabidopsis thaliana]
```

```
Seq. No.
                     163526
  Seq. ID
                     LIB3177-064-P1-K1-C7
  Method
                     BLASTN
  NCBI GI
                     g313151
  BLAST score
                     42
  E value
                     4.0e-14
  Match length
                    74
  % identity
                    95
 NCBI Description A.thaliana ribosomal protein S15 mRNA, complete CDS
 Seq. No.
                    163527
 Seq. ID
                    LIB3177-064-P1-K1-C8
 Method
                    BLASTX
 NCBI GI
                    q4467099
 BLAST score
                    388
 E value
                    8.0e-38
 Match length
                    80
 % identity
                    95
 NCBI Description
                    (AL035538) glycine hydroxymethyltransferase like protein
                    [Arabidopsis thaliana]
 Seq. No.
                    163528
 Seq. ID
                    LIB3177-064-P1-K1-C9
 Method
                    BLASTX
 NCBI GI
                    g4263718
 BLAST score
                    786
 E value
                    4.0e-84
 Match length
                    157
 % identity
 NCBI Description
                   (AC006223) putative DNA topoisomerase III beta [Arabidopsis
                   thaliana]
Seq. No.
                   163529
Seq. ID
                   LIB3177-064-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g3688182
BLAST score
                   604
E value
                   8.0e-63
Match length
                   125
% identity
NCBI Description (AL031804) P-Protein - like protein [Arabidopsis thaliana]
Seq. No.
                   163530
Seq. ID
                   LIB3177-064-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g132102
BLAST score
                   463
E value
                  1.0e-46
Match length
                  87
% identity
                  95
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                  ribulose-bisphosphate carboxylase (\overrightarrow{EC} 4.\overline{1}.1.39) small chain
                  B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana
```

Seq. ID

```
Seq. No.
                   163531
 Seq. ID
                   LIB3177-064-P1-K1-D12
 Method
                   BLASTX
 NCBI GI-
                   g2252828
 BLAST score
                   489
 E value
                   2.0e-49
 Match length
                   118
 % identity
                   85
 NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]
 Seq. No.
                   163532
 Seq. ID
                   LIB3177-064-P1-K1-D2
 Method
                   BLASTX
 NCBI GI
                   q4586047
 BLAST score
                   519
 E value
                   7.0e-53
Match length
                   138
 % identity
                   75
                   (AC007020) putative ferritin protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4588004_gb_AAD25945.1_AF085279_18 (AF085279)
                   hypothetical ferritin subunit [Arabidopsis thaliana]
Seq. No.
                   163533
Seq. ID
                   LIB3177-064-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g1514977
BLAST score
                   305
E value
                   5.0e-28
Match length
                   84
% identity
                   79
NCBI Description (D84669) VM23 [Raphanus sativus]
Seq. No.
                  163534
                  LIB3177-064-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3894186
BLAST score
                  555
E value
                  3.0e-57
Match length
                  118
% identity
                  91
NCBI Description
                  (AC005662) putative embryo-abundant protein [Arabidopsis
                  thaliana]
Seq. No.
                  163535
Seq. ID
                  LIB3177-064-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g3643588
BLAST score
                  104
E value
                  2.0e-51
Match length
                  292
% identity
                  94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163536
```

LIB3177-064-P1-K1-D6

```
Method
                   BLASTX
 NCBI GI
                   g2499609
 BLAST score
                   280
 E value
                   3.0e-25
 Match length
                   53
 % identity
                   100
 NCBI Description
                   MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 5 (MAP KINASE 5)
                   (ATMPK5) >gi_629546_pir__S40471 mitogen-activated protein
                   kinase 5 (EC 2.7.1.-) - Arabidopsis thaliana
                   >gi_457402 dbj_BAA04868_ (D21841) MAP kinase [Arabidopsis
                   thaliana]
 Seq. No.
                   163537
 Seq. ID
                   LIB3177-064-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g4218120
BLAST score
                   461
E value
                   4.0e-46
Match length
                   116
% identity
                   78
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                  163538
Seq. ID
                  LIB3177-064-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  809
E value
                  7.0e-87
Match length
                  153
% identity
                  99
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  163539
Seq. ID
                  LIB3177-064-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g4584351
BLAST score
                  284
E value
                  1.0e-159
Match length
                  336
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome II BAC T12H3 genomic
                  sequence, complete sequence
Seq. No.
                  163540
Seq. ID
                  LIB3177-064-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g132166
BLAST score
                  161
E value
                  3.0e-11
Match length
                  56
% identity
                  66
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048
                  ribulose-bisphosphate carboxylase activase precursor -
                  Arabidopsis thaliana >gi_16471_emb_CAA32429 (X14212)
                  rubisco activase (AA 1 - 473) [Arabidopsis thaliana]
```

a. .

- .

```
Seq. No.
                     163541
 Seq. ID
                     LIB3177-064-P1-K1-E11
 Method
                     BLASTX
 NCBI GI
                     g132074
 BLAST score
                     472
 E value
                     1.0e-47
 Match length
                     96
 % identity
                     95
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
 NCBI Description
                     (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                    ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1.1}.39) small chain
                    Al precursor - Arabidopsis thaliana
 Seq. No.
                    163542
 Seq. ID
                    LIB3177-064-P1-K1-E2
Method
                    BLASTX
NCBI GI
                    g131398
BLAST score
                    58
E value
                    3.0e-49
Match length
                    137
 % identity
                    78
NCBI Description
                    PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                    >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                    - Arabidopsis thaliana >gi_16447 emb CAA39441 (X55970)
                    photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                    >gi_3152571 (AC002986) Match to photosystem II 10kDa
                    polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                    gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                    come from this gene. [Arabidopsis
Seq. No.
                    163543
Seq. ID
                    LIB3177-064-P1-K1-E3
Method
                    BLASTX
NCBI GI
                    g1172872
BLAST score
                    532
E value
                    2.0e-54
Match length
                    103
% identity
NCBI Description
                   CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718
                   drought-inducible cysteine proteinase (\overline{\text{EC}} 3.4.\overline{22}.-) RD19A
                   precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                    (D13042) thiol protease [Arabidopsis thaliana]
                   >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                   cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                   163544
Seq. ID
                   LIB3177-064-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g4512615
BLAST score
                   52
E value
                   9.0e-34
Match length
                   83...
% identity
                   78
NCBI Description
                   (AC004793) Strong similarity to gb X59970 3-isopropylmalate
```

dehydrogenase (IMDH) from Brassica napus. EST gb_F14478



comes from this gene. [Arabidopsis thaliana]

```
Seq. No.
                      163545
  Seq. ID
                      LIB3177-064-P1-K1-E5
  Method
                      BLASTX
  NCBI GI
                      g132102
  BLAST score
                      752
  E value
                      3.0e-80
  Match length
                      145
  % identity
                      97
  NCBI Description
                      RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                      (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                      ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                      B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                      (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                      thaliana]
  Seq. No.
                      163546
  Seq. ID
                      LIB3177-064-P1-K1-E6
  Method
                      BLASTX
  NCBI GI
                      g121902
  BLAST score
                      422
  E value
                      2.0e-41
  Match length
                      136
% identity
                      68
                     HISTONE H1.1 >gi_1070594_pir__HSMU11 histone H1.1 - Arabidopsis thaliana >gi_16317_emb_CAA44314_ (X62458)
  NCBI Description
                      Histone H1 [Arabidopsis thaliana]
  Seq. No.
                     163547
                     LIB3177-064-P1-K1-E7
  Seq. ID
 Method
                     BLASTX
 NCBI GI
                     g541858
 BLAST score
                     48
 E-value
                     8.0e-42 '
 Match length
                     89
 % identity
                     99
 NCBI Description
                     endoxyloglucan transferase - Arabidopsis thaliana
                     >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                     endo-xyloglucan transferase [Arabidopsis thaliana]
 Seq. No.
                     163548
 Seq. ID
                     LIB3177-064-P1-K1-F10
 Method
                     BLASTN
 NCBI GI
                     g2062153
 BLAST score
                                                        , 4° '
                     49
 E value
                     2.0e-18
 Match length
                     73
 % identity
                     41
 NCBI Description
                     Arabidopsis thaliana chromosome III BAC T02004 genomic
                     sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                     163549
 Seq. ID
                     LIB3177-064-P1-K1-F11
 Method
                     BLASTN
 NCBI GI
                     g4539331
```

```
BLAST score
                    173
 E value
                    2.0e-92
 Match length
                    392
 % identity
                    Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13
 NCBI Description
                    (ESSA project)
 Seq. No.
                    163550
 Seq. ID
                    LIB3177-064-P1-K1-F12
 Method
                    BLASTX
 NCBI GI
                    g2143227
 BLAST score
                    167
 E value
                    3.0e-12
 Match length
                    46
 % identity
                    74
 NCBI Description (Y13356) glyoxysomal isocitrate lyase [Brassica napus]
 Seq. No.
                   163551
 Seq. ID
                   LIB3177-064-P1-K1-F2
 Method
                   BLASTN
 NCBI GI
                   g4468801
 BLAST score
                   141
 E value
                   1.0e-73
--Match length
                   212
 % identity
                   98
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
                   (ESSA project)
 Seq. No.
                   163552
                  LIB3177-064-P1-K1-F4
 Seq. ID
 Method
                 ·· BLASTX
NCBI GI
                   g4467099
BLAST score
                   389
E value
                   5.0e-38
Match length
                   75
 % identity
                   100
NCBI Description
                   (AL035538) glycine hydroxymethyltransferase like protein
                   [Arabidopsis thaliana]
Seq. No.
                   163553
Seq. ID
                   LIB3177-064-P1-K1-F5
Method
                   BLASTN
NCBI GI
                   g3449334
BLAST score
                  Ī17
E value
                   3.0e-59
Match length
                   230
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163554
Seq. ID
                  LIB3177-064-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3286693
BLAST score
                  632
E value
                  3.0e-66
Match length
                  127
```

BLAST score

```
% identity
                   100
 NCBI Description (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                   (OEC) in photosystem II [Arabidopsis thaliana]
 Seq. No.
                   163555
 Seq. ID
                   LIB3177-064-P1-K1-F8
 Method
                   BLASTN
 NCBI GI
                   g4159705
 BLAST score
                   20
 E value
                   2.4e-01
 Match length
                   176
 % identity
                   93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MGD8, complete sequence
 Seq. No.
                   163556
 Seq. ID
                   LIB3177-064-P1-K1-F9
 Method
                   BLASTN
 NCBI GI
                   g4741959
 BLAST score
                   96
 E value
                   6.0e-47
Match length
                   150
 % identity
                   91
NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
Seq. No.
                  163557
Seq. ID
                  LIB3177-064-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g4455251
BLAST score
                  482
E value
                  1.0e-48
Match length
                  140
% identity
                  69
NCBI Description
                  (AL035523) magnesium-protoporphyrin IX
                  methyltransferase-like protein [Arabidopsis thaliana]
Seq. No.
                  163558
Seq. ID
                  LIB3177-064-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  311
E value
                  6.0e-29
Match length
                  73
% identity
                  82
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  163559
Seq. ID
                  LIB3177-064-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  q4589445
```

```
E value
                   3.0e-28
 Match length
                   80
 % identity
                   96
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MWL2, complete sequence
                   163560
 Seq. No.
Seq. ID
                   LIB3177-064-P1-K1-G2
Method
                   BLASTN
NCBI GI
                   q3510341
BLAST score
                   149
E value
                   1.0e-78
Match length
                   161
% identity
                   37
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MFC16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163561
Seq. ID
                   LIB3177-064-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q115767
BLAST score
                   645
E value
                   1.0e-67
Match length
                   140
% identity
                   90
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  163562
                  LIB3177-064-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2271485
BLAST score
                  525
E value
                  8.0e-54
Match length
                  105
% identity
                  99
                  (AF009647) arginine decarboxylase [Arabidopsis thaliana]
NCBI Description
                  >gi_3096940_emb_CAA18850.1 (AL023094) arginine
                  decarboxylase SPE2 [Arabidopsis thaliana]
Seq. No.
                  163563
Seq. ID
                  LIB3177-064-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  g259446
BLAST score
                  158
E value
                  1.0e-83
Match length
                  177
% identity
                  100
NCBI Description
                  glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana,
                  C24, mRNA, 680 nt]
```

NCBI GI

q397555

```
Seq. ID
                   LIB3177-064-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g4584523
BLAST score
                   307
E value
                   2.0e-28
Match length
                   61
% identity
                   98
NCBI Description
                   (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3177-064-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g4454037
BLAST score
                   726
E value
                   3.0e-77
Match length
                   139
% identity
                   96
NCBI Description
                   (AL035394) putative major latex protein [Arabidopsis
Seq. No.
                   163566
Seq. ID
                   LIB3177-064-P1-K1-G9
Method
                   BLASTN
NCBI GI
                   g4063737
BLAST score
                   68
E value
                   5.0e-30
Match length
                   96
                   93
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F24D13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163567
Seq. ID
                 LIB3177-064-P1-K1-H10
Method
                  BLASTN
NCBI GI
                   g438448
BLAST score
                   65
E value
                   2.0e-28
Match length
                   101
% identity
                   91
NCBI Description
                  Arabidopsis thaliana carbonic anhydrase (ca180) mRNA,
                   complete cds
Seq. No.
                   163568
Seq. ID
                  LIB3177-064-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4455210
BLAST score
                   557
                  3.0e-57
E value
Match length
                  127
% identity
NCBI Description
                   (AL035440) putative aspartate-tRNA ligase [Arabidopsis
                  thaliana]
Seq. No.
                  163569
Seq. ID
                  LIB3177-064-P1-K1-H3
Method
                  BLASTX
```

```
BLAST score
                    164
 E value
                    2.0e-23
 Match length
                    74
 % identity
                    71
                    (X61664) photosystem I psaH protein [Nicotiana sylvestris]
 NCBI Description
 Seq. No.
                    163570
 Seq. ID
                    LIB3177-064-P1-K1-H4
Method
                    BLASTX
NCBI GI
                    q4741948
BLAST score
                    755
E value
                    2.0e-80
Match length
                    142
% identity
                    100
                   (AF134124) Lhcb2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    163571
Seq. ID
                    LIB3177-064-P1-K1-H5
Method
                    BLASTX
NCBI GI
                    g115470
BLAST score
                    308
E value
                    3.0e-28
Match length
                    133
% identity
NCBI Description
                    CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                    DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase
                   (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                    [Arabidopsis thaliana]
Seq. No.
                    163572
Seq. ID
                   LIB3177-064-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1769905
BLAST score
                   303
                   9.0e-28
E value
Match length
                   99
% identity
                   62
NCBI Description
                    (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                    [Arabidopsis thaliana]
Seq. No.
                   163573
                   LIB3177-064-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4587527
BLAST score
                   167
E value
                   3.0e-12
Match length
                   66
% identity
                   56
NCBI Description
                   (AC007060) Strong similarity to F19I3.2 gi 3033375 putative
                   berberine bridge enzyme from Arabidopsis thaliana BAC
                   gb_AC004238
Seq. No.
                   163574
                   LIB3177-064-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4204285
```

```
BLAST score
                   357
 E value
                   6.0e-34
 Match length
                   133
 % identity
 NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
 Seq. No.
                   163575
 Seq. ID
                   LIB3177-065-P1-K1-A1
 Method
                   BLASTX
NCBI GI
                   q544134
BLAST score
                   140
E value
                   7.0e-50
Match length
                   119
 % identity
                   88
NCBI Description
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
                   >gi_99720_pir__S22863 hypothetical protein - Arabidopsis
                   thaliana >gi_421844_pir__A46260 RecA functional analog
                   DRT100 - Arabidopsis thaliana (fragment)
Seq. No.
                   163576
Seq. ID
                   LIB3177-065-P1-K1-A10
Method
                  BLASTN
NCBI: GI
                  g2618602
BLAST score
                  108
E value
                  7.0e-54
Match length
                  108
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163577
                  LIB3177-065-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4557229
BLAST score
                  174
E value
                  1.0e-12
Match length
                  69
% identity
                  43
NCBI Description
                  angio-associated, migratory cell protein
                  >gi_3121739_sp_Q13685_AAMP_HUMAN ANGIO-ASSOCIATED MIGRATORY
                  CELL PROTEIN >gi_2134759_pir__139383 angio-associated
                  migratory cell protein - human >gi_870803 (M95627)
                  angio-associated migratory cell protein [Homo sapiens]
Seq. No.
                  163578
Seq. ID
                  LIB3177-065-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g1145697
BLAST score
                  631
E value
                  4.0e-66
Match length
                  129
% identity
                  71
NCBI Description
                  (U39485) delta tonoplast integral protein [Arabidopsis
                  thaliana
```

```
Seq. ID
                    LIB3177-065-P1-K1-A2
 Method
                    BLASTX
 NCBI GI
                    g3395441
 BLAST score
                    219
 E value
                    9.0e-18
 Match length
                    62
 % identity
                    58
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    163580
 Seq. ID
                   LIB3177-065-P1-K1-A4
 Method
                   BLASTX
 NCBI GI
                   q1363489
 BLAST score
                    751
 E value
                   4.0e-80
 Match length
                   143
 % identity
                   95
 NCBI Description
                   thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                   thaliana >gi_984052 emb_CAA61592_ (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   163581
Seq. ID
                   LIB3177-065-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g2894596
BLAST score
                   468
E value
                   6.0e-47
Match length
                   107
% identity
                   85
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                   163582
Seq. ID
                   LIB3177-065-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g2342684
BLAST score
                   497
E value
                   2.0e-50
Match length
                   123
% identity
                   84
NCBI Description (AC000106) F7G19.14 [Arabidopsis thaliana]
Seq. No.
                   163583
                   LIB3177-065-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q135467
BLAST score
                   296
E value
                   6.0e-27
Match length
                   69
% identity
                   100
NCBI Description
                  TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4
                   - Arabidopsis thaliana >\overline{gi}_116664\overline{0} (M\overline{21}415) beta-tubulin
                   [Arabidopsis thaliana]
Seq. No.
                   163584
Seq. ID
                  LIB3177-065-P1-K1-A9
Method
```

BLASTX

q1703446

NCBI GI

NCBI GI

```
BLAST score
                   194
 E value
                   2.0e-15
Match length
                   54
 % identity
                   76
 NCBI Description
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                   >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana
                   >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
                   thaliana]
Seq. No.
                   163585
Seq. ID
                   LIB3177-065-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   557
E value
                   2.0e-57
Match length
                   107
% identity
                   98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
Seq. No.
                   163586
                  LIB3177-065-P1-K1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2737904
BLAST score
                  67
E value
                  1.0e-29
Match length
                  79
% identity
                  96
NCBI Description Arabidopsis thaliana retrotransposon TSCL mRNA sequence
Seq. No.
                  163587
                  LIB3177-065-P1-K1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2245031
BLAST score
                  298
E value
                  1.0e-167
Match length
                  318
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  163588
                  LIB3177-065-P1-K1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  318
E value
                  1.0e-179
Match length
                  334
% identity
                  99
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                  163589
Seq. ID
                  LIB3177-065-P1-K1-B3
Method
                  BLASTX
```

BLAST score 500 E value 9.0e-51 Match length 95 % identity 97

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789 (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 163590

Seq. ID LIB3177-065-P1-K1-B4

Method BLASTX
NCBI GI g1708313
BLAST score 390
E value 5.0e-38
Match length 79
% identity 100

NCBI Description HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs 163637

(S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis

thaliana]

Seq. No. 163591

Seq. ID LIB3177-065-P1-K1-B5

Method BLASTX
NCBI GI g115767
BLAST score 488
E value 2.0e-49
Match length 101
% identity 93

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (THCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163592

Seq. ID LIB3177-065-P1-K1-B6

Method BLASTX
NCBI GI g1363489
BLAST score 137
E value 9.0e-09
Match length 35
% identity 77

NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis

thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside

glucohydrolase [Arabidopsis thaliana]

Seq. No. 163593

Seq. ID LIB3177-065-P1-K1-B7

Method BLASTX

NCBI Description

```
NCBI GI
                    g4220457
 BLAST score
                    493
 E value
                    5.0e-50
 Match length
                    112
 % identity
                    38
 NCBI Description
                    (AC006216) Similar to gi_3413714 T19L18.21 putative
                    myrosinase-binding protein from Arabidopsis thaliana BAC
                    gb_AC004747. EST gb_N96478 comes from this gene.
                    [Arabidopsis thaliana]
 Seq. No.
                    163594
 Seq. ID
                   LIB3177-065-P1-K1-C1
 Method
                   BLASTX
 NCBI GI
                   q140508
 BLAST score
                   308
 E value
                   8.0e-29
 Match length
                   65
 % identity
                   88
 NCBI Description
                   PROBABLE INTRON MATURASE >gi_99852_pir__S07168 probable
                   maturase, 63K - white mustard chloroplast
                   >gi_12220_emb_CAA28509_ (X04826) ycf14 (AA1-324) [Sinapis
                   alba]
 Seq. No.
                   163595
 Seq. ID
                   LIB3177-065-P1-K1-C10
 Method
                   BLASTN
 NCBI GI
                   g4741961
 BLAST score
                   216
 E value
                   1.0e-118
Match length
                   238
 % identity
                   98
NCBI Description Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds
Seq. No.
                   163596
Seq. ID
                   LIB3177-065-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g1488255
BLAST score
                   346
E value
                   1.0e-32
Match length
                   90
% identity
                   69
NCBI Description
                  (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
                  >gi_2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase
                  (FAH1) [Arabidopsis thaliana] >gi_3925365 (AF068574)
                  ferulate-5-hydroxylase [Arabidopsis thaliana]
Seq. No.
                  163597
Seq. ID
                  LIB3177-065-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g4662609
BLAST score
                  76
E value
                  5.0e-35
Match length
                  159
% identity
```

complete sequence

Genomic sequence for Arabidopsis thaliana BAC F10A5,

E value

3.0e-17

```
Seq. No.
                    163598
 Seq. ID
                   LIB3177-065-P1-K1-C2
 Method
                   BLASTX
 NCBI GI
                   g3286693
 BLAST .score
                    573
 E value
                    2.0e-59
 Match length
                   118
 % identity
                    99
NCBI Description
                    (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                    (OEC) in photosystem II [Arabidopsis thaliana]
 Seq. No.
                   163599
Seq. ID
                   LIB3177-065-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   589
E value
                   3.0e-61
Match length
                   116
% identity
                   98
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab16\overline{5} - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372\[ emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   163600
Seq. ID
                   LIB3177-065-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   g2760165
BLAST score
                   209
E value
                   1.0e-114
Match length
                   275
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163601
Seq. ID
                   LIB3177-065-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g131211
BLAST score
                   176
E value
                   4.0e-13
Match length
                   36
% identity
                   94
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT: IX (PSI-J)
NCBI Description
                  >gi_1363533_pir__S58571 photosystem I protein psaJ - maize
                  chloroplast >gi_552734 (J04502) ORF42 [Zea mays]
                  >gi_902241_emb_CAA60305_ (X86563) psaJ [Zea mays]
Seq. No.
                  163602
Seq. ID
                  LIB3177-065-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1514639
BLAST score
                  86
```

```
Match length
                    62
 % identity
                   77
 NCBI Description (X85181) alpha-glucan phosphorylase [Spinacia oleracea]
 Seq. No.
                   163603
 Seq. ID
                   LIB3177-065-P1-K1-D1
 Method
                   BLASTX
 NCBI GI
                   q3355472
 BLAST score
                   152
 E value
                   2.0e-10
 Match length
                   41
 % identity
                   66
 NCBI Description
                   (AC004218) disease resistance response protein (206-d) like
                   [Arabidopsis thaliana]
 Seq. No.
                   163604
Seq. ID
                   LIB3177-065-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g4220514
BLAST score
                   83
E value
                   4.0e-09
Match length
                   54
% identity
                   61
NCBI Description
                  (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                   163605
Seq. ID
                   LIB3177-065-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g3236248
BLAST score
                   304
E value
                   6.0e-28
Match length
                   88
% identity
                  70
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                  163606
                  LIB3177-065-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703220
BLAST score
                  441
E value
                  1.0e-43
Match length
                  141
% identity
                  57
NCBI Description
                  AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis
                  thaliana]
Seq. No.
                  163607
Seq. ID
                  LIB3177-065-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g227070
BLAST score
                  165
E value
                  1.0e-11
Match length
                  42
% identity
                  71
NCBI Description ribosomal protein CS-S5 [Spinacia oleracea]
Seq. No.
                  163608
```

Seq. No.

```
Seq. ID
                   LIB3177-065-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   g2264317
BLAST score
                   212
E value
                   1.0e-116
Match length
                   399
% identity
                   94
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163609
Seq. ID
                   LIB3177-065-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   q3282170
BLAST score
                   59
E value
                   8.0e-25
Match length
                   71
                   96
% identity
NCBI Description
                   Arabidopsis thaliana chromosome 1 BAC F8K4 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   163610
Seq. ID
                   LIB3177-065-P1-K1-D7
Method
                 BLASTX
NCBI GI
                   g1055161
BLAST score
                   159
E value
                   1.0e-10
Match length
                   151
% identity
                   32
NCBI Description
                   (U40029) similar to human 100 kDa coactivator (U22055)
                   [Caenorhabditis elegans]
Seq. No.
                   163611
Seq. ID
                   LIB3177-065-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   42
E value
                   3.0e-58
Match length
                   123
% identity
                   95
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP \overline{AB} 140) [Arabidopsis
                  thaliana]
Seq. No.
                  163612
Seq. ID
                  LIB3177-065-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g2760165
BLAST score
                  89
E value
                  2.0e-42
Match length
                  293
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
```

```
Seq. ID
                    LIB3177-065-P1-K1-E1
 Method
                    BLASTX
 NCBI GI
                    g1169235
 BLAST score
                    139
 E value
                    1.0e-08
 Match length
                    74
 % identity
                    46
 NCBI Description
                    DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE)
                    >gi_1073995_pir__B64089 diaminopimelate decarboxylase (dap
                    decarboxylase) (lysA) homolog - Haemophilus influenzae
                    (strain Rd KW20) >gi_1573731 (U32756) diaminopimelate
                    decarboxylase (lysA) [Haemophilus influenzae Rd]
 Seq. No.
                    163614
Seq. ID
                   LIB3177-065-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g2129630
BLAST score
                    436
E value
                   3.0e-43
Match length
                   86
% identity
                   94
NCBI Description
                   lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750
                    (X97023) lamin [Arabidopsis thal\overline{i}ana] >g\overline{i}_33\overline{9}5760 (U7\overline{7}721)
                   unknown [Arabidopsis thaliana]
Seq. No.
                   163615
Seq. ID
                   LIB3177-065-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   g3212102
BLAST score
                   122
E value
                   2.0e-62
Match length
                   170
% identity
                   95
NCBI Description
                   Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   163616
Seq. ID
                   LIB3177-065-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g2062167
BLAST score
                   543
E value
                   9.0e-56
Match length
                   105
% identity
                   97
NCBI Description
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
                   thaliana]
Seq. No.
                   163617
Seq. ID
                   LIB3177-065-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2924772
BLAST score
                   153
E value
                   2.0e-10
Match length
                   37
% identity
                   81
```

NCBI Description (AC002334) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                    163618
  Seq. ID
                    LIB3177-065-P1-K1-E3
 Method
                 - BLASTX
 NCBI GI
                    g2650351
 BLAST score
                    154
 E value
                    2.0e-10
 Match length
                    78
 % identity
                    40
 NCBI Description
                   (AE001085) 3-hydroxyacyl-CoA dehydrogenase (hbd-2)
                    [Archaeoglobus fulgidus]
 Seq. No.
                    163619
 Seq. ID
                    LIB3177-065-P1-K1-E4
 Method
                   BLASTX
 NCBI GI
                   q3334123
 BLAST score
                   395
 E value
                   1.0e-38
 Match length
                   99
 % identity
                   85
                   ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
 NCBI Description
                   >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of
                   mitochondrial FI-ATPase [Arabidopsis thaliana] >gi_2924787
                   (AC002334) mitochondrial F1-ATPase, gamma subunit
                   [Arabidopsis thaliana]
Seq. No.
                   163620
 Seq. ID
                   LIB3177-065-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   g16206
BLAST score
                   75
E value
                   8.0e-35
Match length
                   75
% identity
                   100
NCBI Description A.thaliana Cab mRNA for photossystem I chlorophyll
                   A/B-binding protein
Seq. No.
                   163621
Seq. ID
                  LIB3177-065-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g4567303
BLAST score
                  604
E value
                  6.0e-63
Match length
                  114
% identity
                  100
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                  163622
Seq. ID
                  LIB3177-065-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                  104
E value
                  1.0e-51
Match length
                  204
% identity
                  97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
```

NCBI GI

```
Seq. No.
                    163623
  Seq. ID
                    LIB3177-065-P1-K1-F1
  Method
                    BLASTN
  NCBI GI
                    g3687221
  BLAST score
                    58
  E value
                    2.0e-24
  Match length
                    86
  % identity
                    92
                    Arabidopsis thaliana chromosome II BAC F6F22 genomic
  NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    163624
 Seq. ID
                    LIB3177-065-P1-K1-F10
 Method
                    BLASTN
 NCBI GI
                    q4589444
 BLAST score
                    58
 E value
                    3.0e-24
 Match length
                    140
 % identity
                    95
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                    MWF20, complete sequence
 Seq. No.
                    163625
 Seq. ID
                    LIB3177-065-P1-K1-F4
 Method
                   BLASTX
 NCBI GI
                   g4006879
 BLAST score
                    581
 E value
                   2.0e-60
 Match length
                   113
 % identity
 NCBI Description
                   (Z99707) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   163626
Seq. ID
                   LIB3177-065-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g3953473
BLAST score
                   452
E value
                   4.0e-45
Match length
                   117
% identity
                   80
NCBI Description
                  (ACO02328) F2202.18 [Arabidopsis thaliana]
Seq. No.
                   163627
Seq. ID
                   LIB3177-065-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  g4589428
BLAST score
                  265
E value
                  1.0e-147
Match length
                  289
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MFH8, complete sequence
Seq. No.
                  163628
Seq. ID
                  LIB3177-065-P1-K1-F8
Method
                  BLASTX
```

Seq. ID

```
BLAST score
                    231
  E value
                    2.0e-19
 Match length
                    59
  % identity
                    80
  NCBI Description
                    (AC007119) putative phosphatidylinositol/phophatidylcholine
                    transfer protein [Arabidopsis thaliana]
 Seq. No.
                    163629
 Seq. ID
                    LIB3177-065-P1-K1-F9
 Method
                    BLASTN
 NCBI GI
                    q3869074
 BLAST score
                    46
 E value
                    5.0e-17
 Match length
                    79
 % identity
                    93
                   Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
 NCBI Description
                    MMI9, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    163630
 Seq. ID
                   LIB3177-065-P1-K1-G1
 Method
                   BLASTX
 NCBI GI
                   g231564
 BLAST score
                   390
 E value
                   4.0e-38
 Match length
                   81
 % identity
                   94
 NCBI Description
                   PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR
                   (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP
                   SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE
                   SYNTHASE 2) >gi 166690 (M74820)
                   3-deoxy-D-arabino-heptulosonate 7-phosphate synthase
                   [Arabidopsis thaliana]
Seq. No.
                   163631
Seq. ID
                   LIB3177-065-P1-K1-G10
Method
                   BLASTN
NCBI GI
                   g786465
BLAST score
                   90
E value
                   2.0e-43
Match length
                   133
% identity
                   93
NCBI Description
                  sedoheptulose-1,7-bisphosphatase [Arabidopsis thaliana,
                   C24, Genomic, 2747 nt]
Seq. No.
                   163632
Seq. ID
                  LIB3177-065-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   g4454022
BLAST score
                   32
E value
                  3.0e-09
Match length
                  36
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
                  (ESSAII project)
Seq. No.
                  163633
```

LIB3177-065-P1-K1-G12

Method

BLASTX

```
Method
                   BLASTX
NCBI GI
                   q119975
BLAST score
                    474
                   7.0e-48
E value
Match length
                   98
% identity
                    98
NCBI Description
                   FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin
                    [2Fe-2S] precursor - Arabidopsis thaliana
                   >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                    [Arabidopsis thaliana]
Seq. No.
                   163634
Seq. ID
                   LIB3177-065-P1-K1-G2
Method
                   BLASTN
NCBI GI
                   g2894591
BLAST score
                   137
E value
                   3.0e-71
Match length
                   213
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
                   (ESSAII project)
Seq. No.
                   163635
Seq. ID
                   LIB3177-065-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g1621268
BLAST score
                   524
E value
                   2.0e-53
Match length
                   137
% identity
                   69
NCBI Description
                   (Z81012) unknown [Ricinus communis]
Seq. No.
                   163636
Seq. ID
                   LIB3177-065-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   g4063735
BLAST score
                   107
E value
                   3.0e-53
Match length
                   171
% identity
                   92
NCBI Description
                   Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5
                   cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163637
Seq. ID
                   LIB3177-065-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   q3785997
BLAST score
                   225
E value
                   4.0e-19
Match length
                   66
% identity
NCBI Description
                  (AC005499) putative annexin [Arabidopsis thaliana]
Seq. No.
                   163638
Seq. ID
                   LIB3177-065-P1-K1-G6
```

Seq. No.

```
NCBI GI
                   q2244969
 BLAST score
                   182
 E value
                   5.0e-14
Match length
                   47
 % identity
                   77
NCBI Description
                   (297340) hypothetical gene [Arabidopsis thaliana]
                   >gi_3549643_emb_CAA06433_ (AJ005196) receiver-like protein
                   5 [Arabidopsis thaliana]
 Seq. No.
                   163639
Seq. ID
                   LIB3177-065-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g3869253
BLAST score
                   749
E value
                   7.0e-80
Match length
                   147
% identity
                   100
NCBI Description
                   (U39288) ferredoxin-dependent glutamate synthase precursor
                   [Arabidopsis thaliana]
Seq. No.
                   163640
Seq. ID
                   LIB3177-065-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3157937
BLAST score
                   327
E value
                   7.0e-31
Match length
                   69
% identity
                   99
NCBI Description
                   (AC002131) Identical to aspartic proteinase cDNA gb U51036
                   from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,
                   gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269,
                   gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
                   gb_AA728734, gb
Seq. No.
                   163641
                  LIB3177-065-P1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                  g4454036
BLAST score
                   165
E value
                  7.0e-12
Match length
                  71
% identity
NCBI Description
                   (AL035394) putative major latex protein [Arabidopsis
                  thaliana]
Seq. No.
                  163642
                  LIB3177-065-P1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4159704
BLAST score
                  314
E value
                  1.0e-176
Match length
                  322
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
```

Seq. No.

```
Seq. ID
                   LIB3177-065-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g2244881
BLAST score
                   512
E value
                   4.0e-52
Match length
                   103
% identity
                   61
                  (Z97338) PDR5-like ABC transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                   LIB3177-065-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q2559012
BLAST score
                   361
E value
                   1.0e-34
Match length
                   92
                   76
% identity
                   (AF026293) chaperonin containing t-complex polypeptide 1,
NCBI Description
                   beta subunit; CCT-beta [Homo sapiens] >gi 4090929
                   (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                   [Homo sapiens]
                  163645
Seq. No.
Seq. ID
                  LIB3177-065-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  618
E value
                  2.0e-64
Match length
                  116
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376 emb_CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  163646
                  LIB3177-065-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI ·
                  g3892714
BLAST score
                  611
E value
                  1.0e-63
Match length
                  130
% identity
                  94
                  (AL033545) trehalose-6-phosphate phosphatase-like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  163647
Seq. ID
                  LIB3177-065-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  g1769904
BLAST score
                  120
E value
                  3.0e-61
Match length
                  144
% identity
NCBI Description A.thaliana psbP gene
```

```
Seq. ID
                  LIB3177-065-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g1854386
BLAST score
                  362
E value
                  7.0e-35
Match length
                  88
% identity
                  77
NCBI Description
                  (AB001375) similar to soluble NSF attachment protein [Vitis
                  vinifera]
Seq. No.
                  163649
Seq. ID
                  LIB3177-066-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2851508
BLAST score
                  162
E value
                  1.0e-11
Match length
                  32
% identity
                  97
NCBI Description 60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
                  ribosomal protein L21 (gb L38826). ESTs
                  gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis
                  thaliana] >gi 3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
Seq. No.
                  ·163650
                  LIB3177-066-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454037
BLAST score
                  387
E value
                  4.0e-38
Match length
                  69
% identity
NCBI Description (AL035394) putative major latex protein [Arabidopsis
                  thaliana]
Seq. No.
                  163651
                  LIB3177-066-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2864617
BLAST score
                  428
E value
                  2.0e-42
Match length
                  124
% identity
                  73
NCBI Description (ALO21811) H+-transporting ATP synthase chain9 - like
                  protein [Arabidopsis thaliana]
Seq. No.
                  163652
Seq. ID
                  LIB3177-066-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q3763921
BLAST score
                  200
E value
                  1.0e-15
Match length
                  58
% identity
NCBI Description (AC004450) putative pirin protein [Arabidopsis thaliana]
Seq. No.
                  163653
```

```
Seq. ID
                    LIB3177-066-P1-K1-A5
 Method
                    BLASTX
 NCBI GI
                     g2398527
 BLAST score
                     177
 E value
                    2.0e-13
 Match length
                    36
 % identity
                    97
                   (Y13723) Transcription factor [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    163654
 Seq. ID
                    LIB3177-066-P1-K1-A6
 Method
                    BLASTX
 NCBI GI
                    q2072393
 BLAST score
                    215
 E value
                    7.0e-18
 Match length
                    51
 % identity
 NCBI Description
                    (U29168) similar to human Xeroderma pigmentosum group B DNA
                    repair protein, Swiss-Prot Accession Number P19447
                    [Arabidopsis thaliana]
 Seq. No.
                    163655
 Seq. ID
                    LIB3177-066-P1-K1-A8
 Method
                    BLASTX
 NCBI GI
                    q4263712
 BLAST score
                    335
 E value
                    2.0e-31
Match length
                    96
 % identity
                    73
 NCBI Description
                    (AC006223) putative ribosomal protein S12 [Arabidopsis
                    thaliana]
Seq. No.
                    163656
Seq. ID
                   LIB3177-066-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g136636
BLAST score
                    366
E'value
                    5.0e-35
Match length
                   70
% identity
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594_pdb_1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis Thaliana]
Seq. No.
                   163657
Seq. ID
                   LIB3177-066-P1-K1-B11
Method
                   BLASTN
NCBI GI
                   g4512690
BLAST score
                   239
E value
                   1.0e-132
Match length
```

```
% identity
                    100
 NCBI Description
                    Arabidopsis thaliana chromosome II BAC F11A3 genomic
                    sequence, complete sequence
 Seq. No.
                   . 163658
 Seq. ID
                    LIB3177-066-P1-K1-B12
 Method
                    BLASTX
 NCBI GI
                    g2062161
 BLAST score
                    463
 E value
                    3.0e-47
 Match length
                    102
 % identity
                    52
                    (AC001645) jasmonate inducible protein isolog [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    163659
 Seq. ID
                    LIB3177-066-P1-K1-B2
 Method
                    BLASTN
 NCBI GI
                    g2182287
 BLAST score
                    73
 E value
                    4.0e-33
 Match length
                   129
 % identity
                   89
 NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC T7N9,
                   complete sequence [Arabidopsis thaliana]
 Seq. No.
                   163660
 Seq. ID
                   LIB3177-066-P1-K1-B3
 Method
                   BLASTN
 NCBI GI
                   g2980757
 BLAST score
                   140
 E value
                   3.0e-73
Match length
                   152
 % identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
                   (ESSAII project)
Seq. No.
                   163661
                   LIB3177-066-P1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1402878
BLAST score
                   263
E value
                   3.0e-23
Match length
                   93
% identity
                   58
NCBI Description
                  (X98130) unknown [Arabidopsis thaliana]
Seq. No.
                   163662
Seq. ID
                  LIB3177-066-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  182
E value
                  8.0e-14
Match length
                  51
% identity
                  71
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
```

Seq. ID

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Seq. No.
                    163663
 Seq. ID
                    LIB3177-066-P1-K1-C12
 Method
                    BLASTN
 NCBI GI
                    g2335089
 BLAST score
                    102
 E value
                    3.0e-50
 Match length
                    126
 % identity
                    95
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC T11A7 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    163664
 Seq. ID
                   LIB3177-066-P1-K1-C2
 Method
                   BLASTN
 NCBI GI
                   q16473
 BLAST score
                   375
E value
                   0.0e+00
Match length
                   403
 % identity
                   98
NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer
Seq. No.
                   163665
Seq. ID
                   LIB3177-066-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q2499535
BLAST score
                   352
E value
                   9.0e-34
Match length
                   82
% identity
                   80
NCBI Description
                   2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi 595681
                   (U13238) 2-oxoglutarate/malate translocator [Spinacia
                   oleracea]
Seq. No.
                   163666
Seq. ID
                   LIB3177-066-P1-K1-C5
Method
                   BLASTN
NCBI GI
                   g2264316
BLAST score
                   86
E value
                   2.0e-40
Match length
                   427
% identity
                   39
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163667
Seq. ID
                  LIB3177-066-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g3540210
BLAST score
                  41
E value
                  2.0e-14
Match length
                  77
% identity
                  90
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F5A8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163668
```

LIB3177-066-P1-K1-C8

NCBI GI

```
Method
                      BLASTX
   NCBI GI
                      g4741940
   BLAST score
                      260
   E value
                      3.0e-23
   Match length
                      73
   % identity
                      67
   NCBI Description (AF134120) Lhca2 protein [Arabidopsis thaliana]
   Seq. No.
                     163669
   Seq. ID
                     LIB3177-066-P1-K1-C9
   Method
                     BLASTX
   NCBI GI
                     q1346520
   BLAST score
                     413
   E value
                     2.0e-40
   Match length
                     102
   % identity
                     79
   NCBI Description
                     S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
                     ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
                     >gi_790978_emb_CAA56590_ (X80362) S-adenosyl-L-methionine
                     synthetase [Brassica juncea]
   Seq. No.
                     163670
   Seq. ID
                     LIB3177-066-P1-K1-D1
   Method
                     BLASTN
   NCBI GI
                     g1167960
   BLAST score
                     37
   E value
                     3.0e-11
  Match length
                     343
   % identity
                     36
  NCBI Description Arabidopsis thaliana extensin (atExt1) gene, complete cds
  Seq. No.
                     163671
  Seq. ID
                     LIB3177-066-P1-K1-D12
  Method
                     BLASTX
. NCBI GI
                     g945039
  BLAST score
                     138
  E value
                     7.0e-09
  Match length
                    36
  % identity
                    72
  NCBI Description
                    (U25027) phosphatidylinositol-specific phospholipase C
                     [Glycine max]
  Seq. No.
                    163672
  Seq. ID
                    LIB3177-066-P1-K1-D2
  Method
                    BLASTX
  NCBI GI
                    g2062161
  BLAST score
                    319
  E value
                    2.0e-29
  Match length
                    61
  % identity
                    51
                    (ACO01645) jasmonate inducible protein isolog [Arabidopsis
  NCBI Description
                    thaliana]
  Seq. No.
                    163673
  Seq. ID
                    LIB3177-066-P1-K1-D3
  Method
                    BLASTX
```

E value

7.0e-30

```
BLAST score
                   348
E value
                   8.0e-33
Match length
                   71
% identity
                   48
NCBI Description
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   163674
Seq. ID
                   LIB3177-066-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q2497733
BLAST score
                   203
                   2.0e-16
E value
Match length
                   53
% identity
                   65
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
                   >gi 1177796 (M80567) non-specific lipid transfer protein
                   [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   163675
Seq. ID
                  LIB3177-066-P1-K1-D5
Method
                  BLASTX
NCBI GI
                   q841208
BLAST score
                   309
E value
                   3.0e-28
Match length
                   128
% identity
                   55
                  (U18995) trypsin inhibitor propeptide [Brassica oleracea]
NCBI Description
Seq. No.
                  163676
Seq. ID
                  LIB3177-066-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g2642427
BLAST score
                  58
                  8.0e-24
E value
Match length
                  94
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20D16 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  163677
Seq. No.
Seq. ID
                  LIB3177-066-P1-K1-D8
Method
                  BLASTN
                  g17681
NCBI GI
BLAST score
                  52
E value
                  3.0e-20
Match length
                  208
                  88
% identity
NCBI Description A.thaliana mRNA for Wilm's tumor suppressor homologue
Seq. No.
                  163678
Seq. ID
                  LIB3177-066-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q4510373
BLAST score
                  323
```

```
Match length
                     126
 % identity
                     56
                     (AC007017) putative harpin-induced protein [Arabidopsis
 NCBI Description
                     thaliana]
 Seq. No.
                     163679
 Seq. ID
                     LIB3177-066-P1-K1-E1
 Method
                     BLASTX
 NCBI GI
                     g2369714
 BLAST score
                     237
 E value
                     2.0e-20
 Match length
                     51
 % identity
                     96
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
 Seq. No.
                     163680
Seq. ID
                     LIB3177-066-P1-K1-E10
Method
                     BLASTX
NCBI GI
                     g1169278
BLAST score
                     178
E value
                     2.0e-13
Match length
                     44
% identity
                     86
NCBI Description
                    DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14
                     protein [Arabidopsis thaliana]
Seq. No.
                     163681
Seq. ID
                     LIB3177-066-P1-K1-E11
Method
                    BLASTX
NCBI GI
                    g131398
BLAST score
                     337
E value
                    7.0e-32
Match length
                    70
% identity
                     99
NCBI Description
                    PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                    >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                    photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                    >gi_3152571 (AC002986) Match to photosystem II 10kDa
                    polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                    come from this gene. [Arabidopsis
Seq. No.
                    163682
Seq. ID
                    LIB3177-066-P1-K1-E2
Method
                    BLASTX
NCBI GI
                    g2924779
BLAST score
                    626
E value
                    2.0e-65
Match length
                    149
% identity
NCBI Description
                    (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
                    thaliana] >gi_2981616_dbj_BAA25248 (AB008854)
                    3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                    >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA
```

thiolase [Arabidopsis thaliana]

NCBI GI

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Seq. No.
                   163683
Seq. ID
                   LIB3177-066-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g2791423
BLAST score
                   192
E value
                   1.0e-14
Match length
                   69
% identity
                   54
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
Seq. No.
                   163684
Seq. ID
                   LIB3177-066-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g2129636
BLAST score
                   724
E value
                   6.0e-77
Match length
                   153
% identity
                   91
NCBI Description lipase - Arabidopsis thaliana >gi 1145627 (U38916) lipase
                   [Arabidopsis thaliana]
Seq. No.
                  163685
Seq. ID
                  LIB3177-066-P1-K1-E5
                  BLASTX
Method
                 . g2129636
NCBI GI
BLAST score
                  278
E value
                  1.0e-24
Match length
                  86
% identity
                  65
NCBI Description
                  lipase - Arabidopsis thaliana >gi 1145627 (U38916) lipase
                  [Arabidopsis thaliana]
Seq. No.
                  163686
                  LIB3177-066-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462077
BLAST score
                  397
E value
                  7.0e-39
Match length
                  82
% identity
                  95
                 (Y11871) Oxal protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  163687
Seq. ID
                  LIB3177-066-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2791423
BLAST score
                  207
E value
                  3.0e-16
Match length
                  71
% identity
                  55
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
Seq. No.
                  163688
Seq. ID
                  LIB3177-066-P1-K1-E9
Method
                  BLASTX
```

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```
BLAST score
                   609
 E value
                   2.0e-63
 Match length
                   131
 % identity
 NCBI Description
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
                   region [Arabidopsis thaliana]
 Seq. No.
                   163689
 Seq. ID
                   LIB3177-066-P1-K1-F1
Method
                   BLASTX
 NCBI GI
                   q4469408
 BLAST score
                   260
E value
                   1.0e-22
Match length
                   63
 % identity
                   81
NCBI Description
                   (AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis
                   thaliana] >gi_4469410_gb_AAD21249_ (AF116528) MADS box
                   protein FLOWERING LOCUS F [Arabidopsis thaliana]
Seq. No.
                   163690
Seq. ID
                   LIB3177-066-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q1066163
BLAST score
                   244
E value
                   1.0e-20
Match length
                   48
% identity
                   98
NCBI Description
                   (X93015) glyoxysomal beta-ketoacyl-thiolase [Brassica
                   napus]
Seq. No.
                   163691
                   LIB3177-066-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q731284
BLAST score
                   198
                   3.0e-15
E value
Match length
                   126
% identity
                   37
NCBI Description
                  HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION
                  >gi_1077482_pir_ S51971 probable membrane protein YAL048c -
                  yeast (Saccharomyces cerevisiae) >gi_595536 (U12980)
                  Yal048cp [Saccharomyces cerevisiae]
Seq. No.
                  163692
Seq. ID
                  LIB3177-066-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  g16470
BLAST score
                  171
E value
                  2.0e-91
Match length
                  187
% identity
                  98
NCBI Description
                  Arabidopsis thaliana mRNA for rubisco activase
Seq. No.
                  163693
Seq. ID
                  LIB3177-066-P1-K1-F3
Method
                  BLASTX
NCBI GI
```

q135391

```
BLAST score
                   447
E value
                   1.0e-44
Match length
                   83
% identity
                   100
NCBI Description
                   TUBULIN ALPHA-1 CHAIN >gi_71583_pir__UBMUAM tubulin alpha-1
                   chain - Arabidopsis thaliana >gi_166896 (M21414)
                   alpha-1-tubulin [Arabidopsis thaliana]
Seq. No.
                   163694
Seq. ID
                   LIB3177-066-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q2160166
BLAST score
                   372
                   6.0e-36
E value
Match length
                   101
% identity
                   70
NCBI Description
                   (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                   163695
Seq. ID
                   LIB3177-066-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   g399013
BLAST score
                   593
E value
                   1.0e-61
Match length
                   120
% identity
                   98
NCBI Description
                   ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                   >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)
                   adenylate translocator [Arabidopsis thaliana]
                   >gi_445607_prf 1909354A adenylate translocator
                   [Arabidopsis thaliana]
                   163696
Seq. No.
Seq. ID
                   LIB3177-066-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   q2764941
BLAST score
                   600
E value
                   2.0e-62
                   105
Match length
% identity
                   100
NCBI Description
                   (X98255) transcriptionally stimulated by gibberellins;
                   expressed in meristematic region, and style [Arabidopsis
                   thaliana]
                   163697
Seq. No.
Seq. ID
                   LIB3177-066-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   q2088654
BLAST score
                   484
E value
                   6.0e-49
Match length
                   114
% identity
                   86
NCBI Description
                   (AF002109) 60S acidic ribosomal protein PO isolog
```

[Arabidopsis thaliana]

```
Seq. No.
                   163698
Seq. ID
                   LIB3177-066-P1-K1-F9
Method
                   BLASTN
NCBI GI
                   g1946354
BLAST score
                   163
E value
                   8.0e-87
Match length
                   221
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
                   sequence, complete sequence
Seq. No.
                   163699
Seq. ID
                  LIB3177-066-P1-K1-G11
Method
                  BLASTX
NCBI GI
                   q3193292
BLAST score
                  355
E value
                  6.0e-34
Match length
                  80
% identity
                  88
                  (AF069298) similar to ATPases associated with various
NCBI Description
                  cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
Seq. No.
                  163700
Seq. ID
                  LIB3177-066-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3335371
BLAST score
                  449
E value
                  5.0e-45
Match length
                  96
% identity
                  91
NCBI Description
                  (AC003028) putative ethylene-inducible protein [Arabidopsis
                  thaliana]
Seq. No.
                  163701
Seq. ID
                  LIB3177-066-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g4586249
BLAST score
                  328
E value
                  2.0e-30
Match length
                  140
% identity
NCBI Description
                  (AL049640) putative pollen surface protein [Arabidopsis
                  thaliana]
Seq. No.
                  163702
Seq. ID
                  LIB3177-066-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g131398
BLAST score
                  311
E value
                  2.0e-28 ·
Match length
                  89
% identity
                  71
NCBI Description
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi 72714_pir__F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi_16447 emb_CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
```

```
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                    come from this gene. [Arabidopsis
Seq. No.
                    163703
Seq. ID
                    LIB3177-066-P1-K1-G6
Method
                    BLASTN
NCBI GI
                    g1167960
BLAST score
                    42
E value
                    3.0e-14
Match length
                    244
% identity
                    30
NCBI Description Arabidopsis thaliana extensin (atExt1) gene, complete cds
Seq. No.
                    163704
Seq. ID
                    LIB3177-066-P1-K1-G7
Method
                    BLASTX
NCBI GI
                    g2244798
BLAST score
                    324
E value
                    4.0e-30
Match length
                    62
                   100
% identity
NCBI Description (297336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    163705
Seq. ID
                    LIB3177-066-P1-K1-G8
Method
                    BLASTX
NCBI GI
                    g1769905
BLAST score
                    455
E value
                    2.0e-45
Match length
                    129
% identity
                    69
NCBI Description
                    (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                    [Arabidopsis thaliana]
Seq. No.
                    163706
Seq. ID
                    LIB3177-066-P1-K1-G9
Method
                    BLASTX
NCBI GI
                    g4741960
BLAST score
                    155
E value
                    1.0e-46
                    139
Match length
                    74
% identity
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                    163707
                    LIB3177-066-P1-K1-H10
Seq. ID
Method
                    BLASTN
NCBI GI
                    g3413696
BLAST score
                    297
E value
                    1.0e-166
                    305
Match length
                    99
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T19L18 genomic
```

>gi_3152571 (AC002986) Match to photosystem II 10kDa

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   163708
Seq. ID
                  LIB3177-066-P1-K1-H2
Method
                  BLASTX
NCBI GI
                   g282865
BLAST score
                   323
E value
                  3.0e-30
Match length
                  71
% identity
                  85
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  163709
Seq. ID
                  LIB3177-066-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g1170373
BLAST score
                  668
E value
                  3.0e-70
Match length
                  130
% identity
                  98
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
                  >gi_397482_emb_CAA52684 (X74604) heat shock protein 70
                  cognate [Arabidopsis thaliana]
Seq. No.
                  163710
Seq. ID
                  LIB3177-066-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g2062153
BLAST score
                  102
E value
                  3.0e-50
Match length
                  110
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163711
Seq. ID
                  LIB3177-066-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g4006885
BLAST score
                  58
E value
                  3.0e-24
Match length
                  58
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  163712
Seq. ID
                  LIB3177-066-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  g469113
BLAST score
                  345
E value
                  0.0e + 00
```

```
Match length
                   357
% identity
                   99
NCBI Description A.thaliana (Columbia) Dr4 mRNA
Seq. No.
                   163713
Seq. ID
                   LIB3177-066-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g4510402
BLAST score
                   80
E value
                   1.2e-01
Match length
                   109
% identity
                   45
NCBI Description
                  (AC006587) putative AP2 domain [Arabidopsis thaliana]
Seq. No.
                   163714
                   LIB3177-066-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1702987
BLAST score
                   529
E value
                   4.0e-54
Match length
                   107
% identity
                   100
NCBI Description
                   14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14
                   protein phi chain [Arabidopsis thaliana] >gi 2232146
                   (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis
                   thaliana]
Seq. No.
                   163715
                   LIB3177-066-P1-K1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4559375
BLAST score
                   151
E value
                   2.0e-79
Match length
                   245
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F11C10 genomic
                   sequence, complete sequence
                   163716
Seq. No.
Seq. ID
                   LIB3177-067-P1-K1-A10
Method
                   BLASTN
NCBI GI
                   g469113
BLAST score
                   393
E value
                   0.0e + 00
Match length
                   424
% identity
                   99
NCBI Description A.thaliana (Columbia) Dr4 mRNA
Seq. No.
                  163717
Seq. ID
                  LIB3177-067-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g2832683
BLAST score
                  332
E value
                  6.0e-31
Match length
                  65
                  100
% identity
NCBI Description
                  (AL021712) putative protein [Arabidopsis thaliana]
```

Seq. No.

```
Seq. No.
                   163718
Seq. ID
                   LIB3177-067-P1-K1-A2
Method
                   BLASTN
NCBI GI
                   g4589950
BLAST score
                   210
E value
                   1.0e-114
Match length
                   393
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T28P16 genomic
                   sequence, complete sequence
Seq. No.
                   163719
Seq. ID
                   LIB3177-067-P1-K1-A3
Method
                  BLASTN
NCBI GI
                   g4199934
BLAST score
                   196
E value
                   1.0e-106
Match length
                   216
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  163720
Seq. ID
                  LIB3177-067-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4522012
BLAST score
                  302
E value
                  2.0e-27
                  90
Match length
% identity
                  61
NCBI Description
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
                  163721
Seq. No.
                  LIB3177-067-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q886116
BLAST score
                  651
E value
                  2.0e-68
                  125
Match length
                  98
% identity
NCBI Description
                   (U27609) TCH4 protein [Arabidopsis thaliana] >gi 2952473
                   (AF051338) xyloglucan endotransglycosylase related protein
                  [Arabidopsis thaliana]
                  163722
Seq. No.
Seq. ID
                  LIB3177-067-P1-K1-A7
                  BLASTN
Method
NCBI GI
                  g16363
BLAST score
                  40
E value
                  3.0e-13
Match length
                  103
% identity
                  87
NCBI Description
                  A.thaliana Lhb1B2 gene for photosystem II chlorophyll a/b
                  binding protein
```

Method

BLASTN

```
Seq. ID
                    LIB3177-067-P1-K1-A8
Method
                    BLASTX
NCBI GI
                    g2493810
BLAST score
                    237
E value
                    4.0e-20
Match length
                    43
% identity
                    98
NCBI Description
                    COPROPORPHYRINOGEN III OXIDASE PRECURSOR
                    (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE)
                    >gi_1213067_emb_CAA58038_ (X82831) coproporphyrinogen
                    oxidase [Nicotiana tabacum]
Seq. No.
                    163724
Seq. ID
                    LIB3177-067-P1-K1-B1
Method
                    BLASTX
NCBI GI
                    g3287862
BLAST score
                    339
E value
                    5.0e-32
Match length
                    63
% identity
                    95
NCBI Description
                    PUTATIVE TRYPSIN INHIBITOR T01024.27 PRECURSOR >gi 2289007
                    (AC002335) trypsin inhibitor 2 precursor isolog
                    [Arabidopsis thaliana]
Seq. No.
                    163725
Seq. ID
                    LIB3177-067-P1-K1-B10
Method
                    BLASTN
NCBI GI
                    g4580744
BLAST score
                    133
E value
                    4.0e-69
Match length
                    137
% identity
                    56
NCBI Description
                    Sequence of BAC F15I1 from Arabidopsis thaliana chromosome
                    1, complete sequence
Seq. No.
                    163726
Seq. ID
                    LIB3177-067-P1-K1-B11
Method
                    BLASTX
NCBI GI
                    g549010
BLAST score
                    701
E value
                    3.0e-74
Match length
                    137
% identity
                    100
NCBI Description
                   EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)
                    (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)
                    >gi_322554 pir S31328 omnipotent suppressor protein SUP1
                   homolog (clone G18) - Arabidopsis thaliana
                   >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic
                   early release factor subunit 1-like protein [Arabidopsis
                   thaliana] >gi 1495249 emb CAA66118 (X97486) eRF1-3
                    [Arabidopsis thaliana]
                            41.
Seq. No.
                   163727
Seq. ID
                   LIB3177-067-P1-K1-B12
```

```
NCBI GI
                    q4406805
BLAST score
                    281
E value
                    1.0e-157
Match length
                    429
% identity
                    99
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T27K22 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    163728
Seq. ID
                    LIB3177-067-P1-K1-B2
Method
                    BLASTN
NCBI GI
                    q4199934
BLAST score
                    91
E value
                    4.0e-44
Match length
                    103
% identity
                    74
                    Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                    complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                    LIB3177-067-P1-K1-B4
Method
                    BLASTX
NCBI GI
                    q132110
BLAST score
                    356
E value
                    4.0e-34
Match length
                    76
% identity
                    93
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana)
                    163730
Seq. No.
Seq. ID
                    LIB3177-067-P1-K1-B5
Method
                    BLASTN
NCBI GI
                    q4544381
                    75
BLAST score
                    5.0e-34
E value
Match length
                    79
% identity
                    99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F16F14 genomic
                    sequence, complete sequence
Seq. No.
                    163731
Seq. ID
                  - LIB3177-067-P1-K1-B6
Method
                    BLASTX
NCBI GI
                    g4337175
BLAST score
                    520
                    5.0e-53
E value
Match length
                    131
% identity
                    79
                    (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
```

```
Seq. No.
                    163732
                   LIB3177-067-P1-K1-B8
Seq. ID
Method
                    BLASTX
NCBI GI
                   q1778141
BLAST score
                    528
                                               ٠:٠
E value
                    5.0e-54
Match length
                    138
% identity
                    78
NCBI Description
                   (U66321) phosphate/phosphoenolpyruvate translocator
                   precursor; PPT [Arabidopsis thaliana]
Seq. No.
                    163733
Seq. ID
                   LIB3177-067-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g1170089
BLAST score
                    307
E value
                   1.0e-28
Match length
                    63
% identity
NCBI Description
                   GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
                   >gi_481822_pir__S39542 probable glutathione transferase (EC
                   2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase
                    [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                   S-transferase [Arabidopsis thaliana]
Seq. No.
                   163734
Seq. ID
                   LIB3177-067-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g4741960
BLAST score
                   620
E value
                   1.0e-64
Match length
                   140
% identity
                   85
                   (AF134130) Lhcb6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   163735
Seq. ID
                   LIB3177-067-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g2435406
BLAST score
                   183
E value
                   7.0e-14
Match length
                   49
% identity
                   65
NCBI Description
                   (U83490) thaumatin-like protein [Arabidopsis thaliana]
Seq. No.
                   163736
                   LIB3177-067-P1-K1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4455348
BLAST score
                   140
E value
                   5.0e-73
Match length
                   263
                   98
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8
```

(ESSAII project)

```
Seq. No.
                   163737
Seq. ID
                   LIB3177-067-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3355480
BLAST score
                   242
E value
                   2.0e-20
Match length
                   79
% identity
                   56
NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis
Seq. No.
                   163738
Seq. ID
                   LIB3177-067-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   q2618720
BLAST score
                   132
E value
                   3.0e-68
Match length
                   172
% identity
NCBI Description Arabidopsis thaliana early auxin-induced (IAA16) mRNA,
                   complete cds
Seq. No.
                   163739
Seq. ID
                   LIB3177-067-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   q4056503
BLAST score
                   169
E value
                   3.0e-12
Match length
                   36
% identity
                   92
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                   163740
Seq. ID
                   LIB3177-067-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g1621268
BLAST score
                   373
E value
                   5.0e-36
Match length
                   107
% identity
                   68
NCBI Description (Z81012) unknown [Ricinus communis]
Seq. No.
                  163741
Seq. ID
                  LIB3177-067-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g113026
BLAST score
                   614
E value
                  5.0e-64
Match length
                  132
                  89
% identity
NCBI Description
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                  >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
                  S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
                  napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
                  isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A
```

isocitrate lyase [Brassica napus]

```
Seq. No.
                   163742
Seq. ID
                   LIB3177-067-P1-K1-C9
Method
                   BLASTN
NCBI GI 4
                   g2264318
BLAST score
                   138
E value
                   8.0e-72
Match length
                   226
% identity
                   92
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163743
Seq. ID
                   LIB3177-067-P1-K1-D1
Method
                   BLASTN
NCBI GI
                   g3201608
BLAST score
                   130
E value
                   4.0e-67
Match length
                   157
% identity
                   96
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163744
Seq. ID
                  LIB3177-067-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g4567268
BLAST score
                  261
                 4.0e-23
E value
Match length
                   60
% identity
                   93
NCBI Description
                   (AC006841) putative fructose biphosphate aldolase
                   [Arabidopsis thaliana]
Seq. No.
                  163745
Seq. ID
                  LIB3177-067-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  g3522932
BLAST score
                  165
E value
                  8.0e-88
Match length
                  277
% identity
                  97
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163746
Seq. ID
                  LIB3177-067-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1732570
                  137
BLAST score
                  5.0e-09
E value
                  59
Match length
% identity
NCBI Description
                  (U72153) beta-glucosidase [Arabidopsis thaliana]
                  163747
Seq. No.
```

NCBI GI

```
Seq. ID
                   LIB3177-067-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   q4309683
BLAST score
                   98
E value
                   4.0e-48
Match length
                   154
% identity
                   92
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   163748
Seq. ID
                   LIB3177-067-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   q3883125
BLAST score
                   297
E value
                   1.0e-166
Match length
                   388
% identity
                   95
NCBI Description
                  Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA,
                   complete cds
Seq. No.
                   163749
Seq. ID
                  LIB3177-067-P1-K1-D8
Method
                  BLASTN
NCBI GI
                   q3929648
BLAST score
                  177
E value
                  4.0e-95
Match length
                  205
% identity
                  97
                  Arabidopsis thaliana mRNA for mitochondrial NAD-dependent
NCBI Description
                  malate dehydrogenase
Seq. No.
                  163750
Seq. ID
                  LIB3177-067-P1-K1-E1
Method
                  BLASTN
NCBI GI
                  q3299824
BLAST score
                  43
                  7.0e-16
E value
Match length
                  61
                  92
% identity
NCBI Description
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
                  near 17 cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163751
Seq. ID
                  LIB3177-067-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  g16470
BLAST score
                  98
E value
                  3.0e-48
Match length
                  118
% identity
                  96
NCBI Description Arabidopsis thaliana mRNA for rubisco activase
Seq. No.
                  163752
Seq. ID
                  LIB3177-067-P1-K1-E12
Method
                  BLASTN
```

```
BLAST score
                  163
E value
                  8.0e-87
Match length
                  187
% identity
                  97
NCBI Description
                  Arabidopsis thaliana gibberellin-regulated (GASA4) mRNA,
                  complete cds
Seq. No.
                  163753
Seq. ID
                  LIB3177-067-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  650
                  3.0e-68
E value
                  127
Match length
                  98
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  163754
Seq. No.
Seq. ID '
                  LIB3177-067-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  g47594
BLAST score
                  85
E value
                  4.0e-40
Match length
                  161
                  91
% identity
NCBI Description
                  Synechocystis sp. ndhE gene (partial), psaC gene for
                  photosystem I iron-sulfur protein and ndhD-like ORF
Seq. No.
                  163755
Seq. ID
                  LIB3177-067-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q3283056
BLAST score
                  48
                  3.0e-18
E value
Match length
                  127
% identity
NCBI Description
                  Arabidopsis thaliana one helix protein (OHP) mRNA, complete
                  cds
Seq. No.
                  163756
Seq. ID
                  LIB3177-067-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  393
                  2.0e-38
E value
                  79
Match length
                  96
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
```

B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702

Method

NCBI GI

BLASTX

```
(X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana]
Seq. No.
                    163757
Seq. ID
                    LIB3177-067-P1-K1-E8
Method
                    BLASTX
NCBI GI
                    g115783
BLAST score
                    601
E value
                    1.0e-62
Match length
                    114
% identity
                    99
NCBI Description
                    CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                    chlorophyll a/b binding protein (LHCP \overline{AB} 140) [Arabidopsis
                    thaliana]
                    163758
Seq. No.
Seq. ID
                    LIB3177-067-P1-K1-E9
Method
                    BLASTN
NCBI GI
                    g343376
BLAST score
                    32
E value
                    9.0e-09
Match length
                    59
% identity
                    90
NCBI Description
                    Spinach rps4 gene encoding ribosomal protein S4, complete
                    cds, with Thr-tRNA and Ser-tRNA genes
Seq. No.
                    163759
Seq. ID
                    LIB3177-067-P1-K1-F1
Method
                    BLASTX
NCBI GI
                    g1170089
BLAST score
                    260
E value
                    3.0e-23
Match length
                    64
% identity
                    86
NCBI Description
                   GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
                    >gi_481822_pir__S39542 probable glutathione transferase (EC
                   2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                    S-transferase [Arabidopsis thaliana]
Seq. No.
                    163760
Seq. ID
                    LIB3177-067-P1-K1-F11
Method
                    BLASTX
NCBI GI
                    g4454470
BLAST score
                    344
E value
                    1.0e-32
Match length
                    109
% identity
NCBI Description
                    (AC006234) putative sugar transporter [Arabidopsis
                   thaliana]
Seq. No.
                   163761
Seq. ID
                   LIB3177-067-P1-K1-F12
```

```
BLAST score
                   365
E value
                   6.0e-35
Match length
                   118
% identity
                   64
NCBI Description
                  NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
                   (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__$52286 NADH
                   dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
                   >gi_643090_emb_CAA58887.1 (X84078) NADH dehydrogenase
                   [Arabidopsis thaliana]
Seq. No.
                   163762
Seq. ID
                   LIB3177-067-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q4454479
BLAST score
                   356
E value
                   7.0e-34
Match length
                   74
% identity
                   97
NCBI Description
                   (AC006234) putative riboflavin synthase alpha chain
                   [Arabidopsis thaliana]
Seq. No.
                  163763
Seq. ID
                  LIB3177-067-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1175013
BLAST score
                  221
E value
                  1.0e-18
Match length
                  42
% identity
                  98
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084
NCBI Description
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
Seq. No.
                  163764
Seq. ID
                  LIB3177-067-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3157937
BLAST score
                  259
E value
                  1.0e-22
Match length
                  60
% identity
                  82
NCBI Description
                  (AC002131) Identical to aspartic proteinase cDNA gb U51036
                  from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,
                  gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269,
                  gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
                  gb_AA728734, gb
Seq. No.
                  163765
Seq. ID
                  LIB3177-067-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2493052
BLAST score
                  373
E value
                  5.0e-36
Match length
                  70
% identity
                  100
```

NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL

```
mitochondrial F1-ATPase [Arabidopsis thaliana]
Seq. No.
                   163766
Seq. ID
                   LIB3177-067-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q4538903
BLAST score
                   139
E value
                   9.0e-09
Match length
                   72
% identity
                   43
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
                   163767
Seq. No.
Seq. ID
                   LIB3177-067-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q3695383
BLAST score
                   250
E value
                   1.0e-21
Match length
                   61
                   82
% identity
NCBI Description
                   (AF096370) similar to inorganic pyrophosphatase (Pfam:
                   PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis
                   thalianal
Seq. No.
                   163768
Seq. ID
                   LIB3177-067-P1-K1-G2
Method
                  BLASTX
NCBI GI
                   g2911042
BLAST score
                   357
E value
                   2.0e-34
Match length
                   72
% identity
                   100
NCBI Description
                   (AL021961) Phosphoglycerate dehydrogenase - like protein
                   [Arabidopsis thaliana]
                   163769
Seq. No.
Seq. ID
                  LIB3177-067-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q4490732
BLAST score
                  567
E value
                  1.0e-58
Match length
                  120
% identity
                  88
                  (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                  protein [Arabidopsis thaliana]
                  163770
Seq. No.
Seq. ID
                  LIB3177-067-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q2815905
BLAST score
                  290
                  4.0e-26
E value
Match length
                  98
% identity
                  58
NCBI Description
                  (AF043734) Pros45 proteosome subunit homolog [Drosophila
```

>gi_1655486_dbj BAA13602 (D88377) epsilon subunit of

melanogaster]

NCBI GI

g115767

```
Seq. No.
                   163771
Seq. ID
                   LIB3177-067-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g2851508
BLAST score
                   49
E value
                   2.0e-32
Match length
                   70
% identity
                   100
                   60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to
NCBI Description
                   ribosomal protein L21 (gb_L38\overline{8}26). ESTs
                   gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis
                   thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                   L21 [Arabidopsis thaliana]
Seq. No.
                   163772
Seq. ID
                   LIB3177-067-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   g3063438
BLAST score
                   82
E value
                   3.0e-38
Match length
                   160
% identity
                   88
                   Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   163773
Seq. ID
                   LIB3177-067-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g132102
BLAST score
                   414
E value
                   7.0e-41
Match length
                   88
% identity
                   94
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  163774
                  LIB3177-067-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129640
BLAST score
                  389
E value
                  4.0e-38
Match length
                  84
                  88
% identity
NCBI Description
                  magnesium chelatase chain - Arabidopsis thaliana
                  >gi_1154627 emb CAA92802 (Z68495) magnesium chelatase
                  subunit [Arabidopsis thaliana]
Seq. No.
                  163775
                  LIB3177-067-P1-K1-H10
Seq. ID
Method
                  BLASTX
```

Seq. No.

```
BLAST score
                   624
E value
                   2.0e-66
Match length
                   132
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyl·l
                   a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  163776
Seq. ID
                  LIB3177-067-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1732570
BLAST score
                  277
E value
                  3.0e-25
Match length
                  73
% identity
                  77
NCBI Description
                  (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                  163777
Seq. ID
                  LIB3177-067-P1-K1-H12
Method .
                  BLASTX
NCBI GI
                  g115385
BLAST score
                  687
E value
                  1.0e-72
Match length
                  131
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  163778
Seq. ID
                  LIB3177-067-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  q3212846
BLAST score
                  200
E value
                  1.0e-109
Match length
                  244
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163779
                  LIB3177-067-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4056476
BLAST score
                  113
E value
                  7.0e-57
Match length
                  194
% identity
                  95
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3G5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

```
Seq. ID
                   LIB3177-067-P1-K1-H5
Method
                   BLASTX
 NCBI GI
                   g2119848
 BLAST score
                   513
 E value
                   2.0e-52
Match length
                   95
 % identity
                   100
NCBI Description
                   chlorophyll a/b-binding protein type I precursor Lhb1B1 -
                   Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128229 (AC004077) putative
                   photosystem II type I chlorophyll a/b binding protein
                   [Arabidopsis thaliana] >gi_3337372 (AC004481) putative
                   photosystem II type I chlorophyll a/b binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   163781
Seq. ID
                  LIB3177-067-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g421836
BLAST score
                  142
                  2.0e-09
E value
Match length
                  30
                  97
% identity
                  G-box-binding factor GF14 - Arabidopsis thaliana >gi 553040
NCBI Description
                   (M96855) GF14 [Arabidopsis thaliana]
Seq. No.
                  163782
Seq. ID
                  LIB3177-067-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g3172156
BLAST score
                  189
                  1.0e-102
E value
Match length
                  336
                  98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  163783
Seq. ID
                  LIB3177-067-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g131381
BLAST score
                  597
E value
                  3.0e-62
Match length
                  117
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852
                  photosystem II oxygen-evolving complex protein 1 precursor
                  - Arabidopsis thaliana >gi_22571 emb_CAA36675 (X52428) 33
                  kDa oxygen-evolving protein [Arabidopsis thaliana]
Seq. No.
                  163784
Seq. ID
                  LIB3177-068-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3157944
```

% identity

```
BLAST score
                   561
                   8.0e-58
E value
                   109
Match length
% identity
                   98
NCBI Description
                   (AC002131) Very strong similarity to aminomethyltransferase
                   precursor gb U79769 from Mesembryanthemum crystallinum.
                   ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773,
                   gb_N38038, gb_T13742, gb Z26545, gb T20753 and gb W43123
                   come from this ge
                   163785
Seq. No.
Seq. ID
                   LIB3177-068-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g118514
BLAST score
                   179
E value
                   2.0e-25
Match length
                   88
                   65
% identity
NCBI Description
                   TURGOR-RESPONSIVE PROTEIN 26G >gi 100051 pir S11863
                   aldehyde dehydrogenase homolog - garden pea
                   >gi_20681_emb_CAA38243_ (X54359) 508 aa peptide [Pisum
                   sativum]
Seq. No.
                   163786
Seq. ID
                   LIB3177-068-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   g3421079
BLAST score
                   353
                   0.0e+00
E value
Match length
                   357
% identity
                   100
NCBI Description Arabidopsis thaliana 20S proteasome subunit PAD1 (PAD1)
                   mRNA, complete cds
Seq. No.
                   163787
Seq. ID
                   LIB3177-068-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   582
E value
                   2.0e-60
Match length
                   116
% identity
                   96
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   163788
Seq. ID
                  LIB3177-068-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   g2244829
BLAST score
                   228
E value
                   1.0e-125
Match length
                   404
```

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   163789
Seq. ID
                   LIB3177-068-P1-K1-A4
Method
                   BLASTN
NCBI GI
                   q4756963
BLAST score
                   372
E value
                   0.0e + 00
Match length
                   439
% identity
                   95
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                   163790
Seq. ID
                   LIB3177-068-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g1168201
BLAST score
                   502
E value
                   5.0e-51
Match length
                   116
% identity
                   89
                  14-3-3-LIKE PROTEIN RCI2 >gi_1076394_pir__S47970 RCI1B
NCBI Description
                  protein - Arabidopsis thaliana >gi_531379_emb_CAA52238_
                   (X74141) RCI1B [Arabidopsis thaliana]
Seq. No.
                  163791
Seq. ID
                  LIB3177-068-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g1732570
BLAST score
                  164
E value
                  1.0e-23
Match length
                  57
% identity
                  90
NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                  163792
Seq. ID
                  LIB3177-068-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2262167
BLAST score
                  435
E value
                  3.0e-43
Match length
                  94
% identity
                  (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  163793
Seq. ID
                  LIB3177-068-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  g2244829
BLAST score
                  40
E value
                  3.0e-13
Match length
                  40
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
```

E value

```
Seq. No.
                   163794
 Seq. ID
                   LIB3177-068-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q131398
BLAST score
                   554
                   5.0e-57
E value
Match length
                   140
% identity
                   81
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb CAA39441 (X55970)
                   photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                   >gi_3152571 (AC002986) Match to photosystem II 10kDa
                   polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                   gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb T45400
                   come from this gene. [Arabidopsis
Seq. No.
                   163795
Seq. ID
                   LIB3177-068-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q2062161
BLAST score
                   588
E value
                   4.0e-61
Match length
                   128
% identity
                   53
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   163796
Seq. ID
                  LIB3177-068-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  q438448
BLAST score
                  34
E value
                  4.0e-10
Match length
                  38
                  97
% identity
NCBI Description
                  Arabidopsis thaliana carbonic anhydrase (cal80) mRNA,
                  complete cds
Seq. No.
                  163797
Seq. ID
                  LIB3177-068-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g4741940
BLAST score
                  536
E value
                  6.0e-55
Match length
                  118
% identity
                  60
NCBI Description
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.
                  163798
Seq. ID
                  LIB3177-068-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2760169
BLAST score
                  186
```

1.0e-100

```
Match length
                   350
% identity
                   98
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFB13, complete sequence [Arabidopsis thaliana]
Seq. No.
              ... 163799
Seq. ID
                   LIB3177-068-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g4585882
BLAST score
                   105
E value
                   9.0e-62
Match length
                   127
% identity
                   97
NCBI Description
                   (AC005850) PSI type III chlorophyll a/b-binding protein
                  [Arabidopsis thaliana]
Seq. No.
                   163800
Seq. ID
                   LIB3177-068-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g4454037
BLAST score
                   694
E value
                   2.0e-73
Match length
                   136
% identity
                   94
NCBI Description
                   (AL035394) putative major latex protein [Arabidopsis
                   thaliana)
Seq. No.
                   163801
Seq. ID
                  LIB3177-068-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q1628478
BLAST score
                   463
E value
                  3.0e-46
Match length
                  102
% identity
                  91
                  (X98536) variant histone H2A.Z12 [Xenopus laevis]
NCBI Description
                  >gi 1685280 (U77893) histone H2A.Z variant [Xenopus laevis]
                  >gi_1695198_emb_CAA67148_ (X98535) variant histone H2A.Zl1
                   [Xenopus laevis]
Seq. No.
                  163802
Seq. ID
                  LIB3177-068-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  g3985954
BLAST score
                  95
E value
                  3.0e-46
Match length
                  171
% identity
                  45
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRG21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163803
Seq. ID
                  LIB3177-068-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2129670
BLAST score
                  140
E value
                  2.0e-64
```

```
Match length
                   128
% identity
                   95
                   phosphoinositide-specific phospholipase C - Arabidopsis
NCBI Description
                   thaliana >gi_857374_dbj_BAA09432 (D50804) phosphoinositide
                   specific phospholipase C [Arabidopsis thaliana]
Seq. No.
                   163804
Seq. ID
                   LIB3177-068-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2828267
BLAST score
                   331
E value
                   5.0e-31
Match length
                   92
% identity
                   75
                  (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   163805
Seq. ID
                   LIB3177-068-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g2829868
BLAST score
                   130
E value
                   2.0e-46
Match length
                   117
% identity
                   88
NCBI Description
                   (AC002396) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   163806
Seq. ID
                   LIB3177-068-P1-K1-C10
Method
                  BLASTN
NCBI GI
                   g2618604
BLAST score
                   143
E value
                   1.0e-74
Match length
                   155
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163807
Seq. ID
                  LIB3177-068-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3859536
BLAST score
                  581
E value
                  2.0e-60
Match length
                  112
% identity
                  99
NCBI Description
                  (AF095453) asparagine synthetase [Arabidopsis thaliana]
Seq. No.
                  163808
Seq. ID
                  LIB3177-068-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  q2980757
BLAST score
                  51
E value
                  7.0e-20
Match length
                  127
% identity
                  86
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
                  (ESSAII project)
```

```
Seq. No.
                   163809
Seq. ID
                   LIB3177-068-P1-K1-C2
Method
                   BLASTN
NCBI GI
                   · g3449326
BLAST score
                   217
E value
                   1.0e-119
Match length
                   264
% identity
                   95
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K19M22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163810
Seq. ID
                   LIB3177-068-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g119143
BLAST score
                   278
E value
                   1.0e-24
Match length
                   54
% identity
                   100
NCBI Description
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                   >gi_81606_pir__S06724 translation elongation factor eEF-1
                   alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                   (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1369927_emb_CAA34454_ (X16431) elongation factor
                   1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                   (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                   >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                   >gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                   163811
Seq. ID
                   LIB3177-068-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g2119846
BLAST score
                   440
E value
                   5.0e-44
Match length
                   92
% identity
                   91
NCBI Description
                   chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364 emb_CAA45790 (X64460)
                   photosystem II type I ch\overline{l}oroph\overline{y}ll \overline{a} /b bind\overline{i}ng protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi 3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   163812
Seq. ID
                   LIB3177-068-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1710581
BLAST score
                   417
E value
                   4.0e-41
Match length
                   91
% identity
                   89
NCBI Description
                  60S RIBOSOMAL PROTEIN L9 >gi 2129720_pir S71255 ribosomal
```

protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_

Seq. No.

163818

Seq. No. 163813 Seq. ID LIB3177-068-P1-K1-C6 Method BLASTX NCBI GI g4539302 BLAST score 654 E value 8.0e-69 Match length 129 % identity 96 NCBI Description (AL049480) putative protein [Arabidopsis thaliana] Seq. No. 163814 Seq. ID LIB3177-068-P1-K1-C7 Method BLASTX NCBI GI g4263525 BLAST score 527 E value 8.0e-54 Match length 125 % identity NCBI Description (AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana] Seq. No. 163815 Seq. ID LIB3177-068-P1-K1-C8 Method BLASTX NCBI GI q2129651 BLAST score 762 E value 2.0e-81 Match length 147 % identity 100 NCBI Description myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis thaliana] Seq. No. 163816 Seq. ID LIB3177-068-P1-K1-D10 Method BLASTN NCBI GI q4559375 BLAST score 231 E value 1.0e-127 424 Match length % identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence Seq. No. 163817 Seq. ID LIB3177-068-P1-K1-D11 Method BLASTX NCBI GI q2832605 BLAST score 695 E value 2.0e-73 Match length 153 % identity NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

(X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Method

BLASTX

```
Seq. ID
                   LIB3177-068-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   517
E value
                   7.0e-53
Match length
                   105
% identity
                   95
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   163819
Seq. ID
                   LIB3177-068-P1-K1-D3
Method
                   BLASTN
NCBI GI
                   g2459406
BLAST score
                   202
E value
                   1.0e-110
Match length
                   402
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4P9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163820
Seq. ID
                   LIB3177-068-P1-K1-D4
Method
                   BLASTN
NCBI GI
                   q4519194
BLAST score
                   257
E value
                   1.0e-142
Match .length
                   288
% identity
                   97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHM17, complete sequence
Seq. No∴
                   163821
Seq. ID
                  LIB3177-068-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g1370186
BLAST score
                  516
E value
                  2.0e-52
Match length
                  101
% identity
                  98
NCBI Description
                  (Z73942) RAB7C [Lotus japonicus]
Seq. No.
                  163822
Seq. ID
                  LIB3177-068-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4582787
BLAST score
                  334
E value
                  2.0e-31
Match length
                  77
% identity
                  83
NCBI Description
                  (AJ012281) adenosine kinase [Zea mays]
Seq. No.
                  163823
Seq. ID
                  LIB3177-068-P1-K1-D7
```

```
NCBI GI
                   q2911085
BLAST score
                   345
E value
                   2.0e-39
Match length
                   113
% identity
                   81
NCBI Description
                   (AL021960) photosystem II oxygen-evolving complex protein
                   3-like [Arabidopsis thaliana] >gi 3402748 emb CAA20194.1
                   (AL031187) photosystem II oxygen-evolving complex protein 3

    like [Arabidopsis thaliana]

Seq. No.
                   163824
Seq. ID
                   LIB3177-068-P1-K1-D8
Method
                  BLASTN
NCBI GI
                   a4559344
BLAST score
                   350
E value
                  0.0e+00
Match length
                   404
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F27C12 genomic
                  sequence, complete sequence
Seq. No.
                  163825
Seq. ID
                  LIB3177-068-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q3023516
BLAST score
                  343
E value
                  9.0e-33
Match length
                  78
% identity
                  87
                  PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE PRECURSOR
NCBI Description
                   (DXP SYNTHASE) >gi_1399261 (U27099) DEF [Arabidopsis
                  thaliana]
Seq. No.
                  163826
Seq. ID
                  LIB3177-068-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4725941
BLAST score
                  519
E value
                  6.0e-53
Match length
                  112
% identity
                  86
NCBI Description
                  (AL049730) putative pollen-specific protein [Arabidopsis
                  thaliana]
Seq. No.
                  163827
Seq. ID
                  LIB3177-068-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1175013
BLAST score
                  571
                  5.0e-59
E value
Match length
                  126
% identity
                  89
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir_ S44084
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
```

protein 2a [Arabidopsis thaliana]

```
Seq. No.
                  163828
Seq. ID
                  LIB3177-068-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                   698
E value
                   6.0e-74 "
Match length
                  136
% identity
                  97
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  163829
Seq. ID
                  LIB3177-068-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q3286693
BLAST score
                  618
E value
                  2.0e-64
Match length
                  128
% identity
                  98
                  (Y15433) 33 kDa polypeptide of oxygen-evolving complex
NCBI Description
                  (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                  163830
Seq. ID
                  LIB3177-068-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g1169601
BLAST score
                  743
E value
                  4.0e-79
Match length
                  146
% identity
                  99
                  OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 493068 (U09503) chloroplast omega-6 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  163831
Seq. ID
                  LIB3177-068-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g4581084
BLAST score
                  280
E value
                  1.0e-156
Match length
                  332
% identity
                  99
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  163832
Seq. ID
                  LIB3177-068-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  g4713943
BLAST score
                  98
E value
                  3.0e-48
Match length
                  146
% identity
                  92
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,
```

complete sequence

```
Seq. No.
                    163833
 Seq. ID
                    LIB3177-068-P1-K1-E5
 Method
                    BLASTX
 NCBI GI
                    q4586256
 BLAST score
                    247
                    4.0e-21
 E value
 Match length
                    62
 % identity
                    81
 NCBI Description
                    (AL049640) probable photosystem I chain XI precursor
                    [Arabidopsis thaliana]
 Seq. No.
                   163834
 Seq. ID
                   LIB3177-068-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   q3869069
BLAST score
                   56
E value
                   1.0e-22
Match length
                   389
% identity
                   87
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163835
Seq. ID
                   LIB3177-068-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   508
E value
                   9.0e-52
Match length
                   95
% identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP \overline{AB} 140) [Arabidopsis
                   thaliana]
Seq. No.
                   163836
Seq. ID
                   LIB3177-068-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g421826
BLAST score
                   618
E value
                   2.0e-64
Match length
                   141
% identity
NCBI Description
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                   >gi_298036_emb CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
Seq. No.
                   163837
Seq. ID
                   LIB3177-068-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g4741960
BLAST score
                   478
E value
                   4.0e-48
Match length
                   111
% identity
NCBI Description
                   (AF134130) Lhcb6 protein [Arabidopsis thaliana]
```

```
Seq. No.
                   163838
Seq. ID
                   LIB3177-068-P1-K1-F11
Method
                   BLASTN
NCBI GI
                   g4519190
BLAST score
                   136
E value
                   2.0e-70
Match length
                   464
                   98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K6A12, complete sequence
Seq. No.
                   163839
Seq. ID
                   LIB3177-068-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g3914442
BLAST score
                   518
                   9.0e-53
E value
Match length
                   140
                   74
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                  163840
Seq. ID
                  LIB3177-068-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1145697
BLAST score
                  514
E value
                  2.0e-52
Match length
                  106
% identity
                  53
NCBI Description
                  (U39485) delta tonoplast integral protein [Arabidopsis
                  thaliana]
Seq. No.
                  163841
Seq. ID
                  LIB3177-068-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  g4206762
BLAST score
                  49
E value
                  2.0e-18
Match length
                  334
% identity
                  40
                  Arabidopsis thaliana cell wall-plasma membrane linker
NCBI Description
                  protein homolog (CWLP) mRNA, complete cds
Seq. No.
                  163842
Seq. ID
                  LIB3177-068-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3299824
BLAST score
                  427
E value
                  0.0e + 00
Match length
                  471
% identity
                  97
NCBI Description
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
```

near 17 cM, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   163843
 Seq. ID
                   LIB3177-068-P1-K1-F6
 Method
                   BLASTX
 NCBI GI
                   q282865
 BLAST score
                   670
 E value
                   1.0e-70
Match length
                   133
 % identity
                   72
NCBI Description
                   chlorophyll a/b-binding protein - Arabidopsis thaliana
                   >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                   protein [Arabidopsis thaliana] >gi_166644 (M85150)
                   chlorophyll a/b-binding protein [Arabidopsis thaliana]
                   >gi_4678304 emb_CAB41095.1_ (AL049655) chlorophyll
                   a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                   163844
Seq. ID
                   LIB3177-068-P1-K1-F8
Method
                   BLASTN
NCBI GI
                   q516248
BLAST score
                   200
E value
                   1.0e-109
Match length
                   228
% identity
                   97
NCBI Description A.thaliana gene for porphobilinogen deaminase
Seq. No.
                   163845
Seq. ID
                   LIB3177-068-P1-K1-F9
Method
                   BLASTN
NCBI GI
                   g4220635
BLAST score
                   127
E value
                   3.0e-65
Match length
                   217
% identity
                   91
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163846
                  LIB3177-068-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g421826
BLAST score
                   337
E value
                   9.0e-32
Match length
                  101
% identity
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi 298036 emb CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
Seq. No.
                  163847
Seq. ID
                  LIB3177-068-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q4678268
BLAST score
                  52
E value
                  6.0e-50
Match length
                  103
% identity
NCBI Description
                  (AL049660) putative protein [Arabidopsis thaliana]
```

```
Seq. No.
                   163848
 Seq. ID
                   LIB3177-068-P1-K1-G12
 Method
                   BLASTX
 NCBI GI
                   g4539009
 BLAST score
                   661
 E value
                   2.0e-69
 Match length
                   156
 % identity
                   76
NCBI Description
                  (AL049481) putative protein [Arabidopsis thaliana]
 Seq. No.
                   163849
 Seq. ID
                   LIB3177-068-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   q1175010
BLAST score
                   317
E value
                   1.0e-46
Match length
                   113
% identity
                   88
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540 pir S44082
                   plasma membrane intrinsic protein la - Arabidopsis thaliana
                   >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic
                   protein la [Arabidopsis thaliana]
Seq. No.
                   163850
Seq. ID
                  LIB3177-068-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   619
E value
                   1.0e-64
Match length
                  119
% identity
                  99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  163851
                  LIB3177-068-P1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589412
BLAST score
                  46
E value
                  1.0e-16
Match length
                  155
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F6N7, complete sequence
Seq. No.
                  163852
Seq. ID
                  LIB3177-068-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3914442
BLAST score
                  424
E value
                  7.0e-42
```

```
Match length
                   121
% identity
                   71
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                   >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                   163853
                   LIB3177-068-P1-K1-G7
Seq. ID
Method
                   BLASTX
                   q2809244
NCBI GI
BLAST score
                   449
E value
                   1.0e-44
Match length
                   82
% identity
                   100
NCBI Description
                  (AC002560) F21B7.13 [Arabidopsis thaliana]
Seq. No.
                   163854
Seq. ID
                   LIB3177-068-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   q2289010
BLAST score
                   454
E value
                   1.0e-45
Match length
                   93
% identity
                   97
                   (AC002335) FKBP type peptidyl-prolyl cis-trans isomerase
NCBI Description
                   isolog [Arabidopsis thaliana]
Seq. No.
                   163855
Seq. ID
                  LIB3177-068-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  q3337347
BLAST score
                  162
E value
                  6.0e-86
Match length
                  296
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13P17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163856
Seq. ID
                  LIB3177-068-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g1237123
BLAST score
                  350
E value
                  0.0e+00
Match length
                  350
                  100
% identity
NCBI Description
                  Arabidopsis thaliana photosystem I PSI-N mRNA, nuclear gene
                  encoding chloroplast protein, complete cds
Seq. No.
                  163857
Seq. ID
                  LIB3177-068-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g4406777
BLAST score
                  282
E value
                  4.0e-25
Match length
                  55
% identity
                  95
```

```
NCBI Description
                   (ACO06532) putative zinc-finger protein [Arabidopsis
                    thalianal
 Seq. No.
                    163858
 Seq. ID
                   LIB3177-068-P1-K1-H12
 Method
                   BLASTX
 NCBI GI
                   q2894564
 BLAST score
                   127
 E value
                   9.0e-28
Match length
                   66
 % identity
                   98
NCBI Description
                   (AL021890) putative protein [Arabidopsis thaliana]
 Seq. No.
                   163859
 Seq. ID
                   LIB3177-068-P1-K1-H2
Method
                   BLASTN
 NCBI GI
                   q3298610
BLAST score
                   127
                   2.0e-65
E value
Match length
                   135
% identity
                   99
NCBI Description Arabidopsis thaliana BAC T2H3
Seq. No.
                   163860
Seq. ID
                   LIB3177-068-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   q2760829
BLAST score
                   297
E value
                   1.0e-166
Match length
                   324
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F18A8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163861
Seq. ID
                   LIB3177-068-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g2146741
BLAST score
                   630
E value
                   5.0e-66
Match length
                   119
% identity
                   100
NCBI Description
                   isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) -
                   Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl
                   {\tt diphosphate:dimethylally} \overline{1} \ {\tt diphosphate:isomerase}
                   [Arabidopsis thaliana]
Seq. No.
                   163862
Seq. ID
                  LIB3177-068-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g1477480
BLAST score
                  739
E value
                  1.0e-78
Match length
                  145
% identity
                  52
NCBI Description
                  (U40341) carbamoyl phosphate synthetase large chain
                  [Arabidopsis thaliana]
```

Seq. ID

```
Seq. No.
                   163863
Seq. ID
                   LIB3177-068-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g3449041
BLAST score
                   486
E value
                   3.0e-49
Match length
                   90
% identity
                   97
NCBI Description
                  (U73462) carbonic anhydrase [Arabidopsis thaliana]
Seq. No.
                   163864
                   LIB3177-068-P1-K1-H7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4159706
BLAST score
                   104
E value
                   7.0e-52
Match length
                   127
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MGL6, complete sequence
Seq. No.
                   163865
Seq. ID *
                   LIB3177-068-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g166835
BLAST score
                   525
E value
                   7.0e-54
Match length
                   100
% identity
                   100
NCBI Description
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
                   activase [Arabidopsis thaliana] >gi 2642170 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
Seq. No.
                   163866
Seq. ID
                   LIB3177-068-P1-K1-H9
Method
                  BLASTN
NCBI GI
                   q600388
BLAST score
                   285
E value
                   1.0e-159
Match length
                   306
% identity
                   98
NCBI Description A.thaliana UbcAT3 mRNA for ubiquitin conjugating enzyme E2
Seq. No.
                  163867
Seq. ID
                  LIB3177-069-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g4519192
BLAST score
                  258
E value
                  1.0e-143
Match length
                  262
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MBK21, complete sequence
Seq. No.
                  163868
```

LIB3177-069-P1-K1-A11

```
Method
                    BLASTN
 NCBI GI
                    q2244788
 BLAST score
                    52
 E value
                    1.0e-20
 Match length
                    71
 % identity
                    96
 NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                    fragment No
 Seq. No.
                    163869
                    LIB3177-069-P1-K1-A12
 Seq. ID
Method
                    BLASTN
NCBI GI
                    q1916349
BLAST score
                    121
E value
                    1.0e-61
Match length
                    227
% identity
                    90
NCBI Description
                   Brassica rapa PSI-H subunit (psaH) mRNA, complete cds
Seq. No.
                    163870
Seq. ID
                   LIB3177-069-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g2982285
BLAST score
                   350
E value
                   4.0e-33
Match length
                   69
% identity
                   80
NCBI Description
                   (AF051227) GASA5-like protein [Picea mariana]
Seq. No.
                   163871
                   LIB3177-069-P1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4587564
BLAST score
                   186
E value
                   2.0e-14
Match length
                   37
% identity
                   97
NCBI Description
                   (AC006550) Strong similarity to gb X14017 photosystem I
                   reaction centre subunit II precursor (psaD) from Spinacia
                   oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,
                   gb_N65521, gb_T424\overline{9}8, gb_T419\overline{1}8, gb_N380\overline{2}4
Seq. No.
                   163872
Seq. ID
                   LIB3177-069-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   g4454036
BLAST score
                   535
E value
                   9.0e-55
Match length
                   106
% identity
                   (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   163873
Seq. ID
                   LIB3177-069-P1-K1-A5
Method
                   BLASTN
NCBI GI
                   q3869062
```

Seq. ID

```
BLAST score
                   148
 E value
                   8.0e-78
Match length
                   231
 % identity
                   92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K11I1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163874
Seq. ID
                   LIB3177-069-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g2462929
BLAST score
                   413
E value
                   9.0e-41
Match length
                   87
% identity
                   93
NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                   163875
Seq. ID
                   LIB3177-069-P1-K1-A9
                   BLASTX
Method
NCBI GI
                   q3157924
BLAST score
                   315
                   5.0e-29
E value
Match length
                   80
% identity
                   78
                   (AC002131) Contains homology to extensin-like protein
NCBI Description
                   gb_D83227 from Populus nigra. ESTs gb H76425, gb T13883,
                   gb_T45348, gb_H37743, gb_AA042634, gb Z26960 and gb Z25951
                   come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like
                   protein [Arabidopsis thaliana]
Seq. No.
                   163876
Seq. ID
                   LIB3177-069-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g1168607
BLAST score
                   601
E value
                   1.0e-62
Match length
                   118
% identity
                   98
NCBI Description
                   AUXIN-INDUCED PROTEIN AUX2-11 >gi_16197_emb_CAA37526
                   (X53435) Aux2-11 protein [Arabidopsis thaliana] >gi 454285
                   (L15450) auxin-responsive protein [Arabidopsis thaliana]
Seq. No.
                   163877
Seg. ID
                   LIB3177-069-P1-K1-B12
                   BLASTN
Method
NCBI GI
                   g3927822
BLAST score
                   324
E value
                   0.0e+00
Match length
                   446
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163878
```

LIB3177-069-P1-K1-B2

```
Method
                   BLASTX
 NCBI GI
                   g3242075
 BLAST score
                   299
 E value
                   1.0e-27
 Match length
                   56
 % identity
                   100
 NCBI Description
                   (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis
                   thaliana]
 Seq. No.
                   163879
 Seq. ID
                   LIB3177-069-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   718
E value
                   3.0e-76
Match length
                   134
% identity
                   98
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063 pir RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   163880
Seq. ID
                   LIB3177-069-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   q2264316
BLAST score
                  180
E value
                   1.0e-96
Match length
                   437
% identity
                   40
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                   MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163881
                   LIB3177-069-P1-K1-B5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2288979
BLAST score
                   315
E value
                   1.0e-177
Match length
                   348
% identity
                   97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T01024 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163882
Seq. ID
                  LIB3177-069-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  460
E value
                  3.0e-46
Match length
                  103
% identity
                  88
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
```

Al precursor - Arabidopsis thaliana

Seq. No.

```
Seq. No.
                    163883
 Seq. ID
                    LIB3177-069-P1-K1-B7
 Method
                    BLASTX
 NCBI GI
                    g4263525
 BLAST score
                    602
 E value
                    1.0e-62
 Match length
                    141
 % identity
                    85
 NCBI Description
                   (AC004044) putative photosystem I reaction center subunit
                    II precursor [Arabidopsis thaliana]
 Seq. No.
                   163884
 Seq. ID
                   LIB3177-069-P1-K1-C11
                   BLASTX
Method
NCBI GI
                   g2052379
BLAST score
                    571
E value
                    4.0e-59
Match length
                   106
% identity
                   99
NCBI Description (U66343) calreticulin [Arabidopsis thaliana]
Seq. No.
                   163885
Seq. ID
                   LIB3177-069-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q1653089
BLAST score
                   243
E value
                   1.0e-20
Match length
                   80
% identity
                   56
NCBI Description
                  (D90911) hypothetical protein [Synechocystis sp.]
Seq. No.
                   163886
                   LIB3177-069-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4406816
BLAST score
                   545
                   9.0e-59
E value
Match length
                   119
% identity
                   97
NCBI Description
                  (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
Seq. No.
                   163887
                   LIB3177-069-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   670
E value
                   1.0e-70
Match length
                   125
% identity
                   98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1.}1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
```

```
LIB3177-069-P1-K1-C4
Seq. ID
Method
                      BLASTX
NCBI GI
                      g228408
BLAST score
                      633
E value
                      3.0e-66
Match length
                      124
% identity
                      66
                      calmodulin 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                      163889
Seq. ID
                      LIB3177-069-P1-K1-C6
Method
                      BLASTX
NCBI GI
                      q1076708
BLAST score
                      657
E value
                      4.0e-69
Match length
                      141
% identity
                      27
                      seed tetraubiquitin - common sunflower
NCBI Description
                      >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
>gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
>gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin
[Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
                      putative polyubiquitin [Arabidopsis thaliana]
                      >qi 1096513 prf 2111434A tetraubiquitin [Helianthus
                      annuus] .
Seq. No.
                      163890
Seq. ID
                      LIB3177-069-P1-K1-D1
Method
                      BLASTX
NCBI GI
                      g1362029
BLAST score
                      374
E value
                      5.0e-36
Match length
                      89
% identity
                      72
                      thioglucosidase (EC 3.2.3.1) precursor - rape
NCBI Description
                      >gi 840725 emb CAA55685 (X79080) myrosinase [Brassica
                      napus]
Seq. No.
                      163891
                      LIB3177-069-P1-K1-D10
Seq. ID
Method
                      BLASTX
NCBI GI
                      g4115364
BLAST score
                      429
E value
                      2.0e-42
Match length
                      97
                      87
% identity
NCBI Description
                      (AC005957) putative fatty acid elongase [Arabidopsis
                      thaliana]
Seq. No.
                      163892
Seq. ID
                      LIB3177-069-P1-K1-D11
Method
                      BLASTX
NCBI GI
                      q3953473
BLAST score
                      637
E value
                      8.0e-67
Match length
                      128
```

Seq. ID

```
% identity
NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]
Seq. No.
                   163893
Seq. ID
                   LIB3177-069-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g2764941
BLAST score
                   518
E value
                   7.0e-53
Match length
                   87
% identity
                   100
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                   expressed in meristematic region, and style [Arabidopsis
                   thalianal
Seq. No.
                   163894
Seq. ID
                  LIB3177-069-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g3894183
BLAST score
                   458
E value
                  9.0e-46
Match length
                  130
% identity
                  74
NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]
Seq. No.
                  163895
Seq. ID
                  LIB3177-069-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4138912
BLAST score
                  140
E value
                  8.0e-09
Match length
                  31
% identity
                  77
NCBI Description (AF059487) expansin precursor [Lycopersicon esculentum]
Seq. No.
                  163896
                  LIB3177-069-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2118220
BLAST score
                  235
E value
                  4.0e-20
Match length
                  67
                  75
% identity
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                  (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581)
                  vacuolar H+-pumping ATPase 16 kDa proteol\overline{i}pid [Arabidopsis
                  thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16
                  kDa proteolipid [Arabidopsis thaliana]
                  >gi 3096941 emb CAA18851.1 (AL023094) vacuolar
                  H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                  >gi 4539311 emb CAB38812.1_ (AL035679) H+-transporting
                  ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
                  >gi_4589976_gb_AAD26493.1_AC007195 7 (AC007195) vacuolar
                  H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.
                  163897
```

LIB3177-069-P1-K1-D8

BLAST score

```
Method
                   BLASTX
NCBI GI
                   g4490325
BLAST score
                   461
E value
                   4.0e-46
Match length
                   115
% identity
                   77. --
NCBI Description
                  (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  163898
Seq. ID
                  LIB3177-069-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4544387
BLAST score
                  248
E value
                  1.0e-21
Match length
                   67
% identity
                  76
NCBI Description
                  (AC007047) putative purple acid phosphatase precursor
                   [Arabidopsis thaliana]
Seq. No.
                  163899
Seq. ID
                  LIB3177-069-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1169278
BLAST score
                  361
                  2.0e-34
E value
Match length
                  152
% identity
                  54
NCBI Description DEHYDRIN ERD14 >gi_556474_dbj BAA04569 (D17715) ERD14
                  protein [Arabidopsis thaliana]
Seq. No.
                  163900
Seq. ID
                  LIB3177-069-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q99735
BLAST score
                  587
E value
                  5.0e-61
Match length
                  112
% identity
                  99
NCBI Description
                  L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                  Arabidopsis thaliana (fragment)
Seq. No.
                  163901
Seq. ID
                  LIB3177-069-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                  578
E value
                  8.0e-60
Match length
                  112
% identity
                  100
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  163902
Seq. ID
                  LIB3177-069-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g585165
```

Seq. ID

Method

```
E value
                   3.0e-73
Match length
                  145
% identity
                   88
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                   (G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate
                  1-dehydrogenase (EC 1.1.1.49) - potato
                  >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate
                  1-dehydrogenase [Solanum tuberosum]
Seq. No.
                  163903
Seq. ID
                  LIB3177-069-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4587564
BLAST score
                  575
E value
                  1.0e-59
Match length
                  129
% identity
NCBI Description
                  (AC006550) Strong similarity to gb_X14017 photosystem I
                  reaction centre subunit II precursor (psaD) from Spinacia
                  oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,
                  gb_N65521, gb_T42498, gb_T41918, gb_N38024
Seq. No.
                  163904
Seq. ID
                  LIB3177-069-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q2199574
BLAST score
                  295
E value
                  4.0e-27
Match length
                  61
% identity
                  90
NCBI Description
                  (AF004293) aquaporin [Brassica rapa]
Seq. No.
                  163905
Seq. ID
                  LIB3177-069-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1362051
BLAST score
                  452
E value
                  5.0e-45
                  95
Match length
% identity
                  92
NCBI Description
                  protein kinase 3 - soybean >qi 310582 (L19361) protein
                  kinase 3 [Glycine max]
Seq. No.
                  163906
Seq. ID
                  LIB3177-069-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  q3046854
BLAST score
                  346
E value
                  0.0e+00
Match length
                  378
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRG7, complete sequence [Arabidopsis thaliana]
                  163907
Seq. No.
```

LIB3177-069-P1-K1-F11

BLASTX

NCBI GI

```
NCBI GI
                   q4585935
BLAST score
                   300
E value
                   1.0e-27
Match length
                   69
% identity
                   86
NCBI Description
                   (AC007211) putative chlorophyll A/B binding protein
                   [Arabidopsis thaliana] >gi 4741946 gb AAD28770.1 AF134123 1
                   (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                   163908
Seq. ID
                   LIB3177-069-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q2341034
BLAST score
                   460
                   4.0e-46
E value
Match length
                   92
% identity
                   100
NCBI Description
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                   163909
Seq. ID
                   LIB3177-069-P1-K1-F2
                   BLASTN :
Method
NCBI GI
                   q240069
BLAST_score
                   70
E value
                   7.0e-32
Match length
                   70
                  100
% identity
NCBI Description
                  light-regulated glutamine synthetase isoenzyme [Arabidopsis
                  thaliana, mRNA, 1548 nt]
Seq. No.
                  163910
Seq. ID
                  LIB3177-069-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  q3046854
BLAST score
                  161
E value
                  2.0e-85
Match length
                  288
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRG7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163911
Seq. ID
                  LIB3177-069-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q1169128
BLAST score
                  196
E value
                  1.0e-15
Match length
                  45
% identity
                  82
                  SERINE/THREONINE-PROTEIN KINASE CTR1 >gi_166680 (L08789)
NCBI Description
                  protein kinase [Arabidopsis thaliana] >gi_166682 (L08790)
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                  163912
Seq. ID
                  LIB3177-069-P1-K1-G1
Method
                  BLASTX
```

q4512675

Method

BLASTX



```
BLAST score
                    794
E value
                    4.0e-85
Match length
                    152
% identity
                    100
NCBI Description
                   (AC006931) putative citrate synthase [Arabidopsis thaliana]
Seq. No.
                    163913
Seq. ID
                    LIB3177-069-P1-K1-G10
Method
                    BLASTX
NCBI GI
                    q16374
BLAST score
                    305
E value
                    2.0e-28
                    62
Match length
                    89
% identity
                    (X03908) chlorophyll a/b binding protein (LHCP AB 180)
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    163914
Seq. ID
                    LIB3177-069-P1-K1-G12
                    BLASTN
Method
NCBI GI
                    q3236479
BLAST score
                    89
E value
                    1.0e-42
Match length
                    137
% identity
                    91
                   Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8
NCBI Description
                    cM, complete sequence
                    163915
Seq. No.
Seq. ID
                    LIB3177-069-P1-K1-G2
Method
                    BLASTX
NCBI GI
                    q2956690
BLAST score
                    420
                    3.0e-41
E value
Match length
                    127
% identity
                    54
                    (AJ223306) PSBY [Arabidopsis thaliana] >gi 3414928
NCBI Description
                    (AF079800) PsbY precursor [Arabidopsis thaliana]
Seq. No.
                    163916
Seq. ID
                    LIB3177-069-P1-K1-G3
Method
                    BLASTX
NCBI GI
                    q3157924
BLAST score
                    315
                    6.0e-29
E value
                    80
Match length
% identity
NCBI Description
                    (AC002131) Contains homology to extensin-like protein
                    gb D83227 from Populus nigra. ESTs gb H76425, gb T13883,
                    gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like
                    protein [Arabidopsis thalīana]
Seq. No.
                    163917
                    LIB3177-069-P1-K1-G5
Seq. ID
```

E value

1.0e-43

```
NCBI GI
                   g4587542
BLAST score
                   339
E value
                   2.0e-32
Match length
                   73
% identity
                   90
NCBI Description (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase
                  with GDSL-motif family. ESTs gb_T45815, gb_T45130 and
                  gb_Z38046 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  163918
Seq. ID
                  LIB3177-069-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q3785991
BLAST score
                  329
E value
                  6.0e-31
Match length
                  73
% identity
                  89
NCBI Description (AC005560) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                  163919
Seq. ID
                  LIB3177-069-P1-K1-G7
                  BLASTX
Method
NCBI GI
                  g1769907
BLAST score
                  454
                  2.0e-45
E value
Match length
                  121
% identity
                  76
                  (X92975) xyloglucan endo-transglycosylase [Arabidopsis
NCBI Description
                  thaliana]
                                                             ٠, . .
Seq. No.
                  163920
Seq. ID
                  LIB3177-069-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g2961378
BLAST score
                  255
E value
                  1.0e-22
Match length
                  60
% identity
                  42
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]
Seq. No.
                  163921
Seq. ID
                  LIB3177-069-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  g2264316
BLAST score
                  103
E value
                  9.0e-51
Match length
                  335
% identity
                  42
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163922
Seq. ID
                  LIB3177-069-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  439
```

NCBI GI

```
95
Match length
% identity
                  89
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  163923
Seq. ID
                  LIB3177-069-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3914117
BLAST score
                  582
E value
                  3.0e-60
Match length
                  144
                  81
% identity
NCBI Description
                  NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP
                  KINASE II) >gi_3093480 (AF017640) nucleoside diphosphate
                  kinase type 2 [Arabidopsis thaliana]
Seq. No.
                  163924
Seq. ID
                  LIB3177-069-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q4566505
BLAST score
                  262
E value
                  4.0e-23
Match length
                  84
                  60
% identity
NCBI Description
                  (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI
                  [Hordeum vulgare]
Seq. No.
                  163925
Seq. ID
                  LIB3177-069-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3080401
BLAST score
                  587
                  7.0e-61
E value
Match length
                  116
% identity
                  100
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4455265 emb CAB36801.1 (AL035527) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  163926
Seq. ID
                  LIB3177-069-P1-K1-H3
Method
                  BLASTN
                  g3402745
NCBI GI
BLAST score
                  166
                  3.0e-88
E value
Match length
                  268
% identity
                  93
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
NCBI Description
                  (ESSAII project)
Seq. No.
                  163927
Seq. ID
                  LIB3177-069-P1-K1-H4
Method
                  BLASTN
```

g4519185

```
BLAST score
                  140
E value
                  4.0e-73
Match length
                  192
% identity
                  93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15015, complete sequence
Seq. No.
                  163928
Seq. ID
                  LIB3177-069-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q2244892
BLAST score
                  189
E value
                  8.0e-15
Match length
                  55
% identity
                  64
NCBI Description
                  (Z97338) similarity to cycloartenol synthase [Arabidopsis
                  thaliana]
Seq. No.
                  163929
Seq. ID
                  LIB3177-069-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g2982285
BLAST score
                 350
E value
                  5.0e-33
Match length
                  69
% identity
                  80
NCBI Description (AF051227) GASA5-like protein [Picea mariana]
                  163930
Seq. No.
Seq. ID
                  LIB3177-069-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1899188
BLAST score
                  109
                  8.0e-05
E value
Match length
                  85
% identity
                  13
NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]
Seq. No.
                  163931
Seq. ID
                  LIB3177-069-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3123745
BLAST score
                  411
E value
                  1.0e-41
Match length
                  99
% identity
                  87
NCBI Description (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                  163932
Seq. ID
                  LIB3177-070-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g4115387
BLAST score
                  587
E value
                  5.0e-61
Match length
                  118
                  99
% identity
NCBI Description (AC005967) putative NADP-dependent
```

Method NCBI GI

BLAST score

```
thalianal
Seq. No.
                  163933
Seq. ID
                  LIB3177-070-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q132110
BLAST score
                  702
E value
                  2.0e-74
Match length
                  131
% identity
                  98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  163934
Seq. ID
                  LIB3177-070-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  q4757662
BLAST score
                  232
E value
                  1.0e-127
Match length
                  465
% identity .
                  100
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F10B6 from
                  chromosome I, complete sequence
Seq. No.
                  163935
Seq. ID
                  LIB3177-070-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  g4314354
BLAST score
                  21
                  5.5e-02
E value
                  196
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC T9I22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163936
Seq. ID
                  LIB3177-070-P1-K1-A2
                  BLASTX
Method
NCBI GI
                  g2129772
BLAST score
                  292
E value
                  1.0e-26
                  82
Match length
% identity
                  63
NCBI Description
                  xyloglucan endotransqlycosylase-related protein XTR-7 -
                  Arabidopsis thaliana >gi 1244760 (U43489) xyloglucan
                  endotransglycosylase-related protein [Arabidopsis thaliana]
Seq. No.
                  163937
Seq. ID
                  LIB3177-070-P1-K1-A3
```

glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis

BLASTX

g132110

E value

5.0e-57

```
E value
                    4.0e-56
Match length
                    106
 % identity
                    96
NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                    (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_ RKMUB3
                    ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1}.1.39) small chain
                    B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana]
Seq. No.
                    163938
Seq. ID
                    LIB3177-070-P1-K1-A5
Method
                    BLASTN
NCBI GI
                    q2244991
BLAST score
                    284
E value
                    1.0e-158
Match length
                    466
                    100
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                    fragment No
Seq. No.
                    163939
Seq. ID
                   LIB3177-070-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g3157947
BLAST score
                   814
E value
                   2.0e-87
Match length
                   156
% identity
                   52
NCBI Description
                   (AC002131) Similar to protein gb_Z74962 from Brassica
                   oleracea which is similar to bacterial YRN1 and HEAHIO
                   proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene.
                    [Arabidopsis tha
Seq. No.
                   163940
                   LIB3177-070-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   743
E value
                   4.0e-79
Match length
                   147
% identity
                   97
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   163941
Seq. ID
                   LIB3177-070-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   q1170939
BLAST score
                   554
```

```
Match length
                  115
% identity
                  92
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
Seq. No.
                  163942
Seq. ID
                  LIB3177-070-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q1773330
BLAST score
                  618
                  2.0e-64
E value
Match length
                  141
% identity
                  85
NCBI Description
                  (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
Seq. No.
                  163943
Seq. ID
                  LIB3177-070-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q3892704
BLAST score ·
                  515
                  2.0e-52
E value
Match length
                  93
                  100
% identity
NCBI Description
                 (AL033545) RCc3-like protein [Arabidopsis thaliana]
                  163944
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  790
E value
                  1.0e-84
Match length
                  150
% identity
                  99
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  163945
Seq. ID
                  LIB3177-070-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  717
                  4.0e-76
E value
Match length
                  138
                  99
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
```

>gi_16368_emb_CAA27540_ (X03907) chlorophyll_a/b binding

Seq. ID

```
>gi_16372_emb CAA27541 (X03908) chlorophyll a/b binding
                     protein (LHCP AB 180) [Arabidopsis thaliana]
 Seq. No.
                     163946
 Seq. ID
                     LIB3177-070-P1-K1-B2
 Method
                     BLASTN
 NCBI GI
                     q14342
 BLAST score
                     316
 E value
                     1.0e-178
 Match length
                     316
 % identity
                    100
 NCBI Description A.thaliana mRNA for carbonic anhydrase
 Seq. No.
                    163947
Seq. ID
                    LIB3177-070-P1-K1-B3
Method
                    BLASTX
NCBI GI
                    g115767
BLAST score
                    649
E value
                    4.0e-68
Match length
                    126
% identity
                    99
                    CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
NCBI Description
                    a/b-binding protein ab16\overline{5} - Arabidopsis thaliana
                    >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                    protein (LHCP AB 65) [Arabidopsis thaliana]
                    >gi_16372_emb CAA27541_ (X03908) chlorophyll a/b binding
                    protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                    163948
                    LIB3177-070-P1-K1-B4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3915865
BLAST score
                    414
E value
                    1.0e-40
Match length
                    102
% identity
                    82
NCBI Description
                   40S RIBOSOMAL PROTEIN S4
Seq. No.
                    163949
Seq. ID
                    LIB3177-070-P1-K1-B5
Method
                    BLASTX
NCBI GI
                    q132110
BLAST score
                    731
E value
                    1.0e-77
Match length
                    138
% identity
                    97
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   163950
```

protein (LHCP AB 65) [Arabidopsis thaliana]

LIB3177-070-P1-K1-B6

```
Method
                   BLASTX
NCBI GI
                   q2443751
BLAST score
                   802
E value
                   5.0e-86
Match length
                   159
% identity
                   100
NCBI Description
                   (AF020303) fumarase [Arabidopsis thaliana] >qi 2529676
                   (AC002535) putative fumarase [Arabidopsis thaliana]
Seq. No.
                   163951
Seq. ID
                   LIB3177-070-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   q99696
BLAST score
                   691
E value
                   4.0e-73
Match length
                   134
% identity
                   99
NCBI Description
                  glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                   chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                   >gi_240070_bbs_69728 (S69727) light-regulated glutamine
                   synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                   aa] [Arabidopsis thaliana] >gi_228453 prf 1804333A Gln
                   synthetase [Arabidopsis thaliana]
Seq. No.
                   163952
Seq. ID
                  LIB3177-070-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g4263642
BLAST score
                   423
E value
                  0.0e+00
Match length
                   431
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T13H18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163953
                  LIB3177-070-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  g2194121
NCBI GI
BLAST score
                  612
E value
                  1.0e-65
Match length
                  134
% identity
                  92
                  (AC002062) Strong similarity to Arabidopsis cyclin delta-1
NCBI Description
                   (gb ATCD1). EST gb ATTS4338 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  163954
                  LIB3177-070-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541858
BLAST score
                  785
E value
                  4.0e-84
Match length
                  148
% identity
                  99
NCBI Description
                  endoxyloglucan transferase - Arabidopsis thaliana
```

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>gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan

% identity

80

```
endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.
                   163955
Seq. ID
                   LIB3177-070-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   q1169201
BLAST score
                   414
E value
                   1.0e-40
Match length
                   109
% identity
NCBI Description
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                   >gi_421830_pir__S33707 DRT112 protein - Arabidopsis
                   thaliana > gi_1 166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                   163956
Seq. ID
                   LIB3177-070-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q399307
BLAST score
                   451
E value
                   6.0e-45
Match length
                   143
% identity
NCBI Description
                  PRENYL TRANSFERASE >gi_99282_pir__A40433 prephytoene
                  pyrophosphatase dehydrogenase (crtE) homolog - Cyanophora
                  paradoxa >gi_336639 (M37111) prephytoene pyrophosphate
                  dehydrogenase [Cyanophora paradoxa] >gi 1016130 (U30821)
                  prenyl transferase [Cyanophora paradoxa]
Seq. No.
                  163957
Seq. ID
                  LIB3177-070-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1350680
BLAST score
                  770
E value
                  3.0e-82
Match length
                  149
                  99
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
Seq. No.
                  163958
Seq. ID
                  LIB3177-070-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3608142
BLAST score
                  252
E value
                  1.0e-21
                  126
Match length
% identity
                  43
NCBI Description (AC005314) putative hin1 [Arabidopsis thaliana]
                  163959
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g131398
BLAST score
                  546
E value
                  5.0e-56
Match length
                  140
```

transferase [Arabidopsis thaliana] >gi 4063757 (AC005561)

```
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                   photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                   >gi 3152571 (AC002986) Match to photosystem II 10kDa
                   polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                   come from this gene. [Arabidopsis
Seq. No.
                   163960
Seq. ID
                   LIB3177-070-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   q2384696
                   394
BLAST score
                   3.0e-38
E value
Match length
                   159
% identity
                   51
                  (AF013216) acyl-CoA oxidase [Myxococcus xanthus]
NCBI Description
Seq. No.
                   163961
Seq. ID
                   LIB3177-070-P1-K1-C7
Method
                   BLASTX
                   q2119846
NCBI GI
                   605
BLAST score
                   4.0e-63
E value
                   117
Match length
% identity
NCBI Description
                   chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi_3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   163962
Seq. ID
                   LIB3177-070-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q1732570
BLAST score
                   156
E value
                   2.0e-10
Match length
                   33
% identity
NCBI Description
                   (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                   163963
Seq. ID
                   LIB3177-070-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   q115385
BLAST score
                   447
E value
                   1.0e-44
Match length
                   105
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
```

chlorophyll a/b binding protein [Arabidopsis thaliana]

```
163964
 Seq. No.
 Seq. ID
                    LIB3177-070-P1-K1-D1
 Method
                    BLASTX
 NCBI GI
                    g3286693
 BLAST score
                    790
 E value
                    1.0e-84
* Match length
                    156
 % identity
                    100
 NCBI Description
                    (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                    (OEC) in photosystem II [Arabidopsis thaliana]
 Seq. No.
                    163965
 Seq. ID
                    LIB3177-070-P1-K1-D11
 Method
                    BLASTN
 NCBI GI
                    q2244870
 BLAST score
                    270
 E value
                    1.0e-150
 Match length
                    288
 % identity
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                    fragment No
 Seq. No.
                    163966
 Seq. ID
                    LIB3177-070-P1-K1-D12
 Method
                    BLASTX
 NCBI GI
                    q3024434
 BLAST score
                    528
 E value
                    6.0e-54
 Match length
                   126
 % identity
                    86
                    26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
 NCBI Description
                    PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_
                    (D88663) Tat binding protein 1 [Brassica rapa]
 Seq. No.
                   163967
 Seq. ID
                   LIB3177-070-P1-K1-D3
 Method
                   BLASTX
 NCBI GI
                   q2388710
 BLAST score
                    393
 E value
                   3.0e-38
 Match length
                   110
 % identity
                   68
 NCBI Description
                   (AF017150) betaine aldehyde dehydrogenase [Amaranthus
                   hypochondriacus]
 Seq. No.
                   163968
                   LIB3177-070-P1-K1-D7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1922944
 BLAST score
                   306
 E value
                   5.0e-28
 Match length
                   84
 % identity
                   76 .
 NCBI Description
                   (AC000106) Strong similarity to Picea histone {\tt H2A}
                   (gb X67819). ESTs gb_ATTS3874,gb T46627,gb_T14194 come from
                   this gene. [Arabidopsis thaliana]
```

Match length

456

```
Seq. No.
                  163969
                  LIB3177-070-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132102
BLAST score
                   686
E value
                   2.0e-72
Match length
                  131
% identity
                  98
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B2 precursor - Arabidopsis thaliana >gi 16194 emb CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  163970
Seq. ID
                  LIB3177-070-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q1709687
BLAST score
                  543
E value
                  6.0e-56
Match length
                  109
% identity
                  96
                  PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O)
NCBI Description
                  REDUCTASE) >gi_2129643_pir__S71275 methionine sulfoxide
                  reductase - Arabidopsis thaliana >gi 1279212 emb CAA65991
                   (X97326) methionine sulfoxide reductase [Arabidopsis
                  thaliana]
Seq. No.
                  163971
Seq. ID
                  LIB3177-070-P1-K1-E1
Method
                  BLASTX
NCBI GI '
                  g4741954
BLAST score
                  706
E value
                  8.0e-75
Match length
                  148
% identity
                  91
NCBI Description
                  (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
Seq. No.
                  163972
Seq. ID
                  LIB3177-070-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4680651
BLAST score
                  215
E value
                  3.0e-17
Match length
                  138
% identity
                  38
NCBI Description (AF132940) CGI-06 protein [Homo sapiens]
Seq. No.
                  163973
Seq. ID
                  LIB3177-070-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g4584351
BLAST score
                  456
E value
                  0.0e+00
```

```
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T12H3 genomic
                  sequence, complete sequence
Seq. No.
                  163974
Seq. ID
                  LIB3177-070-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  q4199934
BLAST score
                  35
E value
                  5.0e-10
Match length
                  597
% identity
                  53
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  163975
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-E2
Method
                  BLASTX
                  g4741948
NCBI GI
BLAST score
                  776
                  5.0e-83
E value
Match length
                  146
% identity
                  100
                  (AF134124) Lhcb2 protein [Arabidopsis thaliana]
NCBI Description
                  163976
Seq. No.
                  LIB3177-070-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3204108
BLAST score
                  656
                  6.0e-69
E value
                  136
Match length
% identity
                  89
                  (AJ006764) putative deoxycytidylate deaminase [Cicer
NCBI Description
                  arietinum]
                  163977
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q1769905
BLAST score
                  569
E value
                  1.0e-58
Match length
                  149
% identity
                  74
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  163978
                  LIB3177-070-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  a1769905
BLAST score
                  205
                  1.0e-16
E value
Match length
                  65 -
% identity
                  65
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                  [Arabidopsis thaliana]
```

```
163979
Seq. No.
                   LIB3177-070-P1-K1-E7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2656031
BLAST score
                   80
                   4.0e-37
E value
Match length
                   156
% identity
                   88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   163980
Seq. No.
                   LIB3177-070-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4835233
BLAST score
                   425
                   6.0e-42
E value
                   95
Match length
                   93
% identity
NCBI Description
                   (AL049862) putative protein 1 photosystem II
                   oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                   163981
Seq. ID
                   LIB3177-070-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q2129538
BLAST score
                   53
E value
                   5.0e-16
Match length
                   50
                   88
% identity
NCBI Description
                  AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
Seq. No.
                   163982
Seq. ID
                  LIB3177-070-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2129538
BLAST score
                   265
E value
                   3.0e-23
Match length
                  51
% identity
                  100
NCBI Description
                  AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
Seq. No.
                  163983
Seq. ID
                  LIB3177-070-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  g4584531
BLAST score
                  469
E value
                  0.0e + 00
Match length
                  481
% identity
                  30
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8
                  (ESSA project)
```

163984

Seq. No.

```
Seq. ID
                   LIB3177-070-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q4741940
BLAST score
                   385
                   2.0e-37
E value
Match length
                   71
                   99
% identity
                   (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   163985
Seq. ID
                   LIB3177-070-P1-K1-F12
Method
                   BLASTX
                   q2244979
NCBI GI
                   647
BLAST score
                   7.0e-68
E value
                   132
Match length
% identity
                   99
                   (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
NCBI Description
                   thaliana]
                   163986
Seq. No.
Seq. ID
                   LIB3177-070-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   q3449332
BLAST score
                   401
                   0.0e + 00
E value
                   449
Match length
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSF19, complete sequence [Arabidopsis thaliana]
                   163987
Seq. No.
Seq. ID
                   LIB3177-070-P1-K1-F3
Method
                   BLASTN
NCBI GI
                   q1532162
BLAST score
                   145
                   5.0e-76
E value
                   169
Match length
% identity
                   96
                   Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,
NCBI Description
                   AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14
                   genes, partial cds, AT.I.24-7, ascorbate peroxidase
                   (ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I
                   163988
Seq. No.
                   LIB3177-070-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464987
                   629
BLAST score
E value
                   1.0e-65
Match length
                   116
% identity
                   100
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                   >gi_421858_pir__S32672 ubiquitin--protein ligase (EC
6.3.2.19) UBC10 - Arabidopsis thaliana
                   >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating
```

```
Seq. No.
                  163989
Seq. ID
                  LIB3177-070-P1-K1-F6
                  BLASTN
Method
NCBI GI
                  g1209241
BLAST score
                  124
                  1.0e-63
E value
Match length
                  184
                  92
% identity
                  Arabidopsis thaliana metallothionein mRNA sequence
NCBI Description
                  163990
Seq. No.
                  LIB3177-070-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2764941
BLAST score
                  607
                  3.0e-63
E value
                  106
Match length
% identity
                  100
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  163991
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-F9
                  BLASTX
Method
NCBI GI
                  q2129752
                  413
BLAST score
                  2.0e-40
E value
Match length
                  86
                  97
% identity
                  thioredoxin - Arabidopsis thaliana >gi 992964 emb CAA84612
NCBI Description
                  (Z35475) thioredoxin [Arabidopsis thaliana]
Seq. No.
                  163992
Seq. ID
                  LIB3177-070-P1-K1-G1
Method
                  BLASTN
                  g3449323
NCBI GI
BLAST score
                  364
E value
                  0.0e + 00
Match length
                  368
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MZA15, complete sequence [Arabidopsis thaliana]
                  163993
Seq. No.
                  LIB3177-070-P1-K1-G11
Seq. ID
                  BLASTN
Method
                  q4519195
NCBI GI
BLAST score
                  98
                  1.0e-47
E value
Match length
                  146
% identity
                  62
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
```

enzyme [Arabidopsis thaliana] >qi 349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

MQC12, complete sequence

```
163994
 Seq. No.
 Seq. ID
                   LIB3177-070-P1-K1-G2
                 • BLASTN
 Method
 NCBI GI
                   g4756963
 BLAST score
                   231
 E value
                   1.0e-127
Match length
                   459
 % identity
                   99
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
 NCBI Description
                   (ESSA project)
 Seq. No.
                   163995
 Seq. ID
                   LIB3177-070-P1-K1-G3
 Method
                   BLASTX
 NCBI GI
                   g1351271
 BLAST score
                   185
                   9.0e-14
 E value
 Match length
                   41
 % identity
                   90
 NCBI Description
                   TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
                   >gi_1084309_pir__S52032 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - spinach >gi 806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
                                                             ----
 Seq. No.
                   163996
 Seq. ID
                   LIB3177-070-P1-K1-G4
                   BLASTX
 Method
 NCBI GI
                   g4741960
 BLAST score
                   500
 E value
                   1.0e-50
 Match length
                   116
 % identity
                   84
                   (AF134130) Lhcb6 protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   163997
                   LIB3177-070-P1-K1-G5
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g4567237
 BLAST score
                   404
 E value
                   0.0e + 00
 Match length
                   478
                   100
 % identity
                   Arabidopsis thaliana chromosome II BAC T22F11 genomic
 NCBI Description
                   sequence, complete sequence
                   163998
 Seq. No.
 Seq. ID
                   LIB3177-070-P1-K1-G6
                   BLASTN
 Method
 NCBI GI
                   g2749918
 BLAST score
                   215
                   1.0e-117
 E value
 Match length
                   295
 % identity
                   98
                   Arabidopsis thaliana chromosome I BAC F3I6 genomic
 NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

E value

3.0e-65

```
Seq. No.
                   163999
Seq. ID
                   LIB3177-070-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g2062164
BLAST score
                   520
                   4.0e-53 ·
E value
Match length
                   100
                   100
% identity
NCBI Description
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
Seq. No.
                   164000
Seq. ID
                   LIB3177-070-P1-K1-G8
Method
                 BLASTN
NCBI GI
                   q3452262
BLAST score
                   473
E value
                   0.0e + 00
                   473
Match length
                   100
% identity
NCBI Description
                  Arabidopsis thaliana phosphatidylinositol 4-kinase mRNA,
                   partial cds
                   164001
Seq. No.
Seq. ID
                   LIB3177-070-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   q1361982
BLAST score
                   623
E value
                   4.0e-65
Match length
                   150
                   84
% identity
                   4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis
NCBI Description
                   thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase
                   [Arabidopsis thaliana]
Seq. No.
                   164002
Seq. ID
                   LIB3177-070-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   q115767
BLAST score
                   208
E value
                   1.0e-16
Match length
                   92
% identity
                   54
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >qi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
                   164003
Seq. No.
Seq. ID
                   LIB3177-070-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g4454036
BLAST score
                   624
```

-

```
Match length
                  129
                  89
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
                  164004
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  q3047074
BLAST score
                  44
                  1.0e-15
E value
                  120
Match length
% identity
                  84
NCBI Description Arabidopsis thaliana BAC F21E10
Seq. No.
                  164005
                  LIB3177-070-P1-K1-H12
Seq. ID
Method
                  BLASTX
                  g3860247
NCBI GI
BLAST score
                  450
E value
                  6.0e-45
Match length
                  92
% identity
                  93
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                  164006
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-H3
Method
                  BLASTX
                  g4468807
NCBI GI
BLAST score
                  569
                  6.0e-64
E value
Match length
                  142
% identity
                  84
                  (AL035601) cytochrome P450 monooxygenase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  164007
Seq. No.
                  LIB3177-070-P1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220637
BLAST score
                  419
E value
                  0.0e+00
Match length
                  423
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MIE1, complete sequence [Arabidopsis thaliana]
                  164008
Seq. No.
                  LIB3177-070-P1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3047074
BLAST score
                  439
                  0.0e+00
E value
Match length
                  439
% identity
                  100
```

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No.

164014

```
164009
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-H6
Method
                  BLASTX
                  g1769905
NCBI GI
BLAST score
                  328
                  4.0e-47
E value
Match length
                  106
                  91
% identity
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                  [Arabidopsis thaliana]
Seq. No.
                  164010
                  LIB3177-070-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678385
BLAST score
                  162
                  4.0e-11
E value
                  62
Match length
                  55
% identity
                  (AL049656) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  LIB3177-070-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q585536
BLAST score
                  724
E value
                  6.0e-77
Match length
                  135
                  99
% identity
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
NCBI Description
                  >gi 1362006 pir S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
                  [Arabidopsis thaliana] >gi 871990 emb CAA55786 (X79194)
                  thioglucosidase [Arabidopsis thaliana]
Seq. No.
                  164012
                  LIB3177-070-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3659491
BLAST score
                  404
                  0.0e+00
E value
Match length
                  462
                  100
% identity
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164013
                  LIB3177-071-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510376
BLAST score
                  210
                  1.0e-16
E value
Match length
                  106
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
```

```
LIB3177-071-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129639
BLAST score
                   549
E value
                   1.0e-56
Match length
                   108
% identity
                  99
NCBI Description
                  luminal binding protein (BiP) - Arabidopsis thaliana
                  >gi 1303695 dbj BAA12348 (D84414) luminal binding protein
                   (BiP) [Arabidopsis thaliana]
Seq. No.
                  164015
Seq. ID
                  LIB3177-071-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q3717948
BLAST score
                   446
E value
                  2.0e-44
Match length
                   106
                  89
% identity
                   (AJ005902) vag2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164016
Seq. ID
                  LIB3177-071-P1-K1-A2
Method
                  BLASTX
                  g1922944
NCBI GI
BLAST score
                   351
E value
                  2.0e-33
Match length
                  73
                  97
% identity
                   (AC000106) Strong similarity to Picea histone H2A
NCBI Description
                   (gb_X67819). ESTs gb_ATTS3874,gb_T46627,gb_T14194 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  164017
Seq. ID
                  LIB3177-071-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q2398679
BLAST score
                  407
E value
                  9.0e-40
Match length
                  84
                  90
% identity
                   (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                  synthase [Morinda citrifolia]
                  164018
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q3395441
BLAST score
                  513
                  3.0e-52
E value
Match length
                  98
% identity
                  100
NCBI Description
                  (AC004683) unknown protein [Arabidopsis thaliana]
                  164019
Seq. No.
                  LIB3177-071-P1-K1-A5
Seq. ID
```

BLASTX

Method

Seq. ID

```
NCBI GI
                  g2499973
BLAST `score
                  228
E value
                  1.0e-18
                  105
Match length
                  52
% identity
NCBI Description
                  PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
                  >gi_1465366_emb_CAA66701_ (X98078) photosystem II
                   [Arabidopsis thaliana]
Seq. No.
                  164020
                  LIB3177-071-P1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2160155
BLAST score
                  59
E value
                  1.0e-24
Match length
                  161
                  92
% identity
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  164021
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  q2088654
BLAST score
                  111
                  6.0e-18
E value
Match length
                  58
                  91
% identity
                   (AF002109) 60S acidic ribosomal protein PO isolog
NCBI Description
                   [Arabidopsis thaliana]
                  164022
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1769905
BLAST score
                  572
E value
                  3.0e-59
Match length
                  112
                  99
% identity
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                  [Arabidopsis thaliana]
                  164023
Seq. No.
                  LIB3177-071-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115783
                  600
BLAST score
E value
                  2.0e-62
Match length
                  116
                  98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  164024
Seq. No.
```

LIB3177-071-P1-K1-B1

E value

5.0e-52

```
Method
                  BLASTN
                  q4757411
NCBI GI
                  53
BLAST score
                  6.0e-22
E value
Match length
                  53
% identity
                  62
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXC7, complete sequence
                  164025
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-B10
Method
                  BLASTX
                  q115783
NCBI GI
BLAST score
                  601
                  1.0e-62
E value
Match length
                  113
                  100
% identity
                 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  164026
                  LIB3177-071-P1-K1-B11
Seq. ID
Method
                  BLASTX
                  a135860
NCBI GI
                  576
BLAST score
E value
                  1.0e-59
                  116
Match length
                  100
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic
                  protein gamma - Arabidopsis thaliana
                  >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi 166732
                  (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >gi_445129_prf__1908432B tonoplast intrinsic protein gamma
                  [Arabidopsis thaliana]
Seq. No.
                  164027
Seq. ID
                  LIB3177-071-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2494299
BLAST score
                  167
E value
                  1.0e-11
Match length
                  97
                  40
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT
NCBI Description
                  (EIF-2-BETA) >gi 1732361 (U80269) translation initiation
                  factor 2 beta [Malus domestica]
Seq. No.
                  164028
Seq. ID
                  LIB3177-071-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q417073
                  510
BLAST score
```

Seq. ID

```
Match length
                   116
% identity
                   84
                   GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
NCBI Description
                   >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC
                   1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate
                   synthase [Medicago sativa]
Seq. No.
                   164029
Seq. ID
                   LIB3177-071-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   q131360
BLAST score
                   241
                   3.0e-20
E value
Match length
                   61
% identity
                   80
NCBI Description
                   PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
                   >gi_81727_pir__S02115 photosystem II protein psbK precursor
                   white mustard chloroplast >gi_12209_emb_CAA31909
                   (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
Seq. No.
                   164030
Seq. ID
                   LIB3177-071-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g114591
BLAST score
                   393
                   2.0e-38
E value
Match length
                   80
% identity
                   100
                  ATP SYNTHASE EPSILON CHAIN >gi .81663 pir S01903
NCBI Description
                   H+-transporting ATP synthase (\overline{E}C 3.6.1.3\overline{4}) epsilon chain -
                   Arabidopsis thaliana chloroplast >gi_11334_emb_CAA31381_
                   (X12889) Cf1 ATPase epsilon subunit (AA 1 - 13\overline{2})
                   [Arabidopsis thaliana]
Seq. No.
                   164031
Seq. ID
                  LIB3177-071-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q2341034
                   424
BLAST score
                   6.0e-42
E value
                  87
Match length
                   99
% identity
NCBI Description
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  164032
                  LIB3177-071-P1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3869062
BLAST score
                  141
E value
                  2.0e-73
                  393
Match length
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K11I1, complete sequence [Arabidopsis thaliana]
                  164033
Seq. No.
```

LIB3177-071-P1-K1-B7

```
Method
                   BLASTX
NCBI GI
                   q3182922
BLAST score
                   233
E value
                   2.0e-19
Match length
                   51
% identity
                   94
NCBI Description
                  ADP-RIBOSYLATION FACTOR 1 >gi 1654142 (U38470) small
                   GTP-binding protein ARF [Brassica rapa]
Seq. No.
                   164034
Seq. ID
                   LIB3177-071-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   q3763930
BLAST score
                   415
E value
                   9.0e-41
Match length
                   137
% identity
                   66
                  (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   164035
Seq. ID
                  LIB3177-071-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1169201
BLAST score
                   60
E value
                  5.0e-32
Match length
                  107
% identity
                  76
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi 421830_pir S33707 DRT112 protein - Arabidopsis
                  thaliana >gi 1\overline{66}696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  164036
Seq. ID
                  LIB3177-071-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q1170170
BLAST score
                  349
E value
                  5.0e-33
                  91
Match length
                  76
% identity
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT3 (HD-ZIP PROTEIN 3)
NCBI Description
                  >gi_549889 (U09338) homeobox protein [Arabidopsis thaliana]
                  >gi_549890 (U09339) homeobox protein [Arabidopsis thaliana]
Seq. No.
                  164037
                  LIB3177-071-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132110
BLAST score
                  623
E value
                  4.0e-65
Match length
                  115
                  99
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195 emb CAA32702
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
```

thaliana]

Method

BLASTX

```
Seq. No.
                  164038
Seq. ID
                  LIB3177-071-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g4733953
BLAST score
                  110
E value
                  2.0e-55
Match length
                  150
% identity
                  94
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  164039
Seq. ID
                  LIB3177-071-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2335094
BLAST score
                  101
E value
                  2.0e-57
Match length
                  118
% identity
                  87
NCBI Description
                  (AC002339) putative polygalacturonase [Arabidopsis
                  thaliana]
Seq. No.
                  164040
Seq. ID
                  LIB3177-071-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q4469023
BLAST score
                  259
E value
                  8.0e-23
Match length
                  70
                  70
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                  164041
Seq. ID
                  LIB3177-071-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3885343
BLAST score
                  185
E value
                  7.0e-14
                  99
Match length
                  33
% identity
NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164042
                  LIB3177-071-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2062164
BLAST score
                  156
E value
                  1.0e-58
Match length
                  116
% identity
                  97
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
                  164043
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-C9
```

Match length

157

```
NCBI GI
                   q2398679
BLAST score
                   239
                   2.0e-20
E value
                   59
Match length
% identity
                   81
                   (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                   synthase [Morinda citrifolia]
Seq. No.
                   164044
Seq. ID
                   LIB3177-071-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   q2407281
                   119
BLAST score
                   7.0e-65
E value
Match length
                   132
% identity
                   91
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   164045
Seq. ID
                  LIB3177-071-P1-K1-D10
Method
                  BLASTN
NCBI GI
                   g517330
BLAST score
                   440
E valué
                   0.0e+00
Match length
                   448
% identity
                   100
NCBI Description A.thaliana mRNA for ribosomal protein S10
                  164046
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q2494174
BLAST score
                   615
                  3.0e-64
E value
                  126
Match length
                  97
% identity
                  GLUTAMATE DECARBOXYLASE 1 (GAD 1) >qi 497979 (U10034)
NCBI Description
                  glutamate decarboxylase [Arabidopsis thaliana]
Seq. No.
                  164047
                  LIB3177-071-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4741960
                  593
BLAST score
                  1.0e-61
E value
Match length
                  131
% identity
                  86
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
NCBI Description
                  164048
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  825
                  9.0e-89
E value
```

Match length

127

```
% identity
NCBI Description
                   thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                   thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   164049
Seq. ID
                  LIB3177-071-P1-K1-D4
Method
                  BLASTN
NCBI GI
                   q2760167
BLAST score
                  83
E value
                  7.0e-39
Match length
                   99
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCO15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164050
Seq. ID
                  LIB3177-071-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  q4757394
BLAST score
                  19
E value
                  2.0e-01
Match length
                  74
% identity
                  88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K1904, complete sequence
Seq. No.
                  164051
Seq. ID
                  LIB3177-071-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1710114
BLAST score
                  245
E value
                  4.0e-21
                  74
Match length
                  74
% identity
                 (U53865) PRH26 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164052
Seq. ID
                  LIB3177-071-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  51
E value
                  1.0e-64
Match length
                  121
% identity
                  99
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  164053
Seq. ID
                  LIB3177-071-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g1871199
BLAST score
                  240
E value
                  3.0e-20
```

```
% identity
                   40
NCBI Description (U91318) pM5 (3' partial) [Homo sapiens]
Seq. No.
                   164054
Seq. ID
                   LIB3177-071-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g2924792
BLAST score
                   502
E value
                   7.0e-51
Match length
                   120
% identity
                   82
NCBI Description (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
Seq. No.
                   164055
Seq. ID
                   LIB3177-071-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   589
E value
                   4.0e-61
Match length
                   114
                   97
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thalianal
Seq. No.
                  164056
Seq. ID
                  LIB3177-071-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g4220636
BLAST score
                  235
E value
                  1.0e-129
Match length
                  474
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFB16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164057
Seq. ID
                  LIB3177-071-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g3914740
BLAST score
                  443
                  3.0e-44
E value
                  95
Match length
                  92
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L26 >gi 2160300 dbj BAA18941
                  (D78495) ribosomal protein [Brassica rapa]
Seq. No.
                  164058
                  LIB3177-071-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132074
BLAST score
                  58
E value
                  2.0e-70
Match length
                  136
% identity
                  96
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
```

E value

7.0e-25

```
Al precursor - Arabidopsis thaliana
                   164059
Seq. No.
Seq. ID
                   LIB3177-071-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   q3169169
BLAST score
                   103
E value
                   1.0e-50
                   473
Match length
                   97
% identity
                   Arabidopsis thaliana chromosome II BAC F21P24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164060
Seq. ID
                   LIB3177-071-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g1709825
BLAST score
                   719
E value
                   2.0e-76
Match length
                   151
                   96
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                   164061
Seq. ID
                   LIB3177-071-P1-K1-E6
                   BLASTX
Method
NCBI GI
                   g1345681
BLAST score
                   96
                   8.0e-40
E value
Match length
                   106
                   72
% identity
                   CATALASE ISOZYME 3 >gi 862456 dbj BAA09508 (D55647)
NCBI Description
                   catalase [Cucurbita pepo]
Seq. No.
                   164062
Seq. ID
                   LIB3177-071-P1-K1-E7
Method
                   {\tt BLASTX}
NCBI GI
                   g548355
BLAST score
                   418
E value
                   4.0e-48
Match length
                   139
                   73
% identity
                   NITRATE REDUCTASE 1 (NR1) >gi_486751_pir_S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana
NCBI Description
                   >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase
                   [Arabidopsis thaliana] >gi_448286 prf__1916406A nitrate
                   reductase [Arabidopsis thaliana]
                   164063
Seq. No.
Seq. ID
                   LIB3177-071-P1-K1-E8
Method
                   BLASTX
NCBI GI.
                   g462174
BLAST score
                   54
```

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

```
Match length
                   95
 % identity
 NCBI Description
                   GERANYLGERANYL PYROPHOSPHATE SYNTHETASE PRECURSOR (GGPP
                   SYNTHETASE) (DIMETHYLALLYLTRANSFERASE /
                   GERANYLTRANSTRANSFERASE / FARNESYLTRANSTRANSFERASE
                   >gi_413730 (L25813) geranylgeranyl pyrophosphate synthase
                   [Arabidopsis thaliana]
 Seq. No.
                   164064
Seq. ID
                   LIB3177-071-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q4680212
BLAST score
                   165
E value
                   2.0e-11
Match length
                   106
% identity
                   41
NCBI Description (AF114171) hypothetical protein [Sorghum bicolor]
Seq. No.
                   164065
Seq. ID
                   LIB3177-071-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   g2618602
BLAST score
                   260
E value
                   1.0e-144
Match length
                   450
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164066
                  LIB3177-071-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529674
BLAST score
                   190
E value
                   3.0e-14
Match length
                   69
% identity
                   57
NCBI Description (AC002535) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164067
Seq. ID
                  LIB3177-071-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  q217842
BLAST score
                  33
E value
                  7.0e-09
Match length
                  61
% identity
                  89
NCBI Description A.thaliana mRNA for protein kinase
Seq. No.
                  164068
Seq. ID
                  LIB3177-071-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  q4587525
BLAST score
                  347
E value
                  1.0e-32
Match length
                  145
% identity
                  48
```

BLAST score

225

```
NCBI Description (AC007060) Contains the PF 00650 CRAL/TRIO
                   phosphatidyl-inositol-transfer protein domain. ESTs
                   gb_T76582, gb_N06574 and gb_Z25700 come from this gene.
                    [Arabidopsis thaliana]
Seq. No.
                   164069
Seq. ID
                   LIB3177-071-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q3273743
BLAST score
                   616
E value
                   3.0e-64
Match length
                   118
% identity
                   99
                   (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                   thaliana] >gi_3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
Seq. No.
                   164070
Seq. ID
                   LIB3177-071-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g4455183
BLAST score
                   116
E value
                   9.0e-31
Match length
                   123
% identity
                   60
                   (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   164071
                   LIB3177-071-P1-K1-F6
Seq.-ID
Method
                   BLASTN
NCBI GI
                   g4337026
BLAST score
                   73
E value
                   6.0e-33
Match length
                   161
% identity
                   88
NCBI Description Arabidopsis thaliana MFP2 mRNA, complete cds
Seq. No.
                   164072
                   LIB3177-071-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2618723
BLAST score
                   294
E value
                   1.0e-26
Match length
                   69
% identity
                   86
NCBI Description
                   (U49073) IAA17 [Arabidopsis thaliana] >gi_2921756
                   (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]
                   >gi_4389514_gb_AAB70451_ (AC000104) Identical to
Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs
                   gb H36782 and gb F14074 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   164073
Seq. ID
                  LIB3177-071-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g3688799
```

```
E value
                     5.0e-19
Match length
                     60
% identity
                     80
                     (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
NCBI Description
Seq. No.
                     164074
Seq. ID
                     LIB3177-071-P1-K1-F9
Method
                     BLASTN
NCBI GI
                     g1279568
BLAST score
                     41
                     1.0e-13
E value
Match length
                     72
% identity
                     96
NCBI Description Nicotiana acuminata chloroplast JLB region, 1-250bp
Seq. No.
                     164075
Seq. ID
                     LIB3177-071-P1-K1-G1
Method
                     BLASTX
NCBI GI
                     g4454036
BLAST score
                     796
E value
                     2.0e-85
Match length
                     147
% identity
                     99
                     (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                     thaliana]
                     164076
Seq. No.
Seq. ID
                    LIB3177-071-P1-K1-G10
Method
                    BLASTX
NCBI GI
                    q464707
BLAST score
                     556
E value
                    3.0e-57
Match length
                    110
% identity
                    99
                    40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                    protein S18.A - Arabidopsis thaliana
                    >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                     [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                    S18 ribosomal protein [Arabidopsis thaliana]
                    >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                     [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                    S18 ribosomal protein [Arabidopsis thaliana]
                    >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                    gb R30430 come from this gene. [Arabidopsis thaliana]
                    >gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal
                    protein [Arabidopsis thaliana]
Seq. No.
                    164077
Seq. ID
                    LIB3177-071-P1-K1-G11
Method
                    BLASTX
NCBI GI
                    g3885511
BLAST score
                    396
                    1.0e-38
E value
```

```
Match length
                  105
                  78
% identity
NCBI Description
                  (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
Seq. No.
                  164078
Seq. ID
                  LIB3177-071-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q4490331
BLAST score
                  417
E value
                  6.0e-41
Match length
                  97
% identity
                  84
NCBI Description
                  (AL035656) hypothetical protein [Arabidopsis thaliana]
                  164079
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q3510254
BLAST score
                  352
E value
                  3.0e-33
Match length
                  154
% identity
                  58
                  (AC005310) putative zinc transporter [Arabidopsis thaliana]
NCBI Description
                  164080
Seq. No.
Seq. ID
                  LIB3177-071-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q1749676
BLAST score
                  222
E value
                  4.0e-18
Match length
                  121
% identity
                  40
NCBI Description
                  (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
                  EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
Seq. No.
                  164081
Seq. ID
                  LIB3177-071-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q3914442
BLAST score
                  403
E value
                  2.0e-39
Match length
                  105
% identity
                  78
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                  164082
Seq. ID
                  LIB3177-071-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q3914940
BLAST score
                  125
E value
                  4.0e-09
Match length
                  70
% identity
                  56
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
```

```
[Spinacia oleracea]
Seq. No.
                   164083
Seq. ID
                   LIB3177-071-P1-K1-G8
Method
                  BLASTN
NCBI GI
                   q3402745
BLAST score
                   185
E value
                   1.0e-100
Match length
                   305
% identity
                   96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
                   (ESSAII project)
Seq. No.
                  164084
Seq. ID
                  LIB3177-071-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g2583108
BLAST score
                  498
E value
                  2.0e-50
Match length
                  132
                  78
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.
                  164085
Seq. ID
                  LIB3177-071-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1805652
BLAST score
                  717
E value
                  4.0e-76
Match length
                  140
% identity
                  100
NCBI Description
                  (X98927) thylakoid-bound ascorbate peroxidase [Arabidopsis
                  thaliana]
Seq. No.
                  164086
                  LIB3177-071-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                  353
E value
                  2.0e-33
Match length
                  134
% identity
NCBI Description
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
                  - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine
                  synthase [Spinacia oleracea]
Seq. No.
                  164087
Seq. ID
                  LIB3177-071-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q421826
BLAST score
                  655
E value
                  8.0e-69
Match length
                  147
% identity
                  83
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
```

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase

220 . .

```
>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
                   164088
 Seq. No.
 Seq. ID
                   LIB3177-071-P1-K1-H2
 Method
                   BLASTN
 NCBI GI
                   g4432847
 BLAST score
                   199
 E value
                   1.0e-108
 Match length
                   331
 % identity
                   90
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F13B15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   164089
 Seq. ID
                   LIB3177-071-P1-K1-H4
 Method
                   BLASTX
 NCBI GI
                   g2160158
 BLAST score
                   534
 E value
                   1.0e-54
 Match length
                   103
 % identity
                   99
 NCBI Description
                   (AC000132) Similar to elongation factor 1-gamma
                   (gb EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come
                   from this gene. [Arabidopsis thaliana]
 Seq. No.
                   164090
 Seq. ID
                   LIB3177-071-P1-K1-H5
 Method
                   BLASTN
 NCBI GI
                   g3046847
 BLAST score
                   152
 E value
                   6.0e-80
Match length
                   160
 % identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
 NCBI Description
                   K11J9, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   164091
 Seq. ID
                   LIB3177-071-P1-K1-H6
 Method
                   BLASTX
                   g4741952
 NCBI GI
 BLAST score
                   594
 E value
                   9.0e-62
Match length
                   117
 % identity
                   73
NCBI Description
                   (AF134126) Lhcb3 protein [Arabidopsis thaliana]
 Seq. No.
                   164092
 Seq. ID
                   LIB3177-071-P1-K1-H7
Method
                   BLASTN
NCBI GI
                   q4544435
BLAST score
                   139
E value
                   4.0e-72
a.Match length
                   436
 % identity
                   100
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F14M13 genomic
                   sequence, complete sequence
```

```
Seq. No.
                   164093
Seq. ID
                   LIB3177-071-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g1418990
BLAST score
                   575
E value
                   2.0e-59
Match length
                   155
% identity
                   68
NCBI Description
                   (Z75524) unknown [Lycopersicon esculentum]
Seq. No.
                   164094
Seq. ID
                   LIB3177-071-P1-K1-H9
Method
                   BLASTN
NCBI GI
                   g2246620
BLAST score
                   33
E value
                   3.0e-09
Match length
                   45
                   93
% identity
                   Arabidopsis thaliana salt-stress induced tonoplast
NCBI Description
                   intrinsic protein mRNA, complete cds
Seq. No.
                   164095
Seq. ID
                   LIB3177-072-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q2739371
BLAST score
                   541
E value
                   2.0e-55
Match length
                   110
% identity
                   95
NCBI Description
                   (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                   164096
Seq. ID
                   LIB3177-072-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q1703227
BLAST score
                   229
E value
                   7.0e-19
Match length
                   60
% identity
                   72
NCBI Description
                   ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
                   TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC
                   2.6.1.2) - barley >gi_469148_emb_CAA81231 (Z26322) alanine
                   aminotransferase [Hordeum vulgare]
Seq. No.
                   164097
                   LIB3177-072-P1-K1-A11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3212846
BLAST score
                   142
E value
                   6.0e-74
Match length
                   414
% identity
                   100
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F6E13 genomic
```

sequence, complete sequence [Arabidopsis thaliana]

Method

BLASTX

```
164098
Seq. No.
Seq. ID
                  LIB3177-072-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4455322
BLAST score
                  221
                  6.0e-18
E value
Match length
                   43
                  100
% identity
                  (AL035525) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  164099
Seq. No.
Seq. ID
                  LIB3177-072-P1-K1-A2
                  BLASTX
Method
NCBI GI
                  g3286693
                  703
BLAST score
                  2.0e-74
E value
                  139
Match length
                  100
% identity
                   (Y15433) 33 kDa polypeptide of oxygen-evolving complex
NCBI Description
                   (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                  164100
                  LIB3177-072-P1-K1-A4
Seq. ID
                  BLASTX
Method
                  q4467134
NCBI GI
                  83
BLAST score
                  2.0e-46
E value
                  96
Match length
                  99
% identity
                   (AL035540) protein kinase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164101
                  LIB3177-072-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4757409
BLAST score
                  278
                  1.0e-155
E value
                  462
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MVC8, complete sequence
                  164102
Seq. No.
                  LIB3177-072-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  g4567232
NCBI GI
BLAST score
                  342
                  4.0e-32
E value
                  72
Match length
                  96
% identity
                   (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
NCBI Description
                  thaliana]
                  164103
Seq. No.
Seq. ID
                  LIB3177-072-P1-K1-A7
```

Seq. ID

```
NCBI GI
                  q4406780
BLAST score
                  519
E value
                  5.0e-53
Match length
                  111
% identity
                  84
NCBI Description
                  (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                  164104
Seq. ID
                  LIB3177-072-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q282865
BLAST score
                  647
E value
                  6.0e-68
Match length
                  129
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  164105
Seq. ID
                  LIB3177-072-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q3746065
BLAST score
                  426
E value
                  4.0e-42
Match length
                  126
% identity
                  63
NCBI Description (AC005311) putative lipase [Arabidopsis thaliana]
Seq. No.
                  164106
Seq. ID
                  LIB3177-072-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q3914740
BLAST score
                  418
E value
                  4.0e-41
Match length
                  109
                  77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L26 >gi_2160300 dbj BAA18941
                  (D78495) ribosomal protein [Brassica rapa]
Seq. No.
                  164107
Seq. ID
                  LIB3177-072-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2062164
BLAST score
                  504
E value
                  4.0e-51
                  94
Match length
% identity
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  164108
```

LIB3177-072-P1-K1-B11

Method

BLASTX

```
Method
                   BLASTX
NCBI GI
                   g1200205
BLAST score
                   461
E value
                   4.0e-46
Match length
                   98
% identity
                   88
NCBI Description (X95753) DAG [Antirrhinum majus]
Seq. No.
                   164109
Seq. ID
                   LIB3177-072-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g3915023
BLAST score
                   513
E value
                   3.0e-52
Match length
                   134
% identity
                   75
NCBI Description
                   SUCROSE-PHOSPHATE SYNTHASE 1
                   (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1)
                   >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate
                   synthase [Citrus unshiu]
Seq. No.
                   164110
Seq. ID
                   LIB3177-072-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g3367536
BLAST score
                   412
E value
                   2.0e-40
Match length
                   100
% identity
                   88
NCBI Description
                   (AC004392) Contains similarity to symbiosis-related like
                   protein F1N20.80 gi_2961343 from A. thaliana BAC gb_AL022140. EST gb_T04695 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   164111
Seq. ID
                   LIB3177-072-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q4406775
BLAST score
                   270
E value
                   1.0e-23
Match length
                   119
% identity
                   42
NCBI Description
                  (AC006836) unknown protein [Arabidopsis thaliana]
Seq. No.
                   164112
                   LIB3177-072-P1-K1-B5
Seq. ID
Method
                   BLASTX
                   g4406804
NCBI GI
BLAST score
                   221
                   5.0e-18
E value
Match length
                   50
% identity
                   84
NCBI Description
                  (AC006304) proline iminopeptidase [Arabidopsis thaliana]
Seq. No.
                   164113
                   LIB3177-072-P1-K1-B6
Seq. ID
```

```
NCBI GI
                  g166867
BLAST score
                  697
E value
                  9.0e-74
Match length
                  151
% identity
                  89
                 (J05216) ribosomal protein S11 (probable start codon at bp
NCBI Description
                  67) [Arabidopsis thaliana]
Seq. No.
                  164114
Seq. ID
                  LIB3177-072-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2522417
BLAST score
                  153
E value
                  3.0e-10
Match length
                  29
% identity
                  100
NCBI Description (AF013984) alpha-tubulin [Cryptosporidium parvum]
Seq. No.
                  164115
Seq. ID
                  LIB3177-072-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g4218109
BLAST score
                  166
E value
                  2.0e-88
Match length
                  220
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16
                  (ESSAII project)
Seq. No.
                  164116
                  LIB3177-072-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3153207
BLAST score
                  531
E value
                  3.0e-54
Match length
                  129
                  82
% identity
NCBI Description (AF001949) ATHB-12 [Arabidopsis thaliana]
Seq. No.
                  164117
                 LIB3177-072-P1-K1-C1
Seq. ID
Method .
                  BLASTX
                  g1419090
NCBI GI
BLAST score
                  279
                  9.0e-25
E value
Match length
                  108
% identity
                  53
NCBI Description (X94968) 37kDa chloroplast inner envelope membrane
                 polypeptide precursor [Nicotiana tabacum]
Seq. No.
                 164118
                 LIB3177-072-P1-K1-C10
Seq. ID
Method
                 BLASTX
NCBI GI
                 q4583542
BLAST score
                 608
E value
                 3.0e-63
Match length
                 151
```

```
% identity
                   85
                   (Y16847) 16 kDa polypeptide of oxygen-evolving complex
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   164119
Seq. ID
                   LIB3177-072-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q1076289
BLAST score
                   731
E value
                   9.0e-78
Match length
                   138
% identity
                   98
                  amino acid permease AAP5 - Arabidopsis thaliana
NCBI Description
                   >gi_608673_emb_CAA54632_ (X77501) amino acid permease
                   [Arabidopsis thaliana]
Seq. No.
                   164120
Seq. ID
                   LIB3177-072-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2983755
BLAST score
                  279
E value
                  9.0e-25
Match length
                  86
% identity
                  60
                  (AE000735) ATP-dependent Clp protease proteolytic subunit
NCBI Description
                   [Aquifex aeolicus]
Seq. No.
                  164121
Seq. ID
                  LIB3177-072-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g4754913
BLAST score
                  313
E value
                  1.0e-52
Match length
                  140
% identity
                  74
NCBI Description
                  (AF132854) carbonic anhydrase isoform 1 [Gossypium
                  hirsutum]
Seq. No.
                  164122
Seq. ID
                  LIB3177-072-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3286693
BLAST score
                  657
E value
                  4.0e-69
Match length
                  131
                  100
% identity
NCBI Description
                  (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                  (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                  164123
Seq. ID
                  LIB3177-072-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  552
E value
                  9.0e-57
Match length
                  126
% identity
                  63
```

```
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                   164124
Seq. ID ···
                   LIB3177-072-P1-K1-C7
Method
                   BLASTX
                                                                        ÷.
NCBI GI
                   q4220523
BLAST score
                   823
E value
                   2.0e-88
Match length
                   154
% identity
                   99
NCBI Description
                  (AL035356) putative alliin lyase [Arabidopsis thaliana]
Seq. No.
                   164125
Seq. ID
                   LIB3177-072-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g166834
BLAST score
                   155
E value
                   4.0e-30
Match length
                   69
% identity
                   100
NCBI Description
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
                   activase [Arabidopsis thaliana] >gi_2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
Seq. No.
                   164126
Seq. ID
                   LIB3177-072-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g1351272
BLAST score
                   202
                   2.0e-16
E value
                   39
Match length
% identity
                   97
NCBI Description
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550
                   (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate
                   isomerase [Arabidopsis thaliana]
Seq. No.
                   164127
Seq. ID
                   LIB3177-072-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g4490725
BLAST score
                   787
                   3.0e-84
E value
Match length
                   150
                   100
% identity
NCBI Description
                   (AL035709) endo-xyloglucan transferase-like protein
                   [Arabidopsis thaliana]
                   164128
Seq. No.
Seq. ID
                  LIB3177-072-P1-K1-D10
Method
                  BLASTX
NCBI GI
                   g140285
BLAST score
                   207
                   3.0e-16
E value
Match length
                   42
                   95
% identity
NCBI Description HYPOTHETICAL 19 KD PROTEIN (ORF 168.)
```

```
tabacum]
                    164129
· Seq. No.
  Seq. ID
                    LIB3177-072-P1-K1-D11
  Method
                    BLASTX :
  NCBI GI
                    g2341034
  BLAST score
                    455
  E value
                    2.0e-45
  Match length
                    86
  % identity
                    100
  NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
. Seq. No.
                    164130
  Seq. ID
                    LIB3177-072-P1-K1-D12
  Method
                    BLASTN
  NCBI GI
                    g3985954
  BLAST score
                    398
  E value
                    0.0e + 00
  Match length
                    456
  % identity
                    98
  NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MRG21, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    164131
  Seq. ID
                    LIB3177-072-P1-K1-D2
  Method
                    BLASTN
  NCBI GI
                    g3510343
 BLAST score
                    443
 E value
                    0.0e + 00
 . Match length
                    454
  % identity
                    100
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MJC20, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    164132
  Seq. ID
                    LIB3177-072-P1-K1-D3
 Method .
                    BLASTX
  NCBI GI
                    q4587526
  BLAST score
                    242
  E value
                    2.0e-20
 Match length
                    130
  % identity
                    38
                    (AC007060) Strong similarity to F19I3.2 gi_3033375 putative
  NCBI Description
                    berberine bridge enzyme from Arabidopsis thaliana BAC
                    gb AC004238. ESTs gb_F19886, gb_Z30784 and gb_Z30785 come
                    from this gene
 Seq. No.
                    164133
 Seq. ID
                    LIB3177-072-P1-K1-D4
 Method
                    BLASTN
 NCBI GI
                    q2924505
 BLAST score
                    142
 E value
                    5.0e-74
 Match length
                    240
 % identity
                    100
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13
```

>gi_2924263_emb_CAA77415_ (Z00044) Ycf3 protein [Nicotiana

Seq. No.

164139

(ESSAII project)

```
Seq. No.
                   164134
                  LIB3177-072-P1-K1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                   179
E value
                   5.0e-96
Match length
                   316
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  164135
Seq. ID
                  LIB3177-072-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q3334144
BLAST score
                  336
E value
                  8.0e-35
Match length
                  114
% identity
                  68
NCBI Description G1/S-SPECIFIC CYCLIN C-TYPE >gi 1695698 dbj BAA13181
                  (D86925) C-type cyclin [Oryza sativa]
Seq. No.
                164136
Seq. ID
                  LIB3177-072-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g2264315
BLAST score
                  201
E value
                  1.0e-109
Match length
                  273
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRN17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164137
Seq. ID
                  LIB3177-072-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3402676
BLAST score
                  148
E value
                  2.0e-34
Match length
                  91
                  44
% identity
                  (AC004697) putative myrosinase-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164138
Seq. ID
                  LIB3177-072-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  723
E value
                  8.0e-77
Match length
                  134
% identity
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
```

Seq. No.

```
Seq. ID
                   LIB3177-072-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g461550
BLAST score
                   154
E value
                   2.0e-10
Match length
                   63
% identity
                   60
                   ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_81635_pir__B39732 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma-1 chain precursor, chloroplast -
                   Arabidopsis thaliana >gi_166632 (M61741) ATP synthase
                   gamma-subunit [Arabidopsis thaliana]
Seq. No.
                   164140
Seq. ID
                   LIB3177-072-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g4006827
BLAST score
                   231
E value
                   4.0e-19
Match length
                   145
% identity
                   41
NCBI Description
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                  164141
Seq. ID
                  LIB3177-072-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3687228
BLAST score
                   638
E value
                  8.0e-67
Match length
                  145
% identity
                  87
                  (AC005169) putative malate dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164142
Seq. ID
                  LIB3177-072-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g4220644
BLAST score
                  154
E value
                  4.0e-81
Match length
                  415
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXL8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164143
Seq. ID
                  LIB3177-072-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  g4733968
BLAST score
                  33
E value
                  3.0e-09
Match length
                  227
% identity
                  92
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F12P23 genomic
                  sequence, complete sequence
```

BLASTN

```
Seq. ID
                   LIB3177-072-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g2738248
BLAST score
                   711
E value
                   2.0e-75
Match length
                   151
% identity
                   91
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   164145
Seq. ID
                   LIB3177-072-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   q3702724
BLAST score
                   42
E value
                   2.0e-14
Match length
                   128
% identity
                   94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164146
Seq. ID
                   LIB3177-072-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q1363489
BLAST score
                   746
E value
                   1.0e-79
                   140
Match length
                   97
% identity
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi 984052 emb CAA61592 (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  164147
Seq. ID
                  LIB3177-072-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g132792
BLAST score
                  506
E value
                  2.0e~51
Match length
                  130
% identity
                  75
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi 343153 (M60953)
NCBI Description
                  ribosomal protein CL22 [Pelargonium hortorum]
Seq. No.
                  164148
Seq. ID
                  LIB3177-072-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q4741952
BLAST score
                  415
E value
                  8.0e-41
Match length
                  81
% identity
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  164149
Seq. ID
                  LIB3177-072-P1-K1-F1
```

```
NCBI GI
                  q2828182
BLAST score
                   335
                  0.0e+00
E value
Match length
                  335
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164150
Seq. ID
                  LIB3177-072-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  q2182286
BLAST score
                  401
                  0.0e + 00
E value
Match length
                  409
% identity
                  100
                  Sequence of BAC F20P5 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164151
Seq. ID
                  LIB3177-072-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1169867
BLAST score
                  162
E value
                  5.0e-11
Match length
                  123
% identity
                  13
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                  PROTEIN >gi 881422 (U27537) G beta like protein
                  [Dictyostelium discoideum]
Seq. No.
                  164152
Seq. ID
                  LIB3177-072-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  732
E value
                  7.0e-78
                  139
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  164153
Seq. ID
                  LIB3177-072-P1-K1-F2
                  BLASTX
Method
NCBI GI
                  g2129640
BLAST score
                  748
                  1.0e-79
E value
                  144
Match length
% identity
                  100
NCBI Description
                  magnesium chelatase chain - Arabidopsis thaliana
                  >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase
```

subunit [Arabidopsis thaliana]

```
Seq. No.
                   164154
Seq. ID
                   LIB3177-072-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2880051
BLAST score
                   348
E value
                   8.0e-33
Match length
                   101
% identity
                   71
NCBI Description
                  (AC002340) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   164155
Seq. ID
                   LIB3177-072-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g2494275
BLAST score
                   222
E value
                   4.0e-18
Match length
                   66
% identity
                   62
NCBI Description
                   ELONGATION FACTOR P (EF-P) >gi 1399829 (U59235) elongation
                   factor P [Synechococcus PCC7942]
Seq. No.
                   164156
Seq. ID
                   LIB3177-072-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g4689366
BLAST score
                   146
                   3.0e-09
E value
Match length
                 60
% identity
                   45
NCBI Description (AF134155) RING finger protein [Arabidopsis thaliana]
Seq. No.
                  164157
Seq. ID
                  LIB3177-072-P1-K1-F6
Method
                  BLASTX
                  g3269287
NCBI GI
BLAST score
                  286
E value
                  7.0e-26
Match length
                  95
% identity
                  61
NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]
Seq. No.
                  164158
Seq. ID
                  LIB3177-072-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2832623
BLAST score
                  640
E value
                  4.0e-67
Match length
                  125
% identity
                  98
NCBI Description
                  (AL021711) protein kinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  164159
Seq. ID
                  LIB3177-072-P1-K1-F8
Method
                  BLASTX
```

```
NCBI GI
                        q417103
BLAST score
                        441
                        5.0e-44
E value
                        89
Match length
                        99
% identity
NCBI Description
                        HISTONE H3.2, MINOR >gi 282871 pir S24346 histone
                        H3.3-like protein - Arabidopsis thaliana
                        >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
                        histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                        (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488567 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)
                        histone H3 variant H3.3 [Lycopersicon esculentum]
                        >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
                        >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana
                        tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa]
                        >gi_4038469_gb_AAC97380 (AF109910) histone H3 [Porteresia
                        coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
                        (AL035708) Histon H3 [Arabidopsis thaliana]
Seq. No.
                        164160
Seq. ID
                        LIB3177-072-P1-K1-F9
Method
                        BLASTX
NCBI GI
                        g4581146
BLAST score
                        471
E value
                        1.0e-59
Match length
                        135
                        91
% identity
NCBI Description
                        (AC006919) putative fructose-bisphosphate aldolase,
                        cytoplasmic [Arabidopsis thaliana]
Seq. No.
                        164161
Seq. ID
                        LIB3177-072-P1-K1-G1
Method
                        BLASTX
NCBI GI
                        g2281631
BLAST score
                        646
E value
                        9.0e-68
Match length
                        134
% identity
NCBI Description
                        (AF003096) AP2 domain containing protein RAP2.3
                        [Arabidopsis thaliana]
Seq. No.
                        164162
Seq. ID
                        LIB3177-072-P1-K1-G10
Method
                        BLASTX
NCBI GI
                        q2119846
BLAST score
                        657
E value
                        3.0e-69
                        124
Match length
                        98
% identity
                       chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
```

Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)

NCBI GI

BLASTX

q1480078

photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

```
Seq. No.
                  164163
Seq. ID
                  LIB3177-072-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q1363489
BLAST score
                  689
E value
                  8.0e-73
Match length
                  126
                  100
% identity
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi 984052 emb CAA61592 (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  164164
Seq. ID
                  LIB3177-072-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q3047082
BLAST score
                  262
                . 6.0e-23
E value ·
Match length
                  48
                  94
% identity
NCBI Description
                  (AF058914) similar to Vigna radiata pectinacetylesterase
                  precursor (GB:X99348) [Arabidopsis thaliana]
Seq. No.
                  164165
Seq. ID
                  LIB3177-072-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q480450
BLAST score
                  440
                  1.0e-43
E value
Match length
                  100
                  89
% identity
NCBI Description
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                  thaliana >gi_402552_emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
Seq. No.
                  164166
Seq. ID
                  LIB3177-072-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g4115387
BLAST score
                  605
E value
                  5.0e-63
Match length
                  148
% identity
NCBI Description
                  (AC005967) putative NADP-dependent
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  164167
Seq. ID
                  LIB3177-072-P1-K1-G4
```

```
BLAST score
                    631
                    5.0e-66
  E value
  Match length
                    126
  % identity
                    98
NCBI Description
                    (X99696) shaggy-like protein kinase iota [Arabidopsis
                    thaliana] >gi 2444277 gb AAB71545.1. (AF019927)
                    GSK3/shaggy-like protein kinase [Arabidopsis thaliana]
  Seq. No.
                    164168
  Seq. ID
                    LIB3177-072-P1-K1-G5
  Method
                    BLASTX
  NCBI GI
                    g2435511
  BLAST score
                    506
                    2.0e-51
  E value
  Match length
                    126
  % identity
                    82
  NCBI Description
                    (AF024504) contains similarity to prolyl 4-hydroxylase
                    alpha subunit [Arabidopsis thaliana]
  Seq. No.
                    164169
  Seq. ID
                    LIB3177-072-P1-K1-G6
  Method
                    BLASTN
  NCBI GI
                    q4469002
  BLAST score
                    190
  E value
                    1.0e-102
  Match length
                    459
  % identity
                    100
  NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                    (ESSA project)
  Seq. No.
                    164170
  Seq. ID
                    LIB3177-072-P1-K1-G7
  Method
                    BLASTX
  NCBI GI
                    g3212877
 BLAST score
                    488
 E value
                    3.0e-49
                    114
 Match length
  % identity
                    86
  NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]
  Seq. No.
                    164171
  Seq. ID
                    LIB3177-072-P1-K1-G8
 Method
                    BLASTX
  NCBI GI
                    g531829
  BLAST score
                    155
                    2.0e-10
  E value
 Match length
                    78
  % identity
                    47
                    (U12390) beta-galactosidase alpha peptide [cloning vector
 NCBI Description
                    pSport1]
                    164172
 Seq. No.
- Seq. ID
                    LIB3177-072-P1-K1-G9
                    BLASTX
 Method .
 NCBI GI
                    g115767
 BLAST score
                    736
                    2.0e-78
 E value
```

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```
Match length
                  140
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  164173
                  LIB3177-072-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741952
BLAST score
                  239
E value
                  9.0e-66
Match length
                  136
% identity
                  69
NCBI Description
                 (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  164174
Seq. ID
                  LIB3177-072-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2119846
BLAST score
                  739
                  1.0e-78
E value
Match length
                  141
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  164175
Seq. ID
                  LIB3177-072-P1-K1-H11
Method
                  BLASTX
                g2809255
NCBI GI
BLAST score
                  759
E value
                  5.0e-81
Match length
                  133
% identity
                  100
NCBI Description (AC002560) F21B7.24 [Arabidopsis thaliana]
Seq. No.
                  164176
Seq. ID
                  LIB3177-072-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  687
                  2.0e-72
E value
Match length
                  143
% idențity
                  96
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
```

a/b-binding protein ab165 - Arabidopsis thaliana

```
>gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   164177
Seq. ID
                   LIB3177-072-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q119350
BLAST score
                   237
E value
                   3.0e-63
Match length
                   133
                   97
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                   thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                   [Arabidopsis thaliana]
                   >gi_4581151 gb_AAD24635.1 AC006919 13 (AC006919) enolase
                   (2-phospho-D-glycerate hydroylase); identical to P25696
                   [Arabidopsis thaliana]
Seq. No.
                   164178
Seq. ID
                   LIB3177-072-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q515616
BLAST score
                   190
E value
                   6.0e-68
Match length
                   132
% identity
                   91
NCBI Description
                   (X61608) LHC II Type III chlorophyll a /b binding protein
                   [Brassica napus]
Seq. No.
                   164179
Seq. ID
                   LIB3177-072-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q1170939
BLAST score
                   596
E value
                   6.0e-62
Match length
                   139
% identity
                   84
NCBI Description
                   S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
                   ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                   >gi 1084408 pir S46540 methionine adenosyltransferase (EC
                   2.5.1.6) - tomato >gi 429108 emb CAA80867 (Z24743)
                   S-adenosyl-L-methionine synthetase [Lycopersicon
                   esculentum]
                   164180
Seq. No.
Seq. ID
                   LIB3177-072-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g1755156
BLAST score
                   619
E value
                   1.0e-64
Match length
                   136
% identity
NCBI Description (U75189) germin-like protein [Arabidopsis thaliana]
```

>gi_16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

Seq. ID

Method

NCBI GI

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```
>gi_1755158 (U75190) germin-like protein [Arabidopsis
thaliana] >gi_1755170 (U75196) germin-like protein
[Arabidopsis thaliana] >gi_1755172 (U75197) germin-like
protein [Arabidopsis thaliana] >gi_1755180 (U75201)
germin-like protein [Arabidopsis thaliana] >gi_1755190
(U75206) germin-like protein [Arabidopsis thaliana]
>gi_1934728 (U95035) germin-like protein [Arabidopsis
thaliana] >gi_4154285 (AF090733) germin-like protein 1
[Arabidopsis thaliana] >gi_4666248_dbj_BAA77207.1_ (D89055)
germin-like protein precursor [Arabidopsis thaliana]
```

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```
Seq. No.
                  164181
Seq. ID
                  LIB3177-072-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  g2191157
BLAST score
                  272
E value
                  1.0e-151
Match length
                  442
                  97
% identity
NCBI Description Arabidopsis thaliana BAC IG002P16
Seq. No.
                  164182
Seq. ID
                  LIB3177-072-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q1362078
BLAST score
                  455
E value
                  2.0e-45
Match length
                  113
                  74
% identity
                  endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
NCBI Description
                  - common nasturtium >gi 311835 emb CAA48324 (X68254)
                  cellulase [Tropaeolum majus]
Seq. No.
                  164183
                  LIB3177-072-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741960
BLAST score
                  543
E value
                  1.0e-55
Match length
                  122
% identity
                  85
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  164184
                  LIB3177-073-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4193320
BLAST score
                  420
E value
                  3.0e-41
Match length
                  121
                  69
% identity
NCBI Description (AF045473) histone deacetylase [Zea mays]
                  164185
Seq. No.
```

LIB3177-073-P1-K1-A11

BLASTX

q4567267

BLASTX

```
BLAST score
                   361
E value
                   2.0e-34
Match length
                   66
% identity
                   100
NCBI Description
                   (AC006841) putative zinc finger protein [Arabidopsis
                  thaliana]
                  164186
Seq. No.
Seq. ID
                  LIB3177-073-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q1168607
BLAST score
                  452
E value
                  5.0e-67
Match length
                  131
                  98
% identity
                  AUXIN-INDUCED PROTEIN AUX2-11 >gi 16197 emb CAA37526
NCBI Description
                   (X53435) Aux2-11 protein [Arabidopsis thaliana] >gi 454285
                   (L15450) auxin-responsive protein [Arabidopsis thaliana]
                  164187
Seq. No.
Seq. ID
                  LIB3177-073-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g4585935
BLAST score
                  726
E value
                  4.0e-77
Match length
                  138
                  99
% identity
                  (AC007211) putative chlorophyll A/B binding protein
NCBI Description
                   [Arabidopsis thaliana] >gi 4741946 gb AAD28770.1 AF134123 1
                   (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  164188
Seq. ID
                  LIB3177-073-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g4566614
BLAST score
                  181
E value
                  1.0e-13
Match length
                  49
                  71
% identity
NCBI Description
                  (AF112887) actin depolymerizing factor [Populus alba x
                  Populus tremula]
                  164189
Seq. No.
                  LIB3177-073-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2499973
BLAST score
                  226
                  1.0e-18
E value
Match length
                  105
% identity
                  52
NCBI Description
                  PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
                  >gi_1465366_emb_CAA66701 (X98078) .photosystem II
                  [Arabidopsis thaliana]
Seq. No.
                  164190
Seq. ID
                  LIB3177-073-P1-K1-A5
```

BLAST score

```
NCBI GI
                   g4376158
BLAST score
                   449
E value
                   6.0e-45
Match length
                   107
% identity
                   88
NCBI Description
                  (X98873) aspartate kinase [Arabidopsis thaliana]
Seq. No.
                   164191
Seq. ID
                   LIB3177-073-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g4127456
BLAST score
                   440
E value
                   9.0e-44
Match length
                   97
% identity
                   62
NCBI Description
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
Seq. No.
                   164192
Seq. ID
                   LIB3177-073-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   q136251
BLAST score
                   778
E value
                   3.0e-83
Match length
                   151
                   99
% identity
                  TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR
NCBI Description
                   >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20) <
                   beta chain - Arabidopsis thaliana >gi_166892 (M23872)
                   tryptophan synthase beta subunit [Arabidopsis thaliana]
Seq. No.
                   164193
Seq. ID
                  LIB3177-073-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g3985952
BLAST score
                   445
E value
                   0.0e + 00
Match length
                   469
% identity .
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MRC8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164194
                  LIB3177-073-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4406776
BLAST score
                  351
E value
                  0.0e + 00
Match length
                  462
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F14H2O genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164195
Seq. ID
                  LIB3177-073-P1-K1-B10
Method
                  BLASTN
                  g2618605
NCBI GI
```

```
E value
                   5.0e-11
Match length
                   119
% identity
                   89
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                   MUK11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164196
Seq. ID
                   LIB3177-073-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q4049349
BLAST score
                   508
E value
                   1.0e-51
Match length
                   122
% identity
                   (AL034567) ubiquinol-cytochrome c reductase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   164197
                   LIB3177-073-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q4646206
BLAST score
                   447
E value
                   3.0e-45
Match length
                   1.10
% identity
                   84
                   (AC007230) Contains similarity to gb_D13630 KIAA0005 gene
NCBI Description
                   from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360,
                   gb_T20468, gb_T45191 and gb_AI100459 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   164198
Seq. ID
                   LIB3177-073-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q132090
BLAST score
                   405
E value
                   8.0e-40
Match length
                   80
                   99
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   164199
Seq. ID
                   LIB3177-073-P1-K1-B3
Method
                   BLASTX
                   g115783
NCBI GI
BLAST score
                   566
                   2.0e-58
E value
Match length
                   109
% identity
                   98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
```

thaliana]

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

```
Seq. No.
                  164200
Seq. ID
                  LIB3177-073-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g2182287
BLAST score
                  89
E value
                  2.0e-42
Match length
                  162
                  95
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T7N9,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  164201
Seq. ID
                  LIB3177-073-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2760833
BLAST score
                  340
E value
                  2.0e-32
Match length
                  80
% identity
                  86
NCBI Description
                 (AC003105) unknown protein [Arabidopsis thaliana]
Seq. No.
                  164202
Seq. ID
                  LIB3177-073-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g114330
BLAST score
                  379
                  5.0e-37
E value
Match length
                  78
% identity
                  95
NCBI Description
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
                  >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
                  type 1, plasma membrane - Arabidopsis thaliana >gi_166746
                  (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis
                  thaliana]
Seq. No.
                  164203
                  LIB3177-073-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4835244
BLAST score
                  505
                  3.0e-51
E value
                  145
Match length
                  68
% identity
NCBI Description
                  (AL049862) putative mitochondrial protein [Arabidopsis
                  thaliana]
Seq. No.
                  164204
                  LIB3177-073-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1208408
BLAST score
                  515
                  2.0e-52
E value
                  98
Match length
                  98
% identity
NCBI Description
                  (D14824) nitrite reductase [Arabidopsis thaliana]
                  >gi_2289780 dbj BAA21672 (AB006032) nitrite reductase
```

```
nitrate reductase [Arabidopsis thaliana]
Seq. No.
                   164205
Seq. ID
                   LIB3177-073-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g1363489
BLAST score
                   281
E value
                   2.0e-25
Match length
                   57
% identity
                   93
NCBI Description
                   thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                   thaliana >gi 984052_emb_CAA61592 (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   164206
                   LIB3177-073-P1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539460
BLAST score
                   173
E value
                   2.0e-12
Match length
                   110
% identity
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   164207
Seq. ID
                   LIB3177-073-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g4567269
BLAST score
                   128
E value
                   6.0e-44
Match length
                  100
% identity
                   98
NCBI Description
                  (AC006841) unknown protein [Arabidopsis thaliana]
Seq. No.
                  164208
Seq. ID
                  LIB3177-073-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g2109292
BLAST score
                  240
E value
                  1.0e-132
Match length
                  264
% identity
                  98
NCBI Description
                  Arabidopsis thaliana serine/threonine protein kinase mRNA,
                  complete cds
Seq. No.
                  164209
                  LIB3177-073-P1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1732569
BLAST score
                  75
E value
                  5.0e-34
Match length
                  154
% identity
NCBI Description
                  Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA,
```

[Arabidopsis thaliana] >gi 4335728 gb AAD17406 (AC006248)

complete cds

```
Seq. No.
                  164210
Seq. ID
                  LIB3177-073-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2306917
BLAST score
                   467
E value
                  6.0e-47
Match length
                  113
% identity
NCBI Description
                  (AF003728) plasma membrane intrinsic protein [Arabidopsis
                  thaliana]
Seq. No.
                  164211
Seq. ID
                  LIB3177-073-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  a3335340
BLAST score
                  385
E value
                  3.0e - 37
Match length
                  76
% identity
NCBI Description
                  (AC004512) Strong similarity to xylglucan
                  endo-transglycolsylase (TCH4) gene gb_U27609, first exon
                  contains strong similarity to meri 5 gene gb Z17989 from A.
                  thaliana. EST gb_N37583 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  164212
Seq. ID
                  LIB3177-073-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g4757409
BLAST score
                  116
E value
                  2.0e-58
Match length
                  458
% identity
                  100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MVC8, complete sequence
Seq. No.
                  164213
Seq. ID
                  LIB3177-073-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1066163
BLAST score
                  243
E value
                  1.0e-20
Match length
                  51
% identity
                  92
NCBI Description
                  (X93015) glyoxysomal beta-ketoacyl-thiolase [Brassica
                  napus]
Seq. No.
                  164214
Seq. ID
                  LIB3177-073-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g119194
BLAST score
                  449
E value
                  5.0e-45
Match length
                  93.
                  96
% identity
NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                  >gi 81607 pir S09152 translation elongation factor Tu
```

```
precursor, chloroplast - Arabidopsis thaliana
>gi_22565_emb_CAA36498_ (X52256) elongation factor Tu
precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A
                    elongation factor Tu [Arabidopsis thaliana]
Seq. No.
                    164215
Seq. ID
                    LIB3177-073-P1-K1-D4
Method
                    BLASTX
NCBI GI
                    q4240120
BLAST score
                    375
E value
                    2.0e-36
Match length
                    78
% identity
                    90
                    (AB007801) cytochrome b5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    164216
Seq. ID
                    LIB3177-073-P1-K1-D5
Method
                    BLASTX
NCBI GI
                    q1495269
BLAST score
                    562
E value
                    6.0e-58
Match length
                    136
% identity
                    80
NCBI Description
                    (X97829) product similar to ccr protein, Citrus paradisi;
                    PIR: S52663 [Arabidopsis thaliana]
                    >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis
                    thalianal
                    164217
Seq. No.
Seq. ID
                    LIB3177-073-P1-K1-D6
Method
                    BLASTX
NCBI GI
                    g2271465
BLAST score
                    141
E value
                    4.0e-09
Match length
                    57
% identity
                    49
NCBI Description
                    (AF009563) 3-ketoacyl-CoA synthase [Brassica napus]
Seq. No.
                    164218
Seq. ID
                    LIB3177-073-P1-K1-D7
Method
                    BLASTN
NCBI GI
                    g2252823
BLAST score
                    246
E value
                    1.0e-136
Match length
                    258
% identity
                    99
NCBI Description
                   Arabidopsis thaliana BAC IG005I10
Seq. No.
                    164219
Seq. ID
                    LIB3177-073-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g2827552
BLAST score
                    482
E value
                    8.0e-52
                    143
Match length
% identity
                    35
NCBI Description
                   (AL021635) predicted protein [Arabidopsis thaliana]
```

P. .

```
Seq. No.
                   164220
Seq. ID
                   LIB3177-073-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g543841
BLAST score
                   241
E value
                   2.0e-20
Match length
                   69
% identity
                   76
                   ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__$28875
NCBI Description
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi_4630747_gb_AAD26597.1 AC007236 2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                   164221
Seq. ID
                   LIB3177-073-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g3158376
BLAST score
                   244
                   4.0e-21
E value
Match length
                   51
% identity
                   90
NCBI Description
                  (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                   164222
Seq. ID
                   LIB3177-073-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g189496
BLAST score
                   564
E value
                   4.0e-58
Match length
                   151
% identity
                   68
NCBI Description
                   (M88565) p58 protein kinase [Homo sapiens]
Seq. No.
                  164223
Seq. ID
                  LIB3177-073-P1-K1-E2
Method
                  BLASTX
NCBI GI.
                  g228210
BLAST score
                  449
E value
                  7.0e-45
Match length
                  109
% identity
                  78
NCBI Description
                  granule-bound starch synthase [Solanum tuberosum]
Seq. No.
                  164224
                  LIB3177-073-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618603
BLAST score
                  247
E value
                  1.0e-136
Match length
                  333
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MSL3, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   164225
 Seq. ID
                   LIB3177-073-P1-K1-E5
 Method
                   BLASTX
 NCBI GI
                   g1172873
 BLAST score
                   48
 E value
                   3.0e-29
 Match length
                  . 77
 % identity
                   87
                   CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
 NCBI Description
                   drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                   precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                   (D13043) thiol protease [Arabidopsis thaliana]
 Seq. No.
                   164226
 Seq. ID
                   LIB3177-073-P1-K1-E6
 Method
                   BLASTX
 NCBI GI
                   g4056502
 BLAST score
                   336
 E value
                   1.0e-31
 Match length
                   98
 % identity
                   73
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
 NCBI Description
Seq. No.
                   164227
 Seq. ID
                   LIB3177-073-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g4586256
BLAST score
                   203
E value
                   7.0e-16
Match length
                   58
                   71
 % identity
NCBI Description
                   (AL049640) probable photosystem I chain XI precursor
                   [Arabidopsis thaliana]
Seq. No.
                   164228
Seq. ID
                   LIB3177-073-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g2119848
BLAST score
                   772
E value
                   1.0e-82
Match length
                   151
 % identity
NCBI Description
                   chlorophyll a/b-binding protein type I precursor Lhb1B1 -
                   Arabidopsis thaliana >gi 16366 emb CAA45789 (X64459)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128229 (AC004077) putative
                   photosystem II type I chlorophyll a/b binding protein
                   [Arabidopsis thaliana] >gi_3337372 (AC004481) putative
                   photosystem II type I chlorophyll a/b binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   164229
Seq. ID
                  LIB3177-073-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g404670
BLAST score
                  193
                   6.0e-15
E value
```

E value

5.0e-75

```
Match length
                   54
% identity
                   76
                   (L21154) phytochrome A [Arabidopsis thaliana] >gi 3482934
NCBI Description
                   (AC003970) phytochrome A [Arabidopsis thaliana]
Seq. No.
                   164230
Seq. ID
                   LIB3177-073-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q132074
BLAST score
                   699
E value
                   5.0e-74
Match length
                   136
% identity
                   93
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   164231
Seq. ID
                   LIB3177-073-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   q3763944
BLAST score
                   83
E value
                   5.0e=39
Match length
                   217
% identity
                   94
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                   (ESSAII project)
Seq. No.
                   164232
Seq. ID
                   LIB3177-073-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q3033375
BLAST score
                   274
E value
                   3.0e-24
                   134
Match length
                   39
% identity
NCBI Description
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
                   thaliana]
Seq. No.
                   164233
Seq. ID
                  LIB3177-073-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3983125
BLAST score
                   560
E value
                  1.0e-57
Match length
                  138
                  80
% identity
NCBI Description
                   (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  164234
Seq. ID
                  LIB3177-073-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  708
```

BLASTX

```
Match length
                    130
 % identity
                    100
                    thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
 NCBI Description
                    thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                    glucohydrolase [Arabidopsis thaliana]
 Seq. No.
                    164235
 Seq. ID
                    LIB3177-073-P1-K1-F5
 Method
                    BLASTN
 NCBI GI
                    g4559375
 BLAST score
                    72
 E value
                    2.0e-32
 Match length
                    178
 % identity
 NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic
                   sequence, complete sequence
 Seq. No.
                   164236
 Seq. ID
                   LIB3177-073-P1-K1-F6
 Method
                   BLASTX
 NCBI GI
                   g115767
 BLAST score
                   345
 E value
                   8.0e-33
 Match length
                   82
 % identity
                   83
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   164237
Seq. ID
                   LIB3177-073-P1-K1-F8
Method
                   BLASTN
NCBI GI
                   g2264321
BLAST score
                   337
E value
                   0.0e+00
Match length
                   385
% identity
                   97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                   MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164238
Seq. ID
                   LIB3177-073-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g2245093
BLAST score
                   71
E value
                   4.0e-15
Match length
                  52
% identity
                   87
NCBI Description (Z97343) membrane channel protein [Arabidopsis thaliana]
Seq. No.
                  164239
Seq. ID
                  LIB3177-073-P1-K1-G1
```

BLASTX

```
NCBI GI
                   q117238
BLAST score
                   447
E value
                   2.0e-44
Match length
                   117
% identity
                   78
                   MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN
N€BI Description
                   CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE)
                   >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast
                   - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411)
                   protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana]
                   >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42
                   precursor, chloroplast [Arabidopsis thaliana]
                   >gi_4490290_emb_CAB38561.1 (X51799) chloroplast protein
[Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene
                   [Euglena gracilis]
Seq. No.
                   164240
Seq. ID
                   LIB3177-073-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q2119846
BLAST score
                   693
E value
                   2.0e-73
Match length
                   134
% identity
NCBI Description
                   chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364_emb_CAA45790 (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi_3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   164241
Seq. ID
                   LIB3177-073-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   g3080430
BLAST score
                   243
E value
                   1.0e-134
Match length
                   431
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
                   (ESSAII project)
Seq. No.
                   164242
Seq. ID
                   LIB3177-073-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   g3033373
BLAST score
                   106
                   1.0e-52
E value
                   282
Match length
                   85
% identity
                  Arabidopsis thaliana chromosome II BAC F19I3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164243
Seq. ID
                  LIB3177-073-P1-K1-G2
```

```
NCBI GI
                    q132074
BLAST score
                    618
E value
                    1.0e-64
Match length
                    112
                    100
% identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    Al precursor - Arabidopsis thaliana
Seq. No.
                    164244
Seq. ID
                    LIB3177-073-P1-K1-G3
Method
                    BLASTX
NCBI GI
                    q3947448
BLAST score
                    215
E value
                    3.0e-17
                    141
Match length
                    39
% identity
                    (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA
NCBI Description
                    EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3
                    comes from this gene; cDNA EST yk475f6.5 comes from this
                    gene; cDNA EST yk499g5.5 comes from this gene
                    [Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes
                    from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5
                    comes from this gene [Caenorhabditi
                  164245
Seq. No.
                    LIB3177-073-P1-K1-G4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115385
BLAST score
                    236
                    6.0e-20
E value
                    65
Match length
                    77
% identity
                    CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                    (CAB-4) (LHCP) >qi 166646 (M63931) light-harvesting
                    chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                    164246
Seq. ID
                    LIB3177-073-P1-K1-G5
Method
                    BLASTX
NCBI GI
                    q115767
BLAST score
                    724
                    6.0e-77
E value
Match length
                    139
                    99
% identity .
NCBI Description
                    CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana
                    >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                    protein (LHCP AB 65) [Arabidopsis thaliana]
                    >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                    protein (LHCP AB 180) [Arabidopsis thaliana]
```

164247

Seq. No.

Seq. ID

```
Seq. ID
                  LIB3177-073-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g3859658
BLAST score
                   459
E value
                  0.0e + 00
                   459
Match length
% identity
                  88
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
                   (ESSAII project)
Seq. No.
                  164248
Seq. ID
                  LIB3177-073-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1169201
BLAST score
                  563
E value
                  5.0e-58
Match length
                  138
% identity
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi_421830_pir__S33707 DRT112 protein - Arabidopsis
                  thaliana > gi_1 \overline{66}696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  164249
Seq. ID
                  LIB3177-073-P1-K1-G9 . .
Method
                  BLASTN
NCBI GI
                  q3193282
BLAST score
                  87
                  3.0e-41
E value
Match length
                  320
% identity
                  94
NCBI Description Arabidopsis thaliana BAC T14P8
Seq. No.
                  164250
Seq. ID
                  LIB3177-073-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q166867
BLAST score
                  695
E value
                  2.0e-73
Match length
                  152
% identity
                  89
                  (J05216) ribosomal protein S11 (probable start codon at bp
NCBI Description
                  67) [Arabidopsis thaliana]
Seq. No.
                  164251
                  LIB3177-073-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82512
BLAST score
                  538
E value
                  3.0e-55
Match length
                  109
% identity
                  43
NCBI Description ubiquitin precursor - rice (fragment)
                  >gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza
                  sativa]
                  164252
Seq. No.
```

LIB3177-073-P1-K1-H11

Match length

```
Method
                   BLASTX
NCBI GI
                   q4115387
BLAST score
                   500
E value
                   1.0e-50
Match length
                   98
% identity
                   99
NCBI Description
                   (AC005967) putative NADP-dependent
                   glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                   thaliana]
Seq. No.
                   164253
Seq. ID
                  LIB3177-073-P1-K1-H12
Method
                  BLASTX
NCBI GI
                   g2119846
BLAST score
                  388
                   1.0e-37
E value
Match length
                   74
% identity
                   100
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi 3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
                  164254
Seq. No.
Seq. ID
                  LIB3177-073-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  707
E value
                   6.0e-75
Match length
                  152
                  90
% identity
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi_984052_emb_CAA61592 (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  164255
Seq. ID
                  LIB3177-073-P1-K1-H3
                  BLASTX
Method
NCBI GI
                  q417381
BLAST score
                  438
E value
                  1.0e-43
Match length
                  89
% identity
                  97
NCBI Description
                  NITRILASE 1 >gi_99738 pir S22398 nitrilase (EC 3.5.5.1) -
                  Arabidopsis thaliana \overline{>}gi_{16400} emb_CAA45041_ (X63445)
                  nitrilase I [Arabidopsis thaliana]
Seq. No.
                  164256
Seq. ID
                  LIB3177-073-P1-K1-H4
Method
                  BLASTN .
NCBI GI
                  g555977
BLAST score
                  318
E value
                  1.0e-179
```

BLASTN

```
98
% identity
NCBI Description
                  Arabidopsis thaliana metallothionein-like protein (AtMT-q)
                  mRNA, complete cds
Seq. No.
                  164257
Seq. ID
                  LIB3177-073-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g4467359
BLAST score
                  513
E value
                  3.0e-52
Match length
                  109
% identity
                  89
                  (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164258
Seq. ID
                  LIB3177-073-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  q4539448
BLAST score
                  217
E value
                  1.0e-118
Match length
                  217
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23
NCBI Description
                  (ESSA project)
                  164259
Seq. No.
Seq. ID
                  LIB3177-073-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2119848
BLAST score
                  413
                  2.0e-40
E value
                  116
Match length
                  78
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B1 -
                  Arabidopsis thaliana >gi 16366 emb CAA45789 (X64459)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128229 (AC004077) putative
                  photosystem II type I chlorophyll a/b binding protein
                  [Arabidopsis thaliana] >gi_3337372 (AC004481) putative
                  photosystem II type I chlorophyll a/b binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  164260
                  LIB3177-073-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4469002
                  293
BLAST score
E value
                  1.0e-164
Match length
                  464
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                  (ESSA project)
Seq. No.
                  164261
                  LIB3177-074-P1-K1-A4
Seq. ID
```

· .

BLAST score

```
NCBI GI
                  g2245073
BLAST score
                   63
                   4.0e-27
E value
Match length
                  185
% identity
                  79
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  164262
Seq. ID
                  LIB3177-074-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  g4097337
BLAST score
                  188
E value
                  1.0e-101
Match length
                  235
% identity
                  99
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                  164263
Seq. No.
Seq. ID
                  LIB3177-074-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g1020154
BLAST score.
                  157
                  4.0e-83
E value
Match length
                  265
% identity
                  89
                  Arabidopsis thaliana clone myb6 DNA-binding protein mRNA,
NCBI Description
                  complete cds
Seq. No.
                  164264
Seq. ID
                  LIB3177-074-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g16375
BLAST score
                  41
E value
                  5.0e-14
Match length
                  163
                  78
% identity
                  A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding
NCBI Description
                  protein
Seq. No.
                  164265
Seq. ID
                  LIB3177-074-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2623302
BLAST score
                  586
E value
                  9.0e-61
                  125
Match length
                  92
% identity
NCBI Description
                  (AC002409) putative cysteine proteinase inhibitor
                  [Arabidopsis thaliana]
Seq. No.
                  164266
Seq. ID
                  LIB3177-074-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  g710625
```

```
E value
                  1.0e-123
Match length
                  266
% identity
                  95
NCBI Description Arabidopsis thaliana mRNA for ERD15 protein, complete cds
                  164267
Seq. No.
Seq. ID
                  LIB3177-074-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g3426033
BLAST score
                  172
E value
                  6.0e-92
Match length
                  344
% identity
                  99
NCBI Description Arabidopsis thaliana chromosome II BAC F12C20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164268
Seq. ID
                  LIB3177-074-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2760834
BLAST score
                  694
E value
                  2.0e-73
Match length
                  143
% identity
                  95
NCBI Description
                 (AC003105) putative nitrate transporter [Arabidopsis
                  thaliana]
                  164269
Seq. No.
Seq. ID
                  LIB3177-074-P1-K1-C6
Method
                  BLASTX
                  g3201613
NCBI GI
BLAST score
                  375
E value
                  3.0e-36
Match length
                  100
                  77
% identity
NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]
Seq. No.
                  164270
Seq. ID
                  LIB3177-074-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g4165340
BLAST score
                  184
                  3.0e-99
E value
                  241
Match length
                  96
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164271
Seq. ID
                  LIB3177-074-P1-K1-D1
                  BLASTX
Method
NCBI GI
                  g1345595
BLAST score
                 668
                  2.0e-70
E value
                  150
Match length
                  89
% identity
NCBI Description 14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
```

```
protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14
                  lambda [Arabidopsis thaliana]
Seq. No.
                  164272
                  LIB3177-074-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3492855
BLAST score
                  35
                  1.0e-10
E value
                  79
Match length
% identity
                  84
                  Genomic sequence for Arabidopsis thaliana BAC F20N2,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  164273
Seq. No.
                  LIB3177-074-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4544419
BLAST score
                  575
E value
                  2.0e-59
Match length
                  146
% identity
                  81
                  (AC006955) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164274
                  LIB3177-074-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201613
BLAST score
                  562
E value
                  6.0e-58
                  108
Match length
% identity
                  99
                  (AC004669) glutathione S-transferase [Arabidopsis thaliana]
NCBI Description
                  164275
Seq. No.
                  LIB3177-074-P1-K1-E11
Seq. ID
Method
                  BLASTX
                  g2246621
NCBI GI
                  328
BLAST score
E value
                  5.0e-31
                  78
Match length
                  83
% identity
NCBI Description
                  (AF004393) salt-stress induced tonoplast intrinsic protein
                  [Arabidopsis thaliana]
Seq. No.
                  164276
Seq. ID
                  LIB3177-074-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q1172977
                  344
BLAST score
E value
                  1.0e-32
                  87
Match length
                  82
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
```

>gi_1084332_pir__S53727 14-3-3-like protein (ATF1) Arabidopsis thaliana >gi 953221 (U02565) 14-3-3-like

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.

```
Seq. No.
                  164277
Seq. ID
                  LIB3177-074-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g70753
BLAST score
                  375
                  3.0e-36
E value
Match length
                  79
% identity
                  95
NCBI Description histone H3 - garden pea >gi_82610 pir S00373 histone H3 -
Seq. No.
                  164278
Seq. ID
                  LIB3177-074-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  266
E value
                  1.0e-23
Match length
                  65
% identity
                  74
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  164279
Seq. ID
                  LIB3177-074-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q4220514
BLAST score
                  286
                  7.0e-26
E value
Match length
                  80
% identity
                  64
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  164280
Seq. No.
Seq. ID
                  LIB3177-074-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q585536
BLAST score
                  425
                  5.0e-42
E value
Match length
                  92
                  86
% identity
NCBI Description
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
                  >gi 1362006 pir__S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
                  [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)
                  thioglucosidase [Arabidopsis thaliana]
                                                                    Seq. No.
                  164281
                  LIB3177-074-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q512400
BLAST score
                  205
                  2.0e-38
E value
Match length
                  130
% identity
                  66
NCBI Description (X74947) annexin [Medicago sativa]
```

Seq. ID

```
Seq. ID
                   LIB3177-074-P1-K1-F7
Method
                   BLASTN
NCBI GI
                   g2351064
BLAST score
                   368
E value
                   0.0e + 00
Match length
                   432
% identity
                   96
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164283
Seq. ID
                   LIB3177-074-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g4559372
BLAST score
                   652
E value
                   2.0e-68
Match length
                   140
% identity
                   87
                   (AC006585) putative CONSTANS protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative
                   CONSTANS protein [Arabidopsis thaliana]
Seq. No.
                   164284
Seq. ID
                   LIB3177-074-P1-K1-F9
Method
                   BLASTN
NCBI GI
                   g4454004
BLAST score
                   40
E value
                   2.0e-13
Match length
                   155
% identity
                   77
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
                  (ESSAII project)
Seq. No.
                  164285
Seq. ID
                  LIB3177-074-P1-K1-G1
Method
                   BLASTX
NCBI GI
                  g2446981
BLAST score
                   558
E value
                   1.0e-57
Match length
                   108
% identity
                   99
                  (AB005560) AtGDI2 [Arabidopsis thaliana]
NCBI Description
                  >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis
                  thaliana]
Seq. No.
                  164286
Seq. ID
                  LIB3177-074-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  g1465365
BLAST score
                  45
E value
                  2.0e-16
Match length
                  104
% identity
                  85
NCBI Description
                  A.thaliana mRNA for subunit T of photosystem II
Seq. No.
                  164287
```

LIB3177-074-P1-K1-G12

Seq. No.

```
Method
                   BLASTX
NCBI GI
                   q120675
BLAST score
                   387
E value
                   1.0e-37
Match length
                   97
% identity
                   78
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                   >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                   alba]
Seq. No.
                   164288
Seq. ID
                   LIB3177-074-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g4263525
BLAST score
                   600
                   2.0e-62
E value
                   139
Match length
% identity
                   85
NCBI Description
                   (AC004044) putative photosystem I reaction center subunit
                   II precursor [Arabidopsis thaliana]
Seq. No.
                  164289
Seq. ID
                  LIB3177-074-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g3461810
BLAST score
                  54
È value
                  8.0e-22
Match length
                  160
% identity
                  79
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T17M13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164290
Seq. ID
                  LIB3177-074-P1-K1-H10
                  BLASTN
Method
NCBI GI
                  g3492855
BLAST score
                  52
E value
                  2.0e-20
Match length
                  193
% identity
                  81
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F20N2,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  164291
Seg. ID
                  LIB3177-074-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  g2739359
BLAST score
                  128
E value
                  1.0e-65
Match length
                  413
% identity
                  97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9J22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. ID

```
Seq. ID
                   LIB3177-074-P1-K1-H3
 Method
                   BLASTN
 NCBI GI
                   q972916
 BLAST score
                   45
 E value
                   3.0e-16 <sub>√</sub>
Match length
                   254
 % identity
                   76
 NCBI Description Arabidopsis thaliana IAA7 (IAA7) gene, complete cds
Seq. No.
                   164293
Seq. ID
                   LIB3177-074-P1-K1-H4
Method
                  . BLASTN
NCBI GI
                   g4455321
BLAST score
                   200
E value
                   1.0e-108
Match length
                   361
% identity
                   96
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
                   (ESSAII project)
Seq. No.
                   164294
Seq. ID
                   LIB3177-074-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g3688799
BLAST score
                   380
                   1.0e-36
E value
Match length
                   112
% identity
                   71
NCBI Description
                   (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
                   thaliana]
Seq. No.
                   164295
Seq. ID
                  LIB3177-074-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   q416681
BLAST score
                   202
E value
                   9.0e-16
Match length
                   96
% identity
                   39
NCBI Description
                  ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
                  >gi_280404_pir__S26198 H+-transporting ATP synthase (EC
                  3.6.1.34) delta chain precursor, chloroplast - common
                  tobacco >gi_19787_emb CAA45153 (X63607) chloroplast ATP
                  synthase (delta subunit) [Nicotiana tabacum]
Seq. No.
                  164296
Seq. ID
                  LIB3177-074-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g3075395
BLAST score
                  301
E value
                  2.0e-27
Match length
                  73
% identity
                  78
NCBI Description
                  (AC004484) nodulin-35 homologue [Arabidopsis thaliana]
Seq. No.
                  164297
```

LIB3177-074-P1-K1-H8

% identity

```
Method
                   BLASTX
 NCBI GI
                   q4490732
 BLAST score
                   366
 E value
                   4.0e-35
 Match length :
                   78
 % identity
                   91
                   (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
 NCBI Description
                   protein [Arabidopsis thaliana]
 Seq. No.
                   164298
 Seq. ID
                   LIB3177-074-P1-K1-H9
 Method
                   BLASTX
 NCBI GI
                   q132110
BLAST score
                   413
E value
                   1.0e-40
Match length
                   85
% identity
                   94
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thalianal
Seq. No.
                   164299
Seq. ID
                   LIB3177-075-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g1076393
BLAST score
                   536
E value
                   6.0e-55
Match length
                   110
% identity
                   99
NCBI Description
                  RCI14A protein - Arabidopsis thaliana
                   >gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis
                   thaliana
Seq. No.
                   164300
Seq. ID
                  LIB3177-075-P1-K1-A11
Method
                  BLASTX
NCBI GI
                   g115783
                                                                               : 2 .
BLAST score
                   607
E value
                   4.0e-63
Match length
                   126
% identity
                   96
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP \overline{AB} 140) [Arabidopsis
                  thalianal
Seq. No.
                  164301
Seq. ID
                  LIB3177-075-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q1669387
BLAST score
                  382
E value 🤏
                  6.0e-37
Match length
                  74
```

Seq. No.

```
NCBI Description (U41998) actin 2 [Arabidopsis thaliana]
 Seq. No.
                   164302
 Seq. ID
                   LIB3177-075-P1-K1-A2
 Method
                   BLASTN
 NCBI GI
                   q442528
 BLAST score
                   62
 E value
                   2.0e-26
Match length
                   66
 % identity
                   98
                   HY4=flavin-type blue-light photoreceptor [Arabidopsis
NCBI Description
                   thaliana, ecotype Columbia, Genomic/mRNA, 2458 nt]
Seq. No.
                   164303
Seq. ID
                   LIB3177-075-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g2213632
BLAST score
                   158
E value
                   1.0e-10
Match length
                   98
% identity
                   43
NCBI Description
                  (AC000103) F21J9.24 [Arabidopsis thaliana]
Seq. No.
                   164304
Seq. ID
                   LIB3177-075-P1-K1-A4
Method ·
                   BLASTX
NCBI GI
                   g1769905
BLAST score
                   60·
E value
                   1.0e-48
Match length
                   114
% identity
                   88
NCBI Description
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                   164305
Seq. ID
                   LIB3177-075-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g2947063
BLAST score
                   194
E value
                   8.0e-15
Match length
                   92
% identity
                   (AC002521) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164306
Seq. ID
                  LIB3177-075-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g4589440
BLAST score
                  362
E value
                  0.0e + 00
Match length
                  408
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSD21, complete sequence
```

Seq. ID

```
Seq. ID
                   LIB3177-075-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   q1041702
BLAST score
                   729
E value
                   2.0e-77
Match length -.
                   146
                   90
% identity
NCBI Description
                   (U30476) expansin At-EXP1 [Arabidopsis thaliana]
Seq. No.
                   164308
Seq. ID
                   LIB3177-075-P1-K1-A8
Method
                   BLASTN
NCBI GI
                   g2924651
BLAST score
                   243
E value
                   1.0e-134
Match length
                   405
% identity
                   98
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164309
Seq. ID
                   LIB3177-075-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g132110
                                 d.
BLAST score
                   543
E value
                   8.0e-56
Match length
                   104
% identity
                   98
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   164310
Seq. ID
                   LIB3177-075-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g4539335
BLAST score
                   542
E value
                   4.0e-58
Match length
                   138
                   76
% identity
NCBI Description
                   (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                   164311
Seq. ID
                   LIB3177-075-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q4741952
BLAST score
                   667
E value
                   3.0e-70
                   126
Match length
% identity
                   75
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                   164312
                   LIB3177-075-P1-K1-B12
```

```
Method
                   BLASTX
NCBI GI
                   q120667
BLAST score
                   702
E value
                   2.0e-74
Match length
                  144
% identity
                  97
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                  thaliana >gi_166706 (M64116) cystolic
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  164313
Seq. ID
                  LIB3177-075-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2062164
BLAST score
                  252
E value
                  1.0e-21
                  47
Match length
% identity
                  100
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  164314
Seq. No.
Seq. ID
                  LIB3177-075-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4204285
BLAST score
                  691
E value
                  4.0e-73
Match length
                  138
% identity
                  96
NCBI Description (AC003027) lcl_prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  164315
Seq. ID
                  LIB3177-075-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g115492
BLAST score
                  174
                  2.0e-12
E value
Match length
                  145
% identity
                  31
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
Seq. No.
                  164316
                  LIB3177-075-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q166867
BLAST score
                  599
E value
                  3.0e-62
Match length
                  140
% identity
                  80
NCBI Description (J05216) ribosomal protein S11 (probable start codon at bp
                  67) [Arabidopsis thaliana]
```

% identity

```
Seq. No.
                    164317
 Seq. ID
                    LIB3177-075-P1-K1-B7
 Method
                    BLASTX
 NCBI GI
                    g2829899
 BLAST score
                    134
 E value
                    8.0e-08
 Match length
                    118
 % identity
                    53
                    (AC002311) similar to ripening-induced protein,
 NCBI Description
                    gp_AJ001449_2465015 and major#latex protein,
                    gp_X91961_1107495 [Arabidopsis thaliana]
 Seq. No.
                    164318
 Seq. ID
                    LIB3177-075-P1-K1-B8
Method
                    BLASTX
NCBI GI
                    g132102
BLAST score
                    437
E value
                    2.0e-43
Match length
                    95
% identity
                    92
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir_ RKMUB2
                    ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1.1.39}) small chain
                   B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana]
Seq. No.
                   164319
Seq. ID
                   LIB3177-075-P1-K1-C1
Method
                   BLASTN
                   g4522002
NCBI GI
BLAST score
                   231
E value
                   1.0e-127
Match length
                   418
% identity
                   98
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T23K3 genomic
                   sequence, complete sequence
Seq. No.
                   164320
Seq. ID
                   LIB3177-075-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g2880049
BLAST score
                   628
E value
                   8.0e-66
Match length
                   122
% identity
                   99
NCBI Description
                   (AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   164321
Seq. ID
                   LIB3177-075-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   734
E value
                   4.0e-78
Match length
                   142
```

BLAST score

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  164322
Seq. ID
                  LIB3177-075-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q231660
BLAST score
                  62
                  4.0e-30
E value
Match length
                  139
% identity
                  49
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
Seq. No.
                  164323
Seq. ID
                  LIB3177-075-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2245032
BLAST score
                  173
                  2.0e-12
E value
Match 'length
                  73
% identity
                  52
NCBI Description
                  (297342) gibberellin oxidase homolog [Arabidopsis thaliana]
Seq. No.
                  164324
Seq. ID
                  LIB3177-075-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g2129569
BLAST score
                  387
                  3.0e-66
E value
Match length
                  130
% identity
NCBI Description
                  cytosolic cyclophilin ROC3 - Arabidopsis thaliana
                  >gi 1305455 (U40399) cytosolic cyclophilin [Arabidopsis
                  thaliana] >gi 4581104 gb AAD24594.1 AC005825 1 (AC005825)
                  cytosolic cyclophilin (ROC3) [Arabidopsis thaliana]
Seq. No.
                  164325
Seq. ID
                  LIB3177-075-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q2829918
BLAST score
                  532
E value
                  2.0e-54
Match length
                  104
                  99
% identity
NCBI Description
                  (AC002291) similar to "tub" protein gp U82468 2072162
                  [Arabidópsis thaliana]
Seq. No.
                  164326
Seq. ID
                  LIB3177-075-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4455250
```

```
E value
                    1.0e-09
Match length
                    64
 % identity
                    48
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
Seq. No.
                    164327
                    LIB3177-075-P1-K1-C8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1170089
BLAST score
                    101
E value
                    7.0e-29
Match length
                    74
% identity
                    95
                    GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
NCBI Description
                    >gi_481822_pir__S39542 probable glutathione transferase (EC
                    2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase
                    [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                    S-transferase [Arabidopsis thaliana]
Seq. No.
                    164328
Seq. ID
                    LIB3177-075-P1-K1-C9
Method
                    BLASTX
NCBI GI
                    q132074
BLAST score
                    633
E value
                    6.0e-66
Match length
                    124
                    97
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                    (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                    ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   164329
Seq. ID
                   LIB3177-075-P1-K1-D1
Method
                   BLASTN
NCBI GI
                   g3128142
BLAST score
                   372
E value
                   0.0e+00
Match length
                   418
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MQN23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164330
Seg. ID
                   LIB3177-075-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   697
E value
                   9.0e-74
Match length
                   129
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
```

Al precursor - Arabidopsis thaliana

```
Seq. No.
                   164331
Seq. ID
                   LIB3177-075-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   q4063737
BLAST score
                   133
E value
                   1.0e-68
Match length
                   281
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F24D13 genomic
                 . sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164332
                  LIB3177-075-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1345655
BLAST score
                   358
E value
                   4.0e-34
Match length
                   66
% identity
                  100
                  CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD)
NCBI Description
                  >gi_757535_emb_CAA83508_ (Z31715) cinnamyl alcohol
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  164333
Seq. ID
                  LIB3177-075-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2465923
BLAST score
                  350
E value
                  4.0e-33
Match length
                  105
% identity
                  66
NCBI Description
                   (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                  164334
Seq. ID
                  LIB3177-075-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q2760834
BLAST score
                  436
                  3.0e-43
E value
Match length
                  82
% identity
NCBI Description
                  (AC003105) putative nitrate transporter [Arabidopsis
                  thaliana]
Seq. No.
                  164335
Seq. ID
                  LIB3177-075-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q480450
BLAST score
                  450
E value
                  8.0e-45
Match length
                  102
% identity
                  89
NCBI Description
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                  thaliana >gi_402552_emb_CAA49506 (X69880) ketol-acid
```

reductoisomerase [Arabidopsis thaliana]

```
Seq. No.
                    164336
Seq. ID
                    LIB3177-075-P1-K1-D7
Method
                    BLASTX
NCBI GI
                    q3319921
BLAST score
                    276
E value
                    2.0e-24
Match length
                    99
                    59
% identity
NCBI Description
                    (AJ223388) Hev b 3 [Hevea brasiliensis]
                    >gi_3319923_emb_CAA11304 (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi_3319925_emb_CAA11305 (AJ223390) Hev b 3
[Hevea brasiliensis] >gi_3818475 (AF051317) small rubber
                    particle protein [Hevea brasiliensis]
Seq. No.
                    164337
Seq. ID
                    LIB3177-075-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    q1709825
BLAST score
                    568
E value
                    1.0e-58
Match length
                    130
% identity
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                    (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                    164338
Seq. ID.
                    LIB3177-075-P1-K1-D9
Method
                    BLASTX
NCBI GI
                    q1169201
BLAST score
                    575
E value
                    2.0e-59
Match length
                    139
% identity
NCBI Description
                    DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                    >gi_421830_pir__S33707 DRT112 protein - Arabidopsis
                    thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                    164339
Seq. ID
                    LIB3177-075-P1-K1-E10
Method
                    BLASTX
NCBI GI
                    g2739010
BLAST score
                    286
E value
                    1.0e-25
Match length
                    97
% identity
                    53
NCBI Description (AF022464) CYP77A3p [Glycine max]
Seq. No.
                    164340
Seq. ID
                    LIB3177-075-P1-K1-E11
Method
                    BLASTN
NCBI GI
                    q4559344
BLAST score
                    275
E value
                    1.0e-153
Match length
                    345
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F27C12 genomic
                    sequence, complete sequence
```

i

Match length

```
Seq. No.
                    164341
                    LIB3177-075-P1-K1-E2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1703129
BLAST score
                    483
                    1.0e-48
E value
Match length
                    110
% identity
                    85
                    ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    164342
                    LIB3177-075-P1-K1-E3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4538963
BLAST score
                    547
E value
                    3.0e-56
Match length
                    134
% identity
                    63
NCBI Description
                    (AL049488) chlorophyll a/b-binding protein-like
                    [Arabidopsis thaliana] >gi_4741958 gb AAD28776.1 AF134129 1
                    (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                    164343
Seq. ID
                    LIB3177-075-P1-K1-E4
Method
                    BLASTX
NCBI GI
                    g4218123
BLAST score
                    437
E value
                    3.0e-43
Match length
                    139
% identity
                    66
NCBI Description
                    (AL035353) photosystem I subunit PSI-E-like protein
                    [Arabidopsis thaliana]
Seq. No.
                    164344
Seq. ID
                    LIB3177-075-P1-K1-E5
Method
                    BLASTX
NCBI GI '
                    g115470
BLAST score
                   · 767
E value
                    5.0e-82
Match length
                    147
% identity
                    99
                   CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                    DEHYDRATASE) >gi_320554_pir__$28412 carbonate dehydratase
                    (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                    [Arabidopsis thaliana]
                    164345
Seq. No.
Seq. ID
                   LIB3177-075-P1-K1-E7
Method
                   BLASTX
NCBI GI
                    g115767
BLAST score
                    585
                   1.0e-60
E value
```

Method

BLASTX

```
% identity
                   99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein abl65 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  164346
Seq. ID
                  LIB3177-075-P1-K1-E8
Method
                  BLASTX
                  g3128168
NCBI GI
BLAST score
                  170
E value
                  5.0e-12
Match length
                  65
% identity
                  52
                  (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  164347
Seq. ID
                  LIB3177-075-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  619
E value
                  1.0e-64
Match length
                  118
% identity
                  99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  164348
Seq. ID
                  LIB3177-075-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g3702735
BLAST score
                  329
E value
                  0.0e+00
                  420
Match length
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164349
Seq. ID
                  LIB3177-075-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q4376158
BLAST score
                  626
E value
                  2.0e-65
                  128
Match length
% identity
NCBI Description
                  (X98873) aspartate kinase [Arabidopsis thaliana]
Seq. No.
                  164350
Seq. ID
                  LIB3177-075-P1-K1-F2
```

```
NCBI GI
                   q4510345
BLAST score
                   395
E value
                   2.0e-38
Match length
                  74
% identity
                  100
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3177-075-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  q2696018
BLAST score
                  75
E value
                  6.0e-34
Match length
                  273
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164352
Seq. ID
                  LIB3177-075-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q2879811
BLAST score
                  358
E value .
                  4.0e-34
Match length
                  88
                  78
% identity
NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]
Seq. No.
                  164353
Seq. ID
                  LIB3177-075-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q1076287
BLAST score
                  400
E value
                  5.0e-39
Match length
                  87
% identity
                  90
NCBI Description
                  amine acid permease - Arabidopsis thaliana
                  >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                  [Arabidopsis thaliana]
Seq. No.
                  164354
Seq. ID
                  LIB3177-075-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g2894557
BLAST score
                  54
E value
                  1.0e-21
Match length
                  141
% identity
                  94
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T805
                  (ESSAII project)
Seq. No.
Seq. ID
                  164355
                  LIB3177-075-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2213585
BLAST score
                  745
E value
                  2.0e-79
```

```
Match length
                   140
                   100
% identity
NCBI Description
                  (AC000348) T7N9.5 [Arabidopsis thaliana]
Seq. No.
                  164356
Seq. ID
                  LIB3177-075-P1-K1-G10
Method
                  BLASTX
NCBI GI
                   q4587542
BLAST score
                   706
E value
                  7.0e-75
Match length
                  135
% identity
                   99
NCBI Description
                  (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase
                  with GDSL-motif family. ESTs gb_T45815, gb_T45130 and
                  gb Z38046 come from this gene. [Arabidopsis thaliana]
                  164357
Seq. No.
Seq. ID
                  LIB3177-075-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2245093
BLAST score
                  620
E value
                  9.0e-65
Match length
                  137
% identity
                  90
                  (297343) membrane channel protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164358
Seq. ID
                  LIB3177-075-P1-K1-G12
Method
                  BLASTX
                  q4586057
NCBI GI
                  589
BLAST score
                  4.0e-61
E value
Match length
                  112
% identity
                  98
NCBI Description
                  (AC007020) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164359
Seq. ID
                  LIB3177-075-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  q3193305
BLAST score
                  390
E value
                  0.0e + 00
                  406
Match length
% identity
                  99
NCBI Description Arabidopsis thaliana BAC F3D13
Seq. No.
                  164360
Seq. ID
                  LIB3177-075-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3953473
BLAST score
                  659
E value
                  3.0e-69
                  133
Match length
% identity
                  100
NCBI Description
                  (AC002328) F2202.18 [Arabidopsis thaliana]
```

164361

Seq. No.

% identity

```
Seq. ID
                  LIB3177-075-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g99736
BLAST score
                  118
E value
                  2.0e-64
Match length
                  129
% identity
                  98
NCBI Description
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
                  Arabidopsis thaliana >gi_16187_emb_CAA46814 (X66016)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
Seq. No.
                  164362
Seq. ID
                  LIB3177-075-P1-K1-G6
Method
                  BLASTX
                  q132090
NCBI GI
BLAST score
                  719
E value
                  2.0e-76
Match length
                  132
% identity
                  99
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B1 precursor - Arabidopsis thaliana >gi 16193 emb CAA32700
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  164363
Seq. ID
                  LIB3177-075-P1-K1-G7
Method
                  BLASTX
                  g3158376
NCBI GI
BLAST score
                  371
E value
                  1.0e-35
Match length
                  113
% identity
                  65
NCBI Description
                  (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                  164364
                  LIB3177-075-P1-K1-G8
Seq. ID
Method
                  BLASTX
                  g3193289
NCBI GI
BLAST score
                  108
                  2.0e-57
E value
Match length
                  144
% identity
                  85
NCBI Description
                  (AF069298) similar to several small proteins (~100 aa) that
                  are induced by heat, auxin, ethylene and wounding such as
                  Phašeolus aureus indole-3-acetic acid induced protein ARG
                  (SW:32292) [Arabidopsis thaliana]
Seq. No.
                  164365
Seq. ID
                  LIB3177-075-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  q4490291
BLAST score
                  198
E value
                  1.0e-107
Match length
                  330
```

Method

BLASTX

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
                  (ESSA project)
Seq. No.
                  164366
Seq. ID
                  LIB3177-075-P1-K1-H1
Method
                  BLASTN
NCBI GI .
                  g2264304
BLAST score
                  229
E value
                  1.0e-126
Match length
                  356
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBG8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164367
Seq. ID
                  LIB3177-075-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q4538963
BLAST score
                  581
E value
                  2.0e-60
Match length
                  111
% identity
                  74
NCBI Description
                  (AL049488) chlorophyll a/b-binding protein-like
                  [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                  (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                  164368
Seq. ID
                  LIB3177-075-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  241
E value
                  1.0e-20
Match length
                  65
                  77
% identity
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  164369
Seq. ID
                  LIB3177-075-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  648
E value
                  5.0e-68
Match length
                  121
% identity
                  100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  164370
Seq. No.
Seq. ID
                  LIB3177-075-P1-K1-H2
```

BLAST score

```
NCBI GI
                   g4185509
BLAST score
                   569
                   8.0e-59
E value
Match length
                   115
% identity
                   97
                   (AF102821) actin depolymerizing factor 3 [Arabidopsis
NCBI Description
                   thaliana]
                   164371
Seq. No.
Seq. ID
                   LIB3177-075-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   q4756963
BLAST score
                   313
E value
                   1.0e-176
Match length
                   383
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                   (ESSA project)
Seq. No.
                   164372
                  LIB3177-075-P1-K1-H4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4589410
BLAST score
                   426
E value
                   0.0e + 00
Match length
                   448
                   99 :
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F2015, complete sequence
                  164373
Seq. No.
                  LIB3177-075-P1-K1-H5
Seq. ID
Method
                  BLASTX
                  q3286693
NCBI GI
BLAST score
                   600
                   2.0e-62
E value
                  122
Match length
% identity
                   99
                   (Y15433) 33 kDa polypeptide of oxygen-evolving complex
NCBI Description
                   (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                  164374
Seq. ID
                  LIB3177-075-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  q2347192
BLAST score
                  199
E value
                  2.0e-15
                  49
Match length
                  84
% identity
                   (AC002338) spliceosomal protein U2B isolog [Arabidopsis
NCBI Description
                  thaliana]
                  164375
Seq. No.
Seq. ID
                  LIB3177-075-P1-K1-H8
Method
                  BLASTX
                  q4510345
NCBI GI
```

```
E value
                  1.0e-17
Match length
                  41
% identity
                  90
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                  164376
                  LIB3177-075-P1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q282865
BLAST score
                  360
E value
                  2.0e-34
                  83
Match length
                  82
% identity
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
                  164377
Seq. No.
Seq. ID
                  LIB3177-076-P1-K1-A1
                  BLASTX
Method
NCBI.GI
                  q116392
BLAST score
                  622
E value
                  4.0e-65
                  120
Match length
                  99
% identity
                  CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE)
NCBI Description
                  >gi 66543 pir SYMUCN naringenin-chalcone synthase (EC
                  2.3.1.74) - Arabidopsis thaliana >gi_166670 (M20308)
                  chalcone synthase [Arabidopsis thaliana]
                  164378
Seq. No.
Seq. ID
                  LIB3177-076-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q4585978
BLAST score
                  766
                  7.0e-82
E value
                  150
Match length
                  97
% identity
                  (AC005287) NADP specific isocitrate dehydrogenase
NCBI Description
                  [Arabidopsis thaliana]
                  164379
Seq. No.
Seq. ID
                  LIB3177-076-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q2130028
BLAST score
                  352
                  3.0e - 33
E value
                  86
Match length
                  73
% identity
                  B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604)
NCBI Description
                  HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805)
                  B12Dg1 [Hordeum vulgare]
```

164380

Seq. No.

```
LIB3177-076-P1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4490701
BLAST score
                   131
E value
                  2.0e-67
Match length
                   422
% identity
                   98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18
                   (ESSA project)
Seq. No.
                   164381
                  LIB3177-076-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1619321
BLAST score
                   176
                   3.0e-13
E value
Match length
                   52
% identity
                   65
NCBI Description
                  (Y07563) hin1 [Nicotiana tabacum]
Seq. No.
                  164382
                  LIB3177-076-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2924520
BLAST score
                   596
E value
                  5.0e-62
Match length
                  113
% identity
                   99
NCBI Description
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
                   [Arabidopsis thaliana]
                  164383
Seq. No.
                  LIB3177-076-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132110
BLAST score
                   630
                   6.0e-66
E value
                  118
Match length
                  98
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                 164384
Seq. ID
                  LIB3177-076-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g117238
BLAST score
                  691
                  5.0e-73
E value
                  138
Match length
% identity
                  98
NCBI Description
                  MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN
                  CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE)
```

>gi_81656_pir__S12785 protein ch-42 precursor, chloroplast

- Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No. 164385 Seq. ID LIB3177-076-P1-K1-A6 Method BLASTX NCBI GI g137465 BLAST score 763 E value 2.0e-81 Match length 150 99 % identity

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)

(V-ATPASE 57 KD SUBUNIT) >gi_81637_pir_ A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain -

Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding

subunit of vacuolar ATPase [Arabidopsis thaliana]

 Seq. No.
 164386

 Seq. ID
 LIB3177-076-P1-K1-A7

 Method
 BLASTX

 NCBI GI
 g1169278

 BLAST score
 305

 E value
 6.0e-28

Match length 75
% identity 84
NCRI Description DEF

NCBI Description DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14

protein [Arabidopsis thaliana]

Seq. No. 164387

Seq. ID LIB3177-076-P1-K1-A8

Method BLASTX
NCBI GI g115385
BLAST score 574
E value 2.0e-59
Match length 115
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 164388

Seq. ID LIB3177-076-P1-K1-A9

Method BLASTX
NCBI GI g2494610
BLAST score 327
E value 2.0e-30
Match length 129
% identity 57

NCBI Description CELL DIVISION PROTEIN FTSZ CHLOROPLAST HOMOLOG PRECURSOR

>gi 1079732 (U39877) cpFtsZ [Arabidopsis thaliana]

Seq. No. 164389

```
Seq. ID
                    LIB3177-076-P1-K1-B1
 Method
                    BLASTX
 NCBI GI
                    g543751
 BLAST score
                    633
 E value
                    3.0e-66
                    120
 Match length
                    99
 % identity
 NCBI Description
                    1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
                    (ETHYLENE-FORMING ENZYME) (EFE) >gi_541861_pir JT0755
                    ethylene-forming enzyme - Arabidopsis thaliana
                    >gi_16254_emb_CAA47251_ (X66719) ethylene-forming enzyme
                    [Arabidopsis thaliana]
                    164390
 Seq. No.
 Seq. ID
                    LIB3177-076-P1-K1-B10
 Method
                    BLASTX
 NCBI GI
                    q2493122
 BLAST score
                    251
 E value
                    1.0e-21
                    78
 Match length
                    69
 % identity
 NCBI Description
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
                    SUBUNIT) (TONOPLAST ATPASE 70 KD SUBUNIT) (BN59)
                   >gi_1362024 pir S57790 H+-transporting ATPase (EC
                 3.6.1.35), vacuolar, 70K chain (clone BN59) - rape
                    >gi_558479 (U15604) tonoplast ATPase 70 kDa subunit
                    [Brassica napus]
 Seq. No.
                    164391
 Seq. ID
                    LIB3177-076-P1-K1-B11
 Method
                    BLASTX
 NCBI GI
                    q4741954
 BLAST score
                    588
 E value
                    5.0e-61
 Match length
                    114
 % identity
                    100
 NCBI Description
                   (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
 Seq. No.
                    164392
 Seq. ID
                    LIB3177-076-P1-K1-B12
 Method
                    BLASTX
 NCBI GI
                    g1710549
 BLAST score
                    265
                    2.0e-23
 E value
 Match length
                    49
 % identity
                    98
                    60S RIBOSOMAL PROTEIN L39
 NCBI Description
 Seq. No.
                    164393
 Seq. ID
                   LIB3177-076-P1-K1-B2
 Method
                    BLASTX
 NCBI GI
                   g1864017
 BLAST score
                    524
                   1.0e-53
E value
 Match length
                   101
 % identity
                    99
 NCBI Description
                   (D63396) elongation factor-1 alpha [Nicotiana tabacum]
```

```
Seq. No.
                   164394
Seq. ID
                   LIB3177-076-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g3451065
BLAST score
                   530
                   3.0e-54
E value
Match length
                   114
                   91
% identity
NCBI Description
                   (AL031326) water channel - like protein [Arabidopsis
                   thalianal
Seq. No.
                   164395
Seq. ID
                   LIB3177-076-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g4204265
BLAST score
                   173
                   2.0e-12
E value
Match length
                   123
% identity
                   34
NCBI Description
                  (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                   164396
                  LIB3177-076-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4522012
BLAST score
                   479
E value
                   3.0e-48
Match length
                  153
% identity
                   58
NCBI Description
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164397
Seq. ID
                  LIB3177-076-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g3702315
BLAST score
                  323
E value
                  0.0e+00
Match length
                  429
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T3F17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164398
Seq. ID
                  LIB3177-076-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g4741948
BLAST score
                  519
E value
                  2.0e-58
Match length
                  122
% identity
                  96
NCBI Description
                  (AF134124) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  164399
Seq. ID
                  LIB3177-076-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g3985958
```

Seq. No.

```
BLAST score
                   317
E value
                   1.0e-178
Match length
                   417
 % identity
                   98
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164400
Seq. ID
                   LIB3177-076-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2662375
BLAST score
                   216
E value
                   2.0e-17
Match length
                   115
% identity
                   39
NCBI Description (D89060) oligosaccharyltransferase [Homo sapiens]
Seq. No.
                   164401
Seq. ID
                   LIB3177-076-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   a595768
BLAST score
                   146
E value
                   4.0e-09
Match length
                   47
% identity
                   62
NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]
Seq. No.
                  164402
Seq. ID
                  LIB3177-076-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  708
E value
                  3.0e-76
Match length
                  145
% identity
                  97
NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  164403
                  LIB3177-076-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  729
E value
                  2.0e-77
Match length
                  133
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
```

```
LIB3177-076-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2583125
BLAST score
                   338
E value
                   1.0e-31
Match length
                   113
% identity
                   61
                   (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                   thaliana)
Seq. No.
                   164405
Seq. ID
                   LIB3177-076-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g2832625
BLAST score
                   299
E value
                   3.0e-27
Match length
                   69
% identity
                   81
NCBI Description
                   (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                   164406
Seq. ID
                   LIB3177-076-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   749
E value
                   8.0e-80
Match length
                   138
% identity
                   99
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi 68060 pir RKMUB3
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1}.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   164407
Seq. ID
                  LIB3177-076-P1-K1-C5
Method
                  BLASTN
NCBI GI
                   g3176694
BLAST score
                   279
E value
                   1.0e-155
Match length
                   406
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T14N5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164408
Seq. ID
                  LIB3177-076-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4204285
BLAST score
                  440
E value
                  1.0e-43
Match length
                  149
% identity
                  56
NCBI Description
                  (AC003027) 1cl prt seq No definition line found
```

[Arabidopsis thaliana]

Method

BLASTX

```
Seq. No.
                  164409
Seq. ID
                  LIB3177-076-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2583134
BLAST score
                  234
E value
                  1.0e-19
Match length
                  44
% identity
                  100
NCBI Description (AC002387) putative proline-rich protein [Arabidopsis
                  thaliana]
Seq. No.
                  164410
Seq. ID
                  LIB3177-076-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g4006885
BLAST score
                  143
E value
                  1.0e-74
Match length
                  415
% identity
                  96
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  164411
                  LIB3177-076-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4741950
BLAST score
                  748
E value
                  9.0e-80
Match length
                  140
                100
% identity
NCBI Description (AF134125) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  164412
Seq. ID
                  LIB3177-076-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2829896
BLAST score
                  283
E value
                  3.0e-25
Match length
                  87
% identity
                  62
NCBI Description
                  (AC002311) highly similar to auxin-regulated protein GH3,
                  gp_X60033_18591 [Arabidopsis thaliana]
Seq. No.
                  164413
Seq. ID
                  LIB3177-076-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g4539316
BLAST score
                  671
E value
                  1.0e-70
Match length
                  138
% identity
                  100
NCBI Description
                 (AL035679) putative fructose-bisphosphate aldolase
                  [Arabidopsis thaliana]
Seq. No.
                  164414
Seq. ID
                  LIB3177-076-P1-K1-D2
```

NCBI GI

g687677

```
NCBI GI
                   g2245079
BLAST score
                   295
E value
                   1.0e-26
Match length
                   104
% identity
                   58
NCBI Description
                  (297343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   164415
                   LIB3177-076-P1-K1-D4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4585952
BLAST score
                   63
E value
                   5.0e-27
Match length
                   157
% identity
                   90
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F26F24,
                   complete sequence
Seq. No.
                   164416
                   LIB3177-076-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3219858
BLAST score
                   601
E value
                   2.0e-62
Match length
                   116
% identity
                   100
NCBI Description
                   DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE
                   >gi_2129724_pir_ S71204 RNA polymerase II 13.6 kDa chain -
                   Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II
                   13.6 kDa subunit [Arabidopsis thaliana]
                   >gi_4678938_emb_CAB41329.1_ (AL049711) DNA-directed RNA
                   polymerase II 13.6K chain [Arabidopsis thaliana]
Seq. No.
                   164417
Seq. ID
                  LIB3177-076-P1-K1-D6
Method
                  BLASTX
NCBI GI
                   g2252828
BLAST score
                   374
E value
                  2.0e-48
Match length
                  123
% identity
                  87
NCBI Description
                  (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                  164418
Seq. ID
                  LIB3177-076-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  517
E value
                  1.0e-52
Match length
                  118
% identity
                  85
NCBI Description
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  164419
Seq. ID
                  LIB3177-076-P1-K1-D8
Method
                  BLASTX
```

E value

5.0e-23

```
BLAST score
                   436
E value
                   3.0e-43
Match length
                   88
% identity
                   99
NCBI Description
                  (U19925) unknown [Arabidopsis thaliana]
Seq. No.
                   164420
Seq. ID
                   LIB3177-076-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g1175012
BLAST score
                   521
E value
                   3.0e-53
Match length.
                   112
                   91
% identity
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
NCBI Description
                   B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane
                   protein TMP-B [Arabidopsis thaliana]
Seq. No.
                   164421
Seq. ID
                   LIB3177-076-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   q4056502
BLAST score
                   618
E value
                   2.0e-64
Match length
                   129
% identity
NCBI Description
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.
                  164422
Seq. ID
                  LIB3177-076-P1-K1-E10
Method
                  BLASTX
NCBI GI
                   q541858
BLAST score
                   756
E value
                   1.0e-80
Match length
                  144
% identity
                   99
NCBI Description
                  endoxyloglucan transferase - Arabidopsis thaliana
                  >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
                  transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                  endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.
                  164423
Seq. ID
                  LIB3177-076-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2832642
BLAST score
                  187
E value
                  6.0e-14
Match length
                  96
                  25
% identity
NCBI Description
                  (AL021710) putative protein [Arabidopsis thaliana]
Seq. No.
                  164424
Seq. ID
                  LIB3177-076-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2078350
BLAST score
                  264
```

```
Match length
                   67
% identity
                   81
NCBI Description
                  (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  164425
                  LIB3177-076-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3176694
BLAST score
                   274
E value
                  1.0e-153
Match length
                   403
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T14N5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164426
Seq. ID
                  LIB3177-076-P1-K1-E6
Method
                  BLASTX
                  g4581146
NCBI GI
BLAST score
                  152
                  6.0e-10
E value
Match length
                  31
% identity
                  94
NCBI Description
                  (AC006919) putative fructose-bisphosphate aldolase,
                  cytoplasmic [Arabidopsis thaliana]
Seq. No.
                  164427
Seq. ID
                  LIB3177-076-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2245057
BLAST score
                  409
                  3.0e-40
E value
Match length
                  75
                  100
% identity
NCBI Description
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164428
Seq. ID
                  LIB3177-076-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4240116
BLAST score
                  532
E value
                  2.0e-54
Match length
                  124
% identity
NCBI Description
                  (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
                  thaliana] >gi 4240118 dbj BAA74838 (AB007800)
                  NADH-cytochrome b5 reductase [Arabidopsis thaliana]
Seq. No.
                  164429
Seq. ID
                  LIB3177-076-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q132659
BLAST score
                  372
E value
                  1.0e-35
Match length
                  82
% identity
NCBI Description
                  50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)
```

Seq. No.

164434

```
L13 [Spinacia oleracea]
 Seq. No.
                   164430
Seq. ID
                   LIB3177-076-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g2129578
BLAST score
                   315
E value
                   3.0e-29
Match length
                   62
% identity
                   dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
NCBI Description
                   thaliana >gi_928932_emb_CAA89205 (Z49239) homolog of
                   dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                   >qi 1585435 prf 2124427B diamide resistance gene
                   [Arabidopsis thaliana]
Seq. No.
                   164431
Seq. ID
                   LIB3177-076-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   651
E value
                   2.0e-68
Match length
                   124
% identity
                   100
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir_ A29280 chlorophyll
                  a/b-binding protein ab16\overline{5} - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  164432
Seq. ID
                  LIB3177-076-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g3212846
BLAST score
                  137
E value
                  5.0e-71
Match length
                  364
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164433
Seq. ID
                  LIB3177-076-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  g2618677
BLAST score
                  101
E value
                  2.0e-49
Match length
                  510
% identity
                  47
                  Arabidopsis thaliana BAC F21B7 chromosome 1, complete
NCBI Description
                  sequence [Arabidopsis thaliana]
```

>gi_81483_pir__A32033 ribosomal protein L13 precursor,
chloroplast - spinach >gi_170133 (J04461) ribosomal protein

```
Seq. ID
                   LIB3177-076-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g1169201
BLAST score
                   611
                   1.0e-63
E value
Match length
                   150
% identity
                   83
NCBI Description
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                   >gi 421830_pir__S33707 DRT112 protein - Arabidopsis
                   thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                   164435
Seq. ID
                  LIB3177-076-P1-K1-F4
Method
                   BLASTX
NCBI GI
                  g3850579
BLAST score
                   554
                   4.0e-57
E value
Match length
                   124
% identity
                   85
NCBI Description
                   (AC005278) Strong similarity to gb_D14550 extracellular
                  dermal glycoprotein (EDGP) precursor from Daucus carota.
                  ESTs gb_H37281, gb T44167, gb T21813, gb N38437, gb Z26470,
                  gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373,
                  gb Z34678 an
                  164436
Seq. No.
                  LIB3177-076-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2500430
BLAST score
                  655
E value
                  7.0e-69
Match length
                  127
% identity
                  100
NCBI Description 40S RIBOSOMAL PROTEIN S16
Seq. No.
                  164437
                  LIB3177-076-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006883
BLAST score
                  453
E value
                  3.0e-45
Match length
                  111
                  79
% identity
NCBI Description
                  (Z99707) cysteine proteinase [Arabidopsis thaliana]
Seq. No.
                  164438
Seq. ID
                  LIB3177-076-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q421826
BLAST score
                  633
E value
                  3.0e-66
Match length
                  143
% identity
                  83
NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi_298036_emb_CAA50712 (X71878) CP29 [Arabidopsis
```

thaliana]

Seq. No.

```
164439
Seq. No.
Seq. ID
                  LIB3177-076-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q4218123
BLAST score
                  332
E value
                  3.0e - 34
Match length
                  136
                  58
% identity
NCBI Description
                   (AL035353) photosystem I subunit PSI-E-like protein
                   [Arabidopsis thaliana]
                  164440
Seq. No.
Seq. ID
                  LIB3177-076-P1-K1-G1
Method
                 BLASTX
NCBI GI
                  g1568480
BLAST score
                  648
                  5.0e-68
E value
Match length
                  150
% identity
                  83
NCBI Description
                  (Z71703) cdc2-like protein kinase [Beta vulgaris]
Seq. No.
                  164441
                  LIB3177-076-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  302
E value
                  2.0e-31
Match length
                  118
                  64
% identity
NCBI Description
                  (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  164442
                  LIB3177-076-P1-K1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q625977
BLAST score
                  609
                  1.0e-63
E value
Match length
                  118
                  100
% identity
NCBI Description
                  p40 protein homolog - Arabidopsis thaliana >gi 402904
                  (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  164443
Seq. ID
                  LIB3177-076-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g1175013
BLAST score
                  514
E value
                  2.0e-52
Match length
                  113
% identity
                  88
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir $44084
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
```

Method

BLASTX

```
Seq. ID
                   LIB3177-076-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g3337361
BLAST score
                   338
E value
                   1.0e-31
Match length
                   146
% identity
                   50
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   164445
                   LIB3177-076-P1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4454036
BLAST score
                   729
                   1.0e-77
E value
Match length
                   133
% identity
                   99
                   (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   164446
Seq. ID
                   LIB3177-076-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   g3241922·
BLAST score
                   19
E value
                   1.1e+00
Match length
                   324
                   73
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164447
Seq. ID
                  LIB3177-076-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g4337175
                                                              7.
BLAST score
                  568
                   9.0e-59
E value
Match length
                  111
% identity
                  100
                  (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                  gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                  gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                  gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  164448
Seq. ID
                  LIB3177-076-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  g336917
BLAST score
                  51
E value
                  1.0e-19
Match length
                  135
                  90
% identity
NCBI Description
                  Epifagus virginiana chloroplast complete genome
Seq. No.
                  164449
Seq. ID
                  LIB3177-076-P1-K1-G7
```

Seq. ID

```
NCBI GI
                  g282865
BLAST score
                  670
E value
                  1.0e-70
Match length
                  133
% identity
                  72
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >gi_16207_emb_CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi 4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  164450
                  LIB3177-076-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213583
BLAST score
                  319
E value
                  1.0e-29
Match length
                  125
% identity
                  53
NCBI Description
                 (AC000348) T7N9.3 [Arabidopsis thaliana]
Seq. No.
                  164451
Seq. ID
                  LIB3177-076-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  g2264313
BLAST score
                  160
E value
                  4.0e-85
Match length
                  160
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOP10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164452
Seq. ID
                  LIB3177-076-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q2062161
BLAST score
                 .735
E value
                  3.0e-78
Match length
                  139
% identity
                  50
                 (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                 thaliana
Seq. No.
                  164453
Seq. ID
                  LIB3177-076-P1-K1-H10
Method :
                  BLASTN
NCBI GI
                  g790582
BLAST score
                  377
E value
                  0.0e+00
Match length
                  381
% identity
                  100
NCBI Description
                  Arabidopsis thaliana putative pathogenesis-related protein
                  (ATOZII) mRNA, complete cds
Seq. No.
                  164454
```

LIB3177-076-P1-K1-H11

Method

BLASTX

```
Method
                   BLASTN
NCBI GI
                   g2618603
BLAST score
                   288
E value
                   1.0e-161
Match length
                   296
% identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MSL3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164455
Seq. ID
                   LIB3177-076-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   q1843527
BLAST score
                   302
E value
                   1.0e-27
Match length
                   103
% identity
                   40
NCBI Description
                   (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   164456
Seq. ID
                   LIB3177-076-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g2499973
BLAST score
                   226
E value
                   1.0e-18
Match length
                   103
                   52
% identity
NCBI Description
                   PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
                   >gi_1465366_emb_CAA66701_ (X98078) photosystem II
                   [Arabidopsis thaliana]
Seq. No.
                   164457
Seq. ID
                   LIB3177-076-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   g2351067
BLAST score
                   232
E value
                   1.0e-128
                   360
Match length
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MPO12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164458
Seq. ID
                   LIB3177-076-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g2501021
BLAST score
                   162
E value
                   2.0e-11
Match length
                   38
% identity
                  82
NCBI Description
                  LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)
                  >gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase
                  [Synechocystis sp.]
Seq. No.
                  164459
Seq. ID
                  LIB3177-076-P1-K1-H6
```

Method

BLASTX

```
NCBI GI
                  g3915826
BLAST score
                   461
                   3.0e-46 ·
E value
Match length
                  103
% identity
                  84
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                  164460
Seq. ID
                  LIB3177-076-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                   712
E value
                  2.0e-75
Match length
                  134
                  76
% identity
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  164461
Seq. ID
                  LIB3177-076-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g3046847
BLAST score
                  178
E value
                  1.0e-95
Match length
                  316
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
                  K11J9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164462
Seq. ID
                  LIB3177-077-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  a3688799
BLAST score
                  492
E value
                  7.0e-50
Match length
                  99
                  99
% identity
NCBI Description
                  (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
                  thaliana]
Seq. No.
                  164463
Seq. ID
                  LIB3177-077-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q132090
BLAST score
                  756
E value
                  1.0e-80
Match length
                  139
% identity
                  99
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  164464
Seq. ID
                  LIB3177-077-P1-K1-A12
```

```
NCBI GI
                     g1172873
BLAST score
                     417
E value
                     4.0e-41
Match length
                     95
% identity
                    89
NCBI Description
                    CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                    precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374
                     (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                    164465
                    LIB3177-077-P1-K1-A2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1402908
BLAST score
                    756
E value
                    1.0e-80
Match length
                    146
% identity
                    99
                    (X98315) peroxidase [Arabidopsis thaliana]
NCBI Description
                    >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
[Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)
                    peroxidase [Arabidopsis thaliana]
Seq. No.
                    164466
Seq. ID
                    LIB3177-077-P1-K1-A3
Method
                    BLASTX
NCBI GI
                    g2130096
BLAST score
                    232
E value
                    3.0e-19
Match length
                    115
                    37
% identity
NCBI Description
                    cytochrome P450tyr - sorghum >gi 984543 (U32624) cytochrome
                    P-450 [Sorghum bicolor]
Seq. No.
                    164467
Seq. ID
                    LIB3177-077-P1-K1-A4
Method
                    BLASTN
NCBI GI
                    g4220635
BLAST score
                    283
E value
                    1.0e-158
Match length
                    283
% identity
                    100
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                    MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.
                    164468
                    LIB3177-077-P1-K1-A5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g81600
BLAST score
                    645
E value
                    1.0e-67
Match length
                    144
% identity
                    92
                    chaperonin 60 beta (clone bX) - Arabidopsis thaliana
NCBI Description
                    (fragment)
```

164469

Seq. No.

Method

BLASTX

```
Seq. ID
                  LIB3177-077-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2738248
BLAST score
                   760
E value
                   4.0e-81
Match length
                   153
                   97
% identity
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   164470
Seq. ID
                  LIB3177-077-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g2979540
                   99
BLAST score
                  3.0e-48
E value
                   457
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F17K2 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164471
Seq. ID
                  LIB3177-077-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  q4586019
BLAST score
                  233
E value
                  1.0e-128
                  233
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T3P4 genomic
NCBI Description
                  sequence, complete sequence
                  164472
Seq. No.
Seq. ID
                  LIB3177-077-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g3169169
BLAST score
                  411
                  0.0e+00
E value
                  443
Match length
                  80
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F21P24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164473
                  LIB3177-077-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454037
BLAST score
                  435
                  3.0e-43
E value
                  84
Match length
                  95
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
                  164474
Seq. No.
Seq. ID
                  LIB3177-077-P1-K1-B11
```

```
NCBI GI
                   g464986
BLAST score
                   696
E value
                   1.0e-73
Match length
                   129
                   100
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   'LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis thaliana]
                   >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                   164475
Seq. ID
                   LIB3177-077-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g4165550
BLAST score ·
                   686
E value
                   2.0e-72
Match length
                   143
% identity
                   91
NCBI Description (AJ004915) apgm [Malus domestica]
Seq. No.
                   164476
Seq. ID
                   LIB3177-077-P1-K1-B2
Method
                   BLASTN
                   q4455339
NCBI GI
BLAST score
                   305
E value
                   1.0e-171
Match length
                   305
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
                   (ESSAII project)
Seq. No.
                   164477
Seq. ID
                   LIB3177-077-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g2117612
BLAST score
                   869
E value
                   7.0e-94
Match length
                  157
% identity
                  100
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
Seq. No.
                  164478
Seq. ID
                  LIB3177-077-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g3883125
BLAST score
                  232
E value
                  1.0e-128
Match length
                  263
% identity
                  97
NCBI Description Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA,
```

complete cds

```
Seq. No.
                   164479
 Seq. ID
                   LIB3177-077-P1-K1-B6
 Method
                   BLASTX
 NCBI GI
                   g16225
 BLAST score
                   628
 E value
                   1.0e-65
Match length
                   123
 % identity
                   65
 NCBI Description
                   (Z12023) calmodulin [Arabidopsis thaliana]
 Seq. No.
                   164480
 Seq. ID
                   LIB3177-077-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g4056457
BLAST score
                   472
E value
                   2.0e-47
Match length
                   130
 % identity
                   71
                   (AC005990) ESTs gb 234051 and gb F13722 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
Seq. No.
                   164481
Seq. ID
                   LIB3177-077-P1-K1-B8
Method
                   BLASTN
NCBI GI
                   g3298610
BLAST score
                   145
E value
                   4.0e-76
Match length
                   157
% identity
                   98
NCBI Description Arabidopsis thaliana BAC T2H3
Seq. No.
                   164482
Seq. ID
                   LIB3177-077-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2558662
·BLAST score
                   143
                   6.0e-09
E value
Match length
                   115
% identity
NCBI Description
                  (AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.
                   164483
Seq. ID
                   LIB3177-077-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   q1173104
BLAST score
                   738
E value
                   1.0e-78
Match length
                   150
% identity
                   90
                   RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease
NCBI Description
                   [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease,
                   RNS2 [Arabidopsis thaliana]
                   164484
Seq. No.
Seq. ID
                   LIB3177-077-P1-K1-C10
```

NCBI GI

g135860

```
Method
                   BLASTX
 NCBI GI
                   q3298443
 BLAST score
                   311
 E value
                   2.0e-28
 Match length
                   84
 % identity
                   69.
 NCBI Description
                   (AB010880) chloroplast ribosomal protein L17 [Nicotiana
                   tabacum]
 Seq. No.
                   164485
 Seq. ID
                   LIB3177-077-P1-K1-C11
 Method
                   BLASTX
 NCBI GI
                   g461532
 BLAST score
                   236
 E value
                   9.0e-20
 Match length
                   64
 % identity
                   66
 NCBI Description
                   ADP-RIBOSYLATION FACTOR >gi 1362500 pir D49993
                   ADP-ribosylation factor - Ajellomyces capsulata >gi 407693
                   (L25117) ADP-ribosylation factor [Histoplasma capsulatum]
 Seq. No.
                   164486
 Seq. ID
                   LIB3177-077-P1-K1-C2
 Method
                   BLASTX
-NCBI GI
                   g4115337
 BLAST score
                   764 .
E value
                   1.0e-81
Match length
                   154
 % identity
                   18
NCBI Description
                  (L81141) ubiquitin [Pisum sativum]
Seq. No.
                   164487
Seq. ID
                   LIB3177-077-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   g3985954
BLAST score
                   398
E value
                   0.0e + 00
Match length
                 457
 % identity
                   98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MRG21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164488
Seq. ID
                   LIB3177-077-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   g3985958
BLAST score
                   317
E value
                   1.0e-178
Match length
                   454
% identity
                   95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164489
Seq. ID
                  LIB3177-077-P1-K1-C5
Method
                  BLASTX
```

Match length

```
BLAST score
                     565
  E value
                     2.0e-58
  Match length
                     123
                     63
  % identity
  NCBI Description
                    TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                     (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic
                    protein gamma - Arabidopsis thaliana
                    >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                    protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732
                     (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                    >gi 445129_prf__1908432B tonoplast intrinsic protein gamma
                     [Arabidopsis thaliana]
  Seq. No.
                    164490
  Seq. ID
                    LIB3177-077-P1-K1-C6
  Method
                    BLASTX
  NCBI GI
                    g4455364
  BLAST score
                    255
  E value
                    6.0e-22
  Match length
                    56
  % identity
                    82
                    (AL035524) senescence-associated protein-like [Arabidopsis
  NCBI Description
                    thaliana]
>- Seq. No.
                    164491
                    LIB3177-077-P1-K1-C7
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g3449334
  BLAST score
                    310
  E value
                    1.0e-174
  Match length
                    394
  % identity
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MYH9, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    164492
  Seq. ID
                    LIB3177-077-P1-K1-C8
  Method
                    BLASTX
  NCBI GI
                    g282865
  BLAST score
                    659
  E value
                    3.0e-69
  Match length
                    131
  % identity
                    72
  NCBI Description
                    chlorophyll a/b-binding protein - Arabidopsis thaliana
                    >gi_16207_emb_CAA39534 (X56062) chlorophyll A/B-binding
                    protein [Arabidopsis thaliana] >gi 166644 (M85150)
                    chlorophyll a/b-binding protein [Arabidopsis thaliana]
                    >gi 4678304_emb CAB41095.1 (AL049655) chlorophyll
                    a/b-binding protein [Arabidopsis thaliana]
  Seq. No.
                    164493
  Seq. ID
                    LIB3177-077-P1-K1-C9
 Method
                    BLASTN
 NCBI GI
                    g2618602
 BLAST score
                    216
 E value
                    1.0e-118
```

NCBI GI

g166835

```
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164494
                  LIB3177-077-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2119846
BLAST score
                   763
E value
                   2.0e-81
Match length
                  145
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  164495
Seq. ID
                  LIB3177-077-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g267083
BLAST score
                  560
E value
                  1.0e-57
Match length
                  107
% identity
                  100
NCBI Description
                  TUBULIN BETA-9 CHAIN >gi 320190 pir JQ1593 tubulin beta-9
                  chain - Arabidopsis thaliana >gi_166910 (M84706) beta-9
                  tubulin [Arabidopsis thaliana]
Seq. No.
                  164496
Seq. ID
                  LIB3177-077-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  g4417264
BLAST score
                  45
E value
                  5.0e-16
Match length
                  123
% identity
                  85
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164497
                  LIB3177-077-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911055
BLAST score
                  577
E value
                  2.0e-67
Match length
                  156
% identity
                  87
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  164498
Seq. ID
                  LIB3177-077-P1-K1-D3
Method
                  BLASTX
```

Seq. ID

```
BLAST score
                          303
       E value
                         8.0e-28
       Match length
                         85
       % identity
                         74
       NCBI Description
                         (M86720) ribulose bisphosphate carboxylase/oxygenase
                         activase [Arabidopsis thaliana] >gi 2642170 (AC003000)
                         Rubisco activase [Arabidopsis thaliana]
       Seq. No.
                         164499
       Seq. ID
                         LIB3177-077-P1-K1-D4
       Method
                         BLASTX
       NCBI GI
                         g2055273
       BLAST score
                         344
                         2.0e-32
       E value
                         66
       Match length
       % identity
                         100
       NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
       Seq. No.
                         164500
       Seq. ID
                         LIB3177-077-P1-K1-D5
       Method
                         BLASTX
       NCBI GI
                         q464720
       BLAST score
                         251
       E value
                         2.0e-21
                         50
      . Match length
                         100
       % identity
       NCBI Description
                        40S RIBOSOMAL PROTEIN S28 >gi 409184 (L09755) ribosomal
                         protein S28 [Arabidopsis thalīana]
       Seq. No.
                         164501
       Seq. ID
                        LIB3177-077-P1-K1-D7
       Method
                         BLASTX
NCBI GI
                         q132110
       BLAST score
                         666
       E value
                         4.0e-70
       Match length
                         122
       % identity
                         99
                         RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
       NCBI Description
                         (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                         ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                         B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                         (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                         thaliana]
       Seq. No.
                         164502
                         LIB3177-077-P1-K1-D8
       Seq. ID
       Method
                         BLASTX
       NCBI GI
                         g4585882
       BLAST score
                         570
       E value
                         6.0e-59
       Match length
                         112
       % identity
       NCBI Description
                         (AC005850) PSI type III chlorophyll a/b-binding protein
                         [Arabidopsis thaliana]
       Seq. No.
                         164503
```

LIB3177-077-P1-K1-D9

```
Method
                   BLASTN
NCBI GI
                   g4510360
 BLAST score
                   292
 E value
                   1.0e-163
Match length
                   340
 %_identity
                   96
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F11F19 genomic
                   sequence, complete sequence
Seq. No.
                   164504
Seq. ID
                   LIB3177-077-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g544425
BLAST score
                   424
                   7.0e-42
E value
Match length
                   82
% identity
                   100
NCBI Description
                   GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
                   >gi_419756 pir__S30148 glycine-rich protein (clone AtGRP8)
                   - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                   glycine rich protein [Arabidopsis thaliana] >qi 166658
                   (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)
                   RNA-binding protein [Arabidopsis thaliana]
           . :
Seq. No.
                   164505
                   LIB3177-077-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4741952.
BLAST score
                   709
E value
                   4.0e-75
Match length
                   131
% identity
                   77
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   164506
Seq. ID
                  LIB3177-077-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   g3702735
BLAST score
                   129
E value
                   1.0e-66
Match length
                  164
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164507
Seq. ID
                  LIB3177-077-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g416758
BLAST score
                  780
E value
                  2.0e-83
Match length
                  146
                  99
% identity
                  SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)
NCBI Description
                  carboxypeptidase Y-like protein [Arabidopsis thaliana]
                  >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis
```

et.

thaliana]

```
Seq. No.
                   164508
Seq. ID
                   LIB3177-077-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g4220514
BLAST score
                   438
E value
                   2.0e-43
Match length
                   119
% identity
                   70
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   164509
Seq. ID
                  LIB3177-077-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   g4220638
BLAST score
                   50
E value
                   2.0e-19
Match length
                   173
% identity
                   89
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIF21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164510
Seq. ID
                  LIB3177-077-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                   678
E value
                  1.0e-71
Match length
                  131
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372 emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  164511
Seq. ID
                  LIB3177-077-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q166702
BLAST score
                  663
E value
                  9.0e-70
Match length
                  149
% identity
NCBI Description
                  (M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit
                  [Arabidopsis thaliana]
Seq. No.
                  164512
                  LIB3177-077-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4493904
BLAST score
                  157
E value
                  5.0e-11
Match length
                  53
% identity
                  60
```

```
NCBI Description
                  (AL034558) predicted using hexExon; MAL3P2.26 (PFC0285c),
                  T-complex protein beta subunit, len: 541 aa; Similarity to
                  T-complex proteins beta subunits. C.elegans T-complex
                  protein beta subunit (SW:TCPB CAEEL) BLAST Score: 1527
Seq. No.
                  164513
Seq. ID
                  LIB3177-077-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  q4490324
BLAST score
                  116
E value
                  8.0e-59
Match length
                  124
% identity
                  75
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
                  (ESSA project)
Seq. No.
                  164514
Seq. ID
                  LIB3177-077-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g1542941
BLAST score
                  198
E value
                  2.0e-15
Match length
                  52
% identity
                  81
NCBI Description
                 (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
                  164515
Seq. No.
Seq. ID
                  LIB3177-077-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g294666
BLAST score
                  227
                  1.0e-18
E value
Match length
                  122
% identity
                  43
NCBI Description (L13241) beta-ketoacyl-ACP synthase [Ricinus communis]
Seq. No.
                  164516
                  LIB3177-077-P1-K1-F1
Seq. ID
Method
              BLASTX
NCBI GI
                  g2062157
BLAST score
                  303
E value
                  4.0e-58
Match length
                  120
% identity
NCBI Description
                  (ACO01645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  164517
Seq. ID
                  LIB3177-077-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q2829899
BLAST score
                  593
E value
                  1.0e-61
Match length
                  117
% identity
NCBI Description (AC002311) similar to ripening-induced protein,
                  gp_AJ001449_2465015 and major#latex protein,
```

% identity

100

Seq. No. 164518 Seq. ID LIB3177-077-P1-K1-F11 Method BLASTX NCBI GI q4454037 BLAST score 599 E value 3.0e-62 Match length 112 % identity 99 NCBI Description (AL035394) putative major latex protein [Arabidopsis thaliana] Seq. No. 164519 Seq. ID LIB3177-077-P1-K1-F12 Method BLASTX NCBI GI q4538963 BLAST score 565 E value 3.0e-58 Match length 137 % identity 64 NCBI Description (AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana] Seq. No. 164520 Seq. ID LIB3177-077-P1-K1-F2 Method BLASTX NCBI GI q4454473 BLAST score 365 E value 8.0e-35 Match length 123 % identity 60 NCBI Description (AC006234) putative beta-expansin protein [Arabidopsis thaliana] Seq. No. 164521 LIB3177-077-P1-K1-F3 -Seq. ID Method BLASTX NCBI GI g1702987 BLAST score 592 E value 6.0e-66 Match length 136 % identity 96 NCBI Description 14-3-3-LIKE PROTEIN GF14 PHI >gi 1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana] Seq. No. 164522 Seq. ID LIB3177-077-P1-K1-F5 Method BLASTX NCBI GI g115385 BLAST score 577 E value 1.0e-59 Match length 111

1552 . . . <u>. .</u>

gp_X91961_1107495 [Arabidopsis thaliana]

Match length

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                     (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                     chlorophyll a/b binding protein [Arabidopsis thaliana]
  Seq. No.
                     164523
                    LIB3177-077-P1-K1-F6
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                    g132074
  BLAST score
                     709
  E value
                    1.0e-78
  Match length
                     142
  % identity
                     91
  NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                     (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    Al precursor - Arabidopsis thaliana
  Seq. No.
                    164524
                    LIB3177-077-P1-K1-F8 .
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    q3269280
  BLAST score
                    144
  E value
                    4.0e-75
  Match length
                    311
                    97
* % identity
  NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22
                    (ESSAII project)
  Seq. No.
                    164525
                    LIB3177-077-P1-K1-F9
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    q3851669
  BLAST score
                    126
  E value
                    2.0e-64
  Match length
                    134
  % identity
                    99
  NCBI Description
                    Arabidopsis thaliana J8 mRNA, nuclear gene encoding plastid
                    protein, complete cds
  Seq. No.
                    164526
  Seq. ID
                    LIB3177-077-P1-K1-G1
  Method
                    BLASTN
  NCBI GI
                    q4262221
  BLAST score
                    36
  E value
                    1.0e-10
  Match length
                    242
  % identity
                    86
  NCBI Description
                    Arabidopsis thaliana chromosome II BAC F10A8 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    164527
                    LIB3177-077-P1-K1-G10
  Seq. ID
  Method'
                    BLASTX
  NCBI GI
                    g115385
  BLAST score
                    704
                    1.0e-74
  E value
```

NCBI GI

```
% identity
                   98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  164528
Seq. ID
                  LIB3177-077-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q1076668
BLAST score
                  511
                  4.0e-52
E value
                  109
Match length
% identity
                  87
NCBI Description
                  NADH dehydrogenase (EC 1.6.99.3) - potato
                  >gi 639834 emb CAA58823 (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
Seq. No.
                  164529
Seq. ID
                  LIB3177-077-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q133938
BLAST score
                  560
                  1.0e-57
E value
Match length
                  144
% identity
                  77
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70866 pir R3SP3
                  ribosomal protein S3 - spinach chloroplast
                  >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3
                  [Spinacia oleracea]
Seq. No.
                  164530
                  LIB3177-077-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832241
BLAST score
                  721
                  1.0e-76
E value
Match length
                  151
% identity
NCBI Description
                  (AF030864) nonphototropic hypocotyl 1 [Arabidopsis
                  thaliana]
Seq. No.
                  164531
                  LIB3177-077-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115385
BLAST score
                  548
E value
                  2.0e-56
Match length
                  105
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  164532
Seq. ID
                  LIB3177-077-P1-K1-G4
Method
                  BLASTX
```

q1076413

Method

BLASTX

```
BLAST score
                  756
E value
                  1.0e-80
Match length
                  149
% identity
                  100
                  serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis
NCBI Description
                  thaliana >gi_2146776_pir__S67482 serine O-acetyltransferase
                   (EC 2.3.1.30) - Arabidopsis thaliana >gi 608577 (L34076)
                  serine acetyltransferase [Arabidopsis thaliana]
                  >gi_608677_emb_CAA84371_ (Z34888) serine acetyltransferase
                   [Arabidopsis thaliana] >gi 1093493 prf 2104212A Ser
                  acetyltransferase [Arabidopsis thaliana]
Seq. No.
                  164533
Seq. ID
                  LIB3177-077-P1-K1-G5
Method
                  BLASTN
                  g4454447
NCBI GI
BLAST score
                  328
E value
                  0.0e + 00
Match length
                  344
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  164534
Seq. No.
                  LIB3177-077-P1-K1-G6
Seq. ID
Method
                  BLASTX
                  g3878874
NCBI GI
BLAST score
                  196
                  5.0e-15
E value
Match length
                  140
% identity
                  34
                  (Z69793) R03A10.3 [Caenorhabditis elegans]
NCBI Description
Seq. No.
                  164535
Seq. ID
                  LIB3177-077-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g166781
BLAST score
                  97
                  2.0e-47
E value
Match length
                  160
                  90
% identity
NCBI Description
                  A.thaliana nitrate reductase mRNA, complete cds
                  164536
Seq. No.
Seq. ID
                  LIB3177-077-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q3885511
BLAST score
                  393
                  3.0e-38
E value
Match length
                  99
                  81
% identity
NCBI Description
                  (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
Seq. No.
                  164537
                  LIB3177-077-P1-K1-G9
Seq. ID
```

% identity

```
NCBI GI
                   g3169185
 BLAST score
                   245
E value
                   8.0e-21
Match length
                   62
% identity
                   76
NCBI Description
                  (AC004401) unknown protein [Arabidopsis thaliana]
Seq. No.
                   164538
Seq. ID
                   LIB3177-077-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g4415930
BLAST score
                   572
E value
                   4.0e-59
Match length
                   134
% identity
                   81
NCBI Description
                   (AC006418) unknown protein [Arabidopsis thaliana]
                   >gi_4559389_gb_AAD23049.1_AC006526_14 (AC006526) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   164539
Seq. ID
                   LIB3177-077-P1-K1-H5
                   BLASTX
Method
NCBI GI
                   g3860315
BLAST score
                   310
E value
                   2.0e-28
Match length
                   68
% identity
                   84
NCBI Description
                  (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
Seq. No.
                   164540
Seq. ID
                   LIB3177-077-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q4417280
BLAST score
                   697
E value
                   1.0e-73
Match length
                   154
% identity
                   92
NCBI Description
                  (AC007019) putative ATP synthase [Arabidopsis thaliana]
Seq. No.
                   164541
Seq. ID
                   LIB3177-077-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q4538979
BLAST score
                   170
E value
                   6.0e-12
Match length
                   90
% identity
                   56
NCBI Description
                  (AL049487) putative protein [Arabidopsis thaliana]
Seq. No.
                  164542
Seq. ID
                  LIB3177-077-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  98
E value
                  2.0e-11
Match length
                  69
```

Method

BLASTX

```
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  164543
Seq. ID
                  LIB3177-078-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2062164
BLAST score
                  708
E value
                  5.0e-75
Match length
                  150
% identity
                  58
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164544
Seq. ID
                  LIB3177-078-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2117612
BLAST score
                  821
E value
                  3.0e-88
Match length
                  149
                  100
% identity
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
Seq. No.
                  164545
Seq. ID
                  LIB3177-078-P1-K1-A12
                  BLASTX
Method
NCBI GI
                  g4160280
BLAST score
                  402
E value
                  3.0e-39
Match length
                  135
% identity
                  54
NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]
Seq. No.
                  164546
Seq. ID
                  LIB3177-078-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1531762
BLAST score
                  153
E value
                  4.0e-10
Match length
                  45
% identity
                  69
NCBI Description
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                  thaliana]
                  164547
Seq. No.
Seq. ID
                  LIB3177-078-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q1621268
BLAST score
                  475
E value
                  9.0e-48
Match length
                  127
% identity
                  68
NCBI Description (Z81012) unknown [Ricinus communis]
Sėq. No.
                  164548
Seq. ID
                  LIB3177-078-P1-K1-A4
```

Seq. No.

```
NCBI GI
                   g421826
BLAST score
                   393
E value
                   4.0e-38
Match length
                   76
                   100
% identity
NCBI Description
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                   >gi_298036_emb CAA50712 (X71878) CP29 [Arabidopsis
                   thaliana]
                   164549
Seq. No.
Seq. ID
                  LIB3177-078-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g4522012
BLAST score
                   115
E value
                   2.0e-05
Match length
                  150
                   43
% identity
NCBI Description
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164550
Seq. ID
                  LIB3177-078-P1-K1-A7
Method
                  BLASTX
                  q4586047
NCBI GI
BLAST score
                   470
E value
                  3.0e-47
Match length
                  110
                  81
% identity
NCBI Description
                  (AC007020) putative ferritin protein [Arabidopsis thaliana]
                  >gi_4588004_gb_AAD25945.1_AF085279 18 (AF085279)
                  hypothetical ferritin subunit [Arabidopsis thaliana]
Seq. No.
                  164551
Seq. ID
                  LIB3177-078-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  728
E value
                  2.0e-77
Match length
                  135
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  164552
Seq. ID
                  LIB3177-078-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g4725950
BLAST score
                  218
E value
                  1.0e-17
Match length
                  126
% identity
NCBI Description
                  (AL049730) putative Phospholipase D [Arabidopsis thaliana]
                  >gi_4725951_emb_CAB41722.1_ (AL049730) putative
                  proline-rich protein [Arabidopsis thaliana]
```

```
LIB3177-078-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337356
BLAST score
                  613
E value
                  7.0e-64
Match length
                  136
                  90
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                  164554
Seq. No.
Seq. ID
                  LIB3177-078-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3335340
BLAST score
                  590
                  3.0e-61
E value
                  138
Match length
                  80
% identity
NCBI Description
                  (AC004512) Strong similarity to xylglucan
                  endo-transglycolsylase (TCH4) gene gb_U27609, first exon
                  contains strong similarity to meri 5 gene gb Z17989 from A.
                  thaliana. EST gb N37583 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  164555
Seq. ID
                  LIB3177-078-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2335106
BLAST score
                  142
E value
                  1.0e-08
Match length
                  130
% identity
                  (AC002339) salt inducible protein-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164556
Seq. ID
                  LIB3177-078-P1-K1-B2
                  BLASTX
Method
NCBI GI
                  g3337356
BLAST score
                  359
E value
                  4.0e-34
                  84
Match length
                  89
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
Seq. No.
                  164557
Seq. ID
                  LIB3177-078-P1-K1-B3
Method
                  BLASTN
                  g2828186
NCBI GI
BLAST score
                  73
                  9.0e-33
E value
Match length
                  256
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
```

K18I23, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   164558
Seq. ID
                   LIB3177-078-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g1931647
BLAST score
                   625
E value
                   2.0e-65
Match length
                   138
% identity
                   88
NCBI Description
                   (U95973) endomembrane protein EMP70 precusor isolog
                   [Arabidopsis thaliana]
Seq. No.
                   164559
Seq. ID
                   LIB3177-078-P1-K1-B5
Method .
                   BLASTX
NCBI GI
                   g1550740
BLAST score
                   611
E value
                   1.0e-63
Match length
                   119
% identity
                   99
NCBI Description
                  (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
Seq. No.
                   164560
Seq. ID
                   LIB3177-078-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g4530591
BLAST score
                   690
E value
                   6.0e-73
Match length
                   138
% identity
                   100
                  (AF132475) heme oxygenase 1 [Arabidopsis thaliana]
NCBI. Description
                   >gi_4530593_gb_AAD22108.1_ (AF132476) heme oxygenase 1
                   [Arabidopsis thaliana]
Seq. No.
                  164561
Seq. ID
                  LIB3177-078-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  736
E value
                  2.0e-78
Match length
                  141
% identity
                  99
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir_ A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >qi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  164562
Seq. ID
                  LIB3177-078-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g2477521
BLAST score
                  360
E value
                  0.0e + 00
Match length
                  452
% identity
```

```
NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164563
Seq. ID
                   LIB3177-078-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2506496
BLAST score
                   679
E value
                   1.0e-71
                   130
Match length
% identity
                   100
NCBI Description
                  GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI)
                   >gi 1890156 emb CAA72413 (Y11727) gluthatione
                   S-transferase [Arabidopsis thaliana]
Seq. No.
                   164564
Seq. ID
                   LIB3177-078-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   q3510336
BLAST score
                   140
                   3.0e-73
E value
                   144
Match length
                   99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18J17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164565
Seq. ID
                   LIB3177-078-P1-K1-C10
Method
                   BLASTN
NCBI GI
                  q2264318
BLAST score
                   130
E value
                   4.0e-67
Match length
                  138
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164566
Seq. ID
                  LIB3177-078-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  601
E value
                  1.0e-62
Match length
                  117
% identity
                  73
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  164567
                  LIB3177-078-P1-K1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4468103
BLAST score
                  239
E value
                  1.0e-132
Match length
                  239
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
```

(ESSA project)

BLAST score

```
Seq. No.
                    164568
Seq. ID
                    LIB3177-078-P1-K1-C3
Method
                    BLASTX
NCBI GI
                    g1703108
BLAST score
                    349
E value
                    4.0e-33
Match length
                    68
% identity
                    100
                    ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
NCBI Description
                    thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                    thaliana]
Seq. No.
                    164569
Seq. ID
                    LIB3177-078-P1-K1-C4
Method
                    BLASTN
NCBI GI
                    g3659491
BLAST score
                    416
E value
                    0.0e+00
Match length
                    458
% identity
                    99
NCBI Description
                    Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
                    1, complete sequence [Arabidopsis thaliana]
Seq. No.
                    164570
Seq. ID
                    LIB3177-078-P1-K1-C5
Method
                    BLASTX
NCBI GI
                    g4741940
BLAST score
                    595
E value
                    9.0e-62
Match length
                    110
% identity
NCBI Description
                   (AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.
                    164571
                    LIB3177-078-P1-K1-C6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g399013
BLAST score
                    656
E value
                    6.0e-69
Match length
                    149
% identity
                    83
NCBI Description
                    ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                    (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                    >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                    thaliana (fragment) >gi 16175 emb CAA46518 (X65549)
                    adenylate translocator [Arabidopsis thaliana]
                    >gi_445607_prf _1909354A adenylate translocator
                    [Arabidopsis thaliana]
Seq. No.
                   164572
Seq. ID
                   LIB3177-078-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   q166833
```

```
E value
                   1.0e-15
Match length
                   82
                   100
 % identity
NCBI Description
                   Arabidopisis thaliana ribulose bisphosphate
                   carboxylase/oxygenase activase (rca) gene, complete cds
Seq. No.
                   164573
Seq. ID
                   LIB3177-078-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g3420055
BLAST score
                   644
E value
                   1.0e-67
                   124
Match length
% identity
                   100
.NCBI Description
                  (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                   164574
Seq. ID
                   LIB3177-078-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g4689366
BLAST score
                   381
E value
                   1.0e-36
Match length
                   139
% identity
                   55
NCBI Description (AF134155) RING finger protein [Arabidopsis thaliana]
Seq. No.
                  164575
Seq. ID
                  LIB3177-078-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4006858
BLAST score
                  232
E value
                  2.0e-19
Match length
                  62
% identity
                  (Z99707) cold acclimation protein homolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164576
Seq. ID
                  LIB3177-078-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2738248
BLAST score
                  586
E value
                  7.0e-61
Match length
                  124
% identity
                  96
NCBI Description
                  (U97200) cobalamin-independent methionine synthase
                  [Arabidopsis thaliana]
Seq. No.
                  164577
Seq. ID
                  LIB3177-078-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3660471
BLAST score
                  440
E value
                  1.0e-43
Match length
                  121
% identity
                  69
NCBI Description
                  (AJ001809) succinate dehydrogenase flavoprotein alpha
```

61.

subunit [Arabidopsis thaliana]

```
Seq. No.
                   164578
 Seq. ID
                   LIB3177-078-P1-K1-D12
 Method
                   BLASTX
 NCBI GI
                   g132074
.BLAST score .
                   587
 E value
                   5.0e-61
Match length
                   109
 % identity
                   99
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
 NCBI Description
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
 Seq. No.
                   164579
Seq. ID
                   LIB3177-078-P1-K1-D3
Method
                   BLASTN
NCBI GI
                   g4678340
BLAST score
                   253
E value
                   1.0e-140
Match length
                   368
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11
                   (ESSA project)
Seq. No.
                   164580
Seq. ID
                   LIB3177-078-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g1769905
BLAST score
                   546
E value
                   5.0e-56
Match length
                   144
% identity
                  74
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                  164581
Seq. ID
                  LIB3177-078-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2281115
BLAST score
                  691
E value
                  5.0e-73
Match length
                  153
% identity
                  90
NCBI Description
                  (AC002330) putative cullin-like 1 protein [Arabidopsis
                  thaliana]
Seq. No.
                  164582
Seq. ID
                  LIB3177-078-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4741962
BLAST score
                  479
E value
                  3.0e-48
Match length
                  145
% identity
                  54
NCBI Description (AF134131) PsbS protein [Arabidopsis thaliana]
```

NCBI GI

```
Seq. No.
                    164583
 Seq. ID
                    LIB3177-078-P1-K1-D8
 Method
                    BLASTX
 NCBI GI
                    g3688799
 BLAST score
                    666
 E value
                    4.0e-70
 Match length
                    133
 % identity
                    99
                    (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    164584
 Seq. ID
                   LIB3177-078-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   g3420042
BLAST score
                   136
E value
                   2.0e-70
Match length
                   420
 % identity
                   98
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T13E15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164585
Seq. ID
                   LIB3177-078-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1621539
BLAST score
                   529
E value
                   4.0e-60
Match length
                   126
% identity
                   45
NCBI Description
                   (U28415) annexin-like protein [Arabidopsis thaliana]
Seq. No.
                   164586
Seq. ID
                   LIB3177-078-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g3402716
BLAST score
                   218
E value
                   1.0e-17
Match length
                   114
% identity
                   47
NCBI Description
                   (AC004261) unknown protein [Arabidopsis thaliana]
Seq. No.
                   164587
Seq. ID
                   LIB3177-078-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g3288823
BLAST score
                   639
E value
                   6.0e-67
Match length
                  127
% identity
                   100
NCBI Description
                  (AF063852) FUS5 [Arabidopsis thaliana]
Seq. No.
                  164588
Seq. ID
                  LIB3177-078-P1-K1-E12
Method
                  BLASTN
```

22041 .

g3702730

```
BLAST score
                   90
E value
                   4.0e-43
Match length
                   97
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MAB16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164589
Seq. ID
                   LIB3177-078-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2781354
BLAST score
                   683
                   4.0e-72
E value
Match length
                   128
                   100
% identity
NCBI Description
                  (AC003113) F2401.10 [Arabidopsis thaliana]
Seq. No.
                   164590
Seq. ID
                  LIB3177-078-P1-K1-E4
Method
                   BLASTN
NCBI GI
                  q516248
BLAST score
                   85
                   5.0e-40
E value
Match length
                  92
                  99
% identity
NCBI Description A.thaliana gene for porphobilinogen deaminase
Seq. No.
                  164591
Seq. ID
                  LIB3177-078-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g1514639
BLAST score
                  726
                  4.0e-77
E value
Match length
                  150
% identity
                  93
NCBI Description
                 (X85181) alpha-glucan phosphorylase [Spinacia oleracea]
Seq. No.
                  164592
Seq. ID
                  LIB3177-078-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g4733953
BLAST score
                  326
                  0.0e + 00
E value
Match length
                  350
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
                  sequence, complete sequence
Seq. No.
                  164593
Seq. ID
                  LIB3177-078-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g4467094
BLAST score
                  72
E value
                  3.0e - 32
Match length
                  154
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
```

(ESSA project)

```
Seq. No.
                   164594
Seq. ID
                   LIB3177-078-P1-K1-F1
Method
                   BLASTN
NCBI GI
                  g1279569
BLAST score
                   86
                   2.0e-40
E value
Match length
                   260
% identity
                  90
NCBI Description Nicotiana acuminata chloroplast JLA region, 1-1028bp
Seq. No.
                  164595
Seq. ID
                  LIB3177-078-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g416652
BLAST score
                  415
E value
                  1.0e-40
Match length
                  136
% identity
                  59
                  PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
NCBI Description
                  PCNT107) >gi_19793_emb_CAA39707_ (X56266) auxin-induced
                  protein [Nicotiana tabacum]
Seq. No.
                  164596
Seq. ID
                  LIB3177-078-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1071912
BLAST score
                  649
                  4.0e-68
E value
Match length
                  138
                  94
% identity
                  cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis
NCBI Description
                  thaliana >gi 572517_emb_CAA57344_ (X81698) cysteine
                  synthase [Arabidopsis thaliana]
Seq. No.
                  164597
Seq. ID
                  LIB3177-078-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g464707
BLAST score
                  637
E value
                  1.0e-66
Match length
                  128
% identity
                  97
                  40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
NCBI Description
                  protein S18.A - Arabidopsis thaliana
                  >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_434343_emb CAA82273 (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb Z28701, DNA gb Z23165 from A.
                  thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                  gb_R30430 come from this gene. [Arabidopsis thaliana]
```

```
protein [Arabidopsis thaliana]
 Seq. No.
                    164598
 Seq. ID
                   LIB3177-078-P1-K1-F2
 Method
                   BLASTN
 NCBI GI
                   g4454447
BLAST score
                   368
 E value
                   0.0e + 00
Match length
                   455
 % identity
                   98
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F5H14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   164599
Seq. ID
                   LIB3177-078-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g4835235
BLAST score
                   241
E value
                   2.0e-20
                   103
Match length
% identity
                   49
NCBI Description
                   (AL049862) putative protein [Arabidopsis thaliana]
Seq. No.
                   164600
Seq. ID
                   LIB3177-078-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   657
E value
                   4.0e-69
Match length
                   122
% identity
                   98
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1.1}.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   164601
                   LIB3177-078-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4490330
BLAST score
                   773
E value
                   1.0e-82
Match length
                   151
% identity
                   91
                   (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   164602
Seq. ID
                  LIB3177-078-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g4741962
BLAST score
                  478
E value
                   4.0e-48
Match length
                  132
```

>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal

NCBI GI

```
% identity
                   57
NCBI Description (AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.
                   164603
Seq. ID
                  LIB3177-078-P1-K1-F8
Method ~~
                  BLASTX
NCBI GI
                  q3063697
BLAST score
                   812
                   3.0e-87
E value
Match length
                  151
% identity
                  99
                  (AL022537) putative myb-protein (partial) [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  164604
Seq. ID
                  LIB3177-078-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3776001
BLAST score
                  638
E value
                  8.0e-67
Match length
                  128
% identity
                  95
NCBI Description
                  (AJ010464) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  164605
Seq. ID
                  LIB3177-078-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  752
E value
                  3.0e-80
Match length
                  143
% identity
NCBI Description
                 chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  164606
Seq. ID
                  LIB3177-078-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g4587541
BLAST score
                  700
E value
                  4.0e-74
Match length
                  137
% identity
                  (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase
NCBI Description
                  with GDSL-motif family. ESTs gb T44453, gb T04815,
                  gb_T45993, gb_R30138, gb_AI0995\overline{7}0 and gb_T\overline{2}2281 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  164607
                  LIB3177-078-P1-K1-G12
Seq. ID
Method
                  BLASTX
```

g1362002

E value

8.0e-44

```
BLAST score
                   278
E value
                   4.0e-25
Match length
                   58
% identity
                   95
NCBI Description
                   protein kinase 1 - Arabidopsis thaliana >gi 166817 (L05561)
                   protein kinase [Arabidopsis thaliana]
                                                                           ٠, .
Seq. No.
                   164608
Seq. ID
                   LIB3177-078-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g3128205
BLAST score
                   687
E value
                   1.0e-72
Match length
                   151
% identity
                   89
NCBI Description
                   (AC004077) putative pyruvate dehydrogenase complex E1 beta
                   subunit [Arabidopsis thaliana]
Seq. No.
                   164609
Seq. ID
                   LIB3177-078-P1-K1-G3
Method
                   BLASTN
NCBI GI
                   g3201608
BLAST score
                   218
E value
                   1.0e-119
Match length
                   448
                   100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164610
Seq. ID
                  LIB3177-078-P1-K1-G4
                  {\tt BLASTX}
Method
NCBI GI
                   g4455210
BLAST score
                   348
                   7.0e-33
E value
Match length
                   77
% identity
                   86
                   (AL035440) putative aspartate-tRNA ligase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   164611
Seq. ID
                  LIB3177-078-P1-K1-G5
Method
                  BLASTN
                  g3201608
NCBI GI
BLAST score
                   40
E value
                   3.0e-13
Match length
                  76
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  164612
Seq. No.
Seq. ID
                  LIB3177-078-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  g3540210
BLAST score
                  91
```

Match length

```
Match length
                   155
% identity
                   100
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F5A8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164613
Seq. ID
                  LIB3177-078-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q282865
BLAST score
                   666
E value
                   4.0e-70
Match length
                   132
                  72
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi 4678304 emb CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  164614
Seq. ID
                  LIB3177-078-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                  733
                  5.0e-78
E value
Match length
                  150
% identity
NCBI Description
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                  >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
Seq. No.
                  164615
Seq. ID
                  LIB3177-078-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2506443
BLAST score
                  364
E value
                  4.0e-35
Match length
                  75
% identity
                  99
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi_2117520 pir JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi 1402885 emb CAA66816 (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) [Arabidopsis thaliana]
Seq. No.
                  164616
Seq. ID
                  LIB3177-078-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q2317729
BLAST score
                  694
E value
                  2.0e-73
```

.

```
99
   % identity
  NCBI Description
                     (AF013627) reversibly glycosylated polypeptide-1
                     [Arabidopsis thaliana]
  Seq. No.
                     164617
· Seq. ID
                     LIB3177-078-P1-K1-H10
  Method
                     BLASTX
  NCBI GI
                     g2191138
  BLAST score
                     391
  E value
                     4.0e-38
  Match length
                     80
  % identity
                     99
  NCBI Description
                     (AF007269) A_IG002N01.18 gene product [Arabidopsis
                     thaliana]
  Seq. No.
                     164618
  Seq. ID
                     LIB3177-078-P1-K1-H11
  Method
                     BLASTX
  NCBI GI
                     g3461817
  BLAST score
                     301
  E value
                     2.0e-27
  Match length
                     134
                     45
  %_identity
  NCBI Description
                    (AC004138) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     164619
  Seq. ID
                     LIB3177-078-P1-K1-H12
  Method
                     BLASTX
  NCBI GI
                     g4582468
  BLAST score
                     570
  E value
                     7.0e-59
  Match length
                     118
  % identity
                     98
                    (AC007071) putative 40S ribosomal protein; contains
  NCBI Description
                     C-terminal domain [Arabidopsis thaliana]
  Seq. No.
                     164620
  Seq. ID
                     LIB3177-078-P1-K1-H2
  Method
                     BLASTX
  NCBI GI
                     g4584541
  BLAST score
                     592
                     2.0e-61
  E value
  Match length
                     115
                     100
  % identity
                     (AL049608) 3-hydroxyisobutyryl-coenzyme A hydrolase-like
  NCBI Description
                     protein [Arabidopsis thaliana]
  Seq. No.
                     164621
  Seq. ID
                     LIB3177-078-P1-K1-H3
  Method
                     BLASTX
  NCBI GI
                     g3249086
  BLAST score
                     217
                     2.0e-17
  E value
  Match length
                     148
  % identity
                     66
                     (AC004473) Contains similarity to 21 KD subunit of the
  NCBI Description
                     Arp2/3 protein complex (ARC21) gb_AF006086 from Homo
```

Seq. No. 164622 Seq. ID LIB3177-078-P1-K1-H4 Method BLASTX NCBI GI g2062164 BLAST score 528 4.0e-54 E value Match length 101 % identity 99 NCBI Description (ACO01645) jasmonate inducible protein isolog [Arabidopsis thaliana] Seq. No. 164623 Seq. ID LIB3177-078-P1-K1-H5 BLASTX Method NCBI GI g4262174 BLAST score 774 E value 8.0e-83 Match length 144 99 % identity NCBI Description (AC005508) 9058 [Arabidopsis thaliana] Seq. No. 164624 Seq. ID LIB3177-078-P1-K1-H6 Method BLASTX NCBI GI g1173218 BLAST score 494 E value 6.0e-50 Match length 109 % identity 90 NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] Seq. No. 164625 Seq. ID LIB3177-078-P1-K1-H8 Method BLASTX NCBI GI g3261659 BLAST score 119 9.0e-10 E value Match length 90 % identity 42 NCBI Description (Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis] Seq. No. 164626 Seq. ID LIB3177-079-P1-K1-A1 Method BLASTN NCBI GI g4581084 BLAST score 278 E value 1.0e-155 360 Match length % identity 100 NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic

sapiens. EST gb Z37222 comes [Arabidopsis thaliana]

sequence, complete sequence

NCBI GI

```
Seq. No.
                  164627
Seq. ID
                  LIB3177-079-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2104677
BLAST score
                   232
E value
                   3.0e-19
Match length
                  111
% identity
                   49
NCBI Description
                  (X97904) transcription factor [Vicia faba]
Seq. No.
                  164628
Seq. ID
                  LIB3177-079-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1170203
                  335
BLAST score
                  2.0e-31
E value
                  93
Match length
                  72
% identity
NCBI Description
                  GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >qi 454359
                   (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]
                  164629
Seq. No.
                LIB3177-079-P1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3776029
BLAST score
                  771
E value
                  2.0e-82
                  151
Match length
                  100
% identity
NCBI Description
                  (AJ010476) RNA helicase [Arabidopsis thaliana]
                  164630
Seq. No.
Seq. ID
                  LIB3177-079-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  q857373
BLAST score
                  233
E value
                  1.0e-128
Match length
                  314
% identity
                  100
NCBI Description
                  Arabidopsis thaliana mRNA for phosphoinositide specific
                  phospholipase C, complete cds
Seq. No.
                  164631
                  LIB3177-079-P1-K1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4454004
BLAST score
                  245
                  1.0e-135
E value
Match length
                  285
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
NCBI Description
                  (ESSAII project)
                  164632
Seq. No.
Seq. ID
                  LIB3177-079-P1-K1-A5
Method
                  BLASTX
```

g1495269

Method

BLASTX

```
BLAST score
                   388
E value
                   1.0e-37
Match length
                   112
% identity
                   71
NCBI Description
                   (X97829) product similar to ccr protein, Citrus paradisi;
                   PIR: S52663 [Arabidopsis thaliana]
                   >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis
                   thaliana]
Seq. No.
                   164633
Seq. ID
                   LIB3177-079-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q232031
BLAST score
                   332
E value
                   4.0e-31
Match length
                   115
% identity
                   54
NCBI Description
                  ELONGATION FACTOR 1 BETA' >gi_322851_pir S29224
                  translation elongation factor eEF-1 beta chain - rice
                  >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza sativa]
Seq. No.
                  164634
Seq. ID
                  LIB3177-079-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  q166695
BLAST score
                  43
E value
                  2.0e-15
Match length
                  51
                  96
% identity
NCBI Description
                  Arabidopsis thaliana recombination and DNA-damage
                  resistance protein (DRT112) mRNA, complete cds
Seq. No.
                  164635
Seq. ID
                  LIB3177-079-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g4262180
BLAST score
                  511
E value
                  4.0e-52
Match length
                  99
% identity
                  94
NCBI Description
                  (AC005508) 29621 [Arabidopsis thaliana]
Seq. No.
                  164636
Seq. ID
                  LIB3177-079-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3047117
BLAST score
                  440
E value
                  8.0e-44
Match length
                  117
% identity
                  74
NCBI Description
                  (AF058919) similar to ATP-dependent RNA helicases
                  [Arabidopsis thaliana]
Seq. No.
                  164637
Seq. ID
                  LIB3177-079-P1-K1-B11
```

```
NCBI GI
                   q4741960
BLAST score
                   507
E value
                   2.0e-51
                   116
Match length
                   84
% identity
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                   164638
Seq. ID
                   LIB3177-079-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q1402908
BLAST score
                   670
E value
                   1.0e-70
                   129
Match length
% identity
                   100
NCBI Description
                   (X98315) peroxidase [Arabidopsis thaliana]
                   >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
[Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)
                   peroxidase [Arabidopsis thaliana]
Seq. No.
                   164639
Seq. ID
                   LIB3177-079-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g1708577
                   293
BLAST score.
E value
                   1.0e-26
                   68
Match length
                   68
% identity
                   TRYPSIN INHIBITOR 2 PRECURSOR (MTI-2)
NCBI Description
                   >gi_2129818_pir__S65661 trypsin inhibitor 2 - white mustard
                   >gi_1054853_emb_CAA58994_ (X84208) trypsin inhibitor 2
                   [Sinapis alba] >gi_2791356_emb_CAA76116 (Y16190) trypsin
                   inhibitor 2 [Sinapis alba]
                   164640
Seq. No.
Seq. ID
                   LIB3177-079-P1-K1-B3
                   BLASTX
Method
NCBI GI
                   g3261659
BLAST score
                   166
E value
                   1.0e-11
Match length
                   66
% identity
NCBI Description
                   (Z81368) hypothetical protein Rv2419c [Mycobacterium
                   tuberculosis]
                   164641
Seq. No.
                   LIB3177-079-P1-K1-B4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3236479
BLAST score
                   137
                   5.0e-71
E value
Match length
                   365
                   97
% identity
                  Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8 .
NCBI Description
                   cM, complete sequence
```

164642

Seq. No.

```
Seq. ID
                    LIB3177-079-P1-K1-B5
Method
                    BLASTX
NCBI GI
                    g1170089
BLAST score
                    656
E value
                    5.0e-69
.Match length
                    129
% identity
                    100
                   GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
NCBI Description
                    >gi_481822_pir_ S39542 probable glutathione transferase (EC
                    2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                    S-transferase [Arabidopsis thaliana]
Seq. No.
                    164643
Seq. ID
                    LIB3177-079-P1-K1-B6
Method
                    BLASTX
NCBI GI
                    g3176690
BLAST score
                    736
E value
                    3.0e-78
Match length
                    155
% identity
                    99
NCBI Description
                   (AC003671) Similar to ubiquitin ligase gb D63905 from S.
                    cerevisiae. EST gb_R65295 comes from this gene.
                    [Arabidopsis thaliana]
Seq. No.
                    164644
Seq. ID
                    LIB3177-079-P1-K1-B7
Method
                    BLASTX
NCBI GI
                    g1402914
BLAST score
                    463
                    2.0e-46
E value
                    92
Match length
                    100
% identity
NCBI Description (X98318) peroxidase [Arabidopsis thaliana]
Seq. No.
                    164645
Seq. ID
                   LIB3177-079-P1-K1-B8
Method
                   BLASTX
NCBI GI
                    g3702323
BLAST score
                    410
E value
                    3.0e-40
Match length
                    93
% identity
                    85
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                 164646
                   LIB3177-079-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2281086
BLAST score
                   182
E value
                   1.0e-13
Match length
                   62
                   52
% identity
                   (AC002333) indole-3-acetate beta-glucosyltransferase isolog
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No.

164652

```
Seq. No.
                   164647
Seq. ID
                   LIB3177-079-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   g3367500
BLAST score
                   108
E value
                   1.0e-53
Match length
                   398
                   100
% identity
                   REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                   TO: 93489, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164648
Seq. ID
                   LIB3177-079-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   g2980757
BLAST score
                   286
E value
                   1.0e-160
Match length
                   343
% identity
                   95
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
                   (ESSAII project)
Seq. No.
                   164649
Seq. ID
                   LIB3177-079-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   q3738275
BLAST score
                   384
E value
                   0.0e + 00
Match length
                   384
                   100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164650
Seq. ID
                   LIB3177-079-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q132074
BLAST score
                   602
E value
                   1.0e-62
Match length
                   110
% identity
                   100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1}.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  164651
                  LIB3177-079-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  449
E value
                  7.0e-45
Match length
                  109
% identity
                  78
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
```

```
Seq. ID
                   LIB3177-079-P1-K1-C3
Method
                   BLASTX
 NCBI GI
                   g2407802
 BLAST score
                   359
E value
                   4.0e-34
Match length
                   75
 % identity
                   97
NCBI Description
                   (Y12576) histone H2B [Arabidopsis thaliana]
Seq. No.
                   164653
Seq. ID
                   LIB3177-079-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q2160182
BLAST score
                   188
E value
                   4.0e-14
Match length
                   133
% identity
                   38
NCBI Description
                   (AC000132) ESTs gb_ATTS1236, gb_T43334, gb_N97019, gb AA395203
                   come from this gene. [Arabidopsis thaliana]
Seq. No.
                   164654
Seq. ID
                   LIB3177-079-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g2911042
BLAST score
                   579
E value
                   6.0e-60
Match length
                   120
% identity
NCBI Description
                   (AL021961) Phosphoglycerate dehydrogenase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   164655
Seq. ID
                   LIB3177-079-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g2244750
BLAST score
                   421
E value
                   1.0e-41
Match length
                   85
% identity
                   95
NCBI Description
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                  >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
Seq. No.
                  164656
Seq. ID
                  LIB3177-079-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2708751
BLAST score
                  210
E value
                  8.0e-17
Match length
                  78
% identity
                  58
NCBI Description
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164657
Seq. ID
                  LIB3177-079-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2832625
```

BLASTX

```
BLAST score
                   330
 E value
                   7.0e-31
Match length
                   70
% identity
                   86
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
 Seq. No.
                   164658
Seq. ID
                   LIB3177-079-P1-K1-C9
Method
                   BLASTN
NCBI GI
                   g2342673
BLAST score
                   245
E value
                   1.0e-135
Match length
                   249
% identity
                   100
NCBI Description
                  Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164659
Seq. ID
                   LIB3177-079-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   q2815404
BLAST score
                   158
E value
                   9.0e-84
Match length
                   222
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMG4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164660
Seq. ID
                  LIB3177-079-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  508
E value
                  7.0e-52
Match length
                  104
% identity
                  68
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  164661
Seq. ID
                  LIB3177-079-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  g2351062
BLAST score
                  182
E value
                  8.0e-98
                  394
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164662
                  LIB3177-079-P1-K1-D2
Seq. ID
```

NCBI GI

بيتخذ

```
NCBI GI
                   g1621268
BLAST score
                   149
E value
                   4.0e-10
Match length
                   35
% identity
                   80
NCBI Description
                   (Z81012) unknown [Ricinus communis]
Seq. No.
                   164663
Seq. ID
                   LIB3177-079-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g2739371
BLAST score
                   571
E value
                   5.0e-59
Match length
                   110
                   100
% identity
NCBI Description
                  (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                   164664
Seq. ID
                   LIB3177-079-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g132102
BLAST score
                   726
E value
                   4.0e-77
Match length
                   140
                   97
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   164665
Seq. ID
                   LIB3177-079-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   q2673901
BLAST score
                   255
E value
                   1.0e-141
Match length
                   438
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T24P15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164666
Seq. ID
                   LIB3177-079-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g2244762
BLAST score
                   478
E value
                   4.0e-48
Match length
                   119
% identity
                   75
NCBI Description
                  (Z97335) major latex protein [Arabidopsis thaliana]
Seq. No.
                  164667
                  LIB3177-079-P1-K1-D7
Seq. ID
Method
                  BLASTX
```

g2642215

```
BLAST score
                    185
 E value
                    7.0e-14
 Match length
                    34
 % identity
                   100
 NCBI Description
                   (AF030386) NOI protein [Arabidopsis thaliana]
 Seq. No.
                   164668
 Seq. ID
                   LIB3177-079-P1-K1-D8
 Method
                   BLASTX
NCBI GI
                   g4678322
 BLAST score
                   530
E value
                   2.0e-54
 Match length
                   121
 % identity
                   87
 NCBI Description
                   (AL049658) putative protein [Arabidopsis thaliana]
 Seq. No.
                   164669
 Seq. ID
                   LIB3177-079-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g2880049
BLAST score
                   265
E value
                   4.0e-23
Match length
                   102
% identity
                   55
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                 . 164670
Seq. ID
                   LIB3177-079-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1619300
BLAST score
                   385
E value
                   3.0e - 37
Match length
                   81
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   164671
Seq. ID
                   LIB3177-079-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g2842490
BLAST score
                   447
E value
                   2.0e-44
Match length
                  120
% identity
                  73
NCBI Description
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  164672
Seq. ID
                  LIB3177-079-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g4503523
BLAST score
                  172
E value
                  3.0e-27
Match length
                  154
% identity
                  47
NCBI Description
                  UNKNOWN >gi 2351378 (U54558) translation initiation factor
                  eIF3 p66 subunit [Homo sapiens] >gi_4200328_emb_CAA18440_
                  (AL022313) EIF3-P66 [Homo sapiens]
```

```
Seq. No.
                     164673
  Seq. ID
                     LIB3177-079-P1-K1-E12
  Method
                     BLASTX
  NCBI GI
                     g2191138
  BLAST score
                     597
  E value
                     5.0e-62
  Match length
                     119
  % identity
                     99
  NCBI Description
                     (AF007269) A IG002N01.18 gene product [Arabidopsis
  Seq. No.
                     164674
  Seq. ID
                    LIB3177-079-P1-K1-E2
  Method
                    BLASTN
  NCBI GI
                     g2244991
  BLAST score
                     309
  E value
                    1.0e-173
  Match length
                    414
  % identity
                    100
  NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                    fragment No
  Seq. No.
                    164675
  Seq. ID
                    LIB3177-079-P1-K1-E3
 Method
                    BLASTX
. NCBI GI
                    g4507131
 BLAST score
                    329
 E value
                    1.0e-30
 Match length
                    74
 % identity
                    78
 NCBI Description
                    small nuclear ribonucleoprotein polypeptide F
                    >gi_1085384_pir__S55053 Sm protein F - human
                    >gi_806564_emb_CAA59688_ (X85372) Sm protein F [Homo
                    sapiens]
 Seq. No.
                    164676
 Seq. ID
                    LIB3177-079-P1-K1-E4
 Method
                    BLASTN
 NCBI GI
                    g3033373
 BLAST score
                    120
 E value
                    8.0e-61
 Match length
                    132
 % identity
                    82
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F19I3 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   164677
 Seq. ID
                   LIB3177-079-P1-K1-E5
 Method
                   BLASTN
 NCBI GI
                   q3883123
 BLAST score
                   181
 E value
                   2.0e-97
 Match length
                   224
 % identity
                   97
 NCBI Description
                   Arabidopsis thaliana arabinogalactan-protein (AGP3) mRNA,
```

complete cds

BLASTN

```
Seq. No.
                   164678
Seq. ID
                   LIB3177-079-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g4678328
BLAST score
                   387
E value
                   2.0e-37
Match length
                   128
                   57
% identity
NCBI Description
                   (AL049658) aldehyde dehydrogenase (NAD+)-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   164679
Seq. ID
                   LIB3177-079-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   g2275194
BLAST score
                   73
                   7.0e-33
E value
Match length
                   130
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T08I13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164680
Seq. ID
                   LIB3177-079-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   g16249
BLAST score
                   97
E value
                   2.0e-47
Match length
                   104
                   98
% identity
NCBI Description A.thaliana mRNA for Cu, Zn superoxide dismutase
Seq. No.
                   164681
Seq. ID
                   LIB3177-079-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   q3869065
BLAST score
                   273
E value
                   1.0e-152
Match length
                   331
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K24M7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164682
Seq. ID
                  LIB3177-079-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g4587681
BLAST score
                  484
E value
                  8.0e-49
Match length
                  94
% identity
                  100
NCBI Description
                  (AC007197) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  164683
Seq. ID
                  LIB3177-079-P1-K1-F11
```

```
NCBI GI
                   q2828186
BLAST score
                   231
                   1.0e-127
E value
Match length
                   442
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18I23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164684
                   LIB3177-079-P1-K1-F12
Seq. ID
Method
                   BLASTX
                   q4835226
NCBI GI
BLAST score
                   171
                   3.0e-12
E value
Match length
                   54
% identity
                   59
NCBI Description
                  (AL049862) putative protein [Arabidopsis thaliana]
Seq. No.
                   164685
Seq. ID
                   LIB3177-079-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g4218123
BLAST score
                   423
                   1.0e-41
E value
Match length
                   136
% identity
                   65
NCBI Description
                   (AL035353) photosystem I subunit PSI-E-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   164686
Seq. ID
                   LIB3177-079-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q115767
BLAST score
                   670
                   1.0e-70
E value
                   124
Match length
% identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540 (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   164687
Seq. ID
                   LIB3177-079-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   q1399275
BLAST score
                   490
                   2.0e-49
E value
                   108
Match length
                   85
% identity
NCBI Description
                   (U31835) calmodulin-domain protein kinase CDPK isoform 6
                   [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis
```

thaliana]

```
Seq. No.
                   164688
Seq. ID
                   LIB3177-079-P1-K1-F7
Method
                   BLASTN
NCBI GI
                   g16375
BLAST score
                   75
E valué
                  .9.0e-35
Match length
                   83
% identity
                   98
NCBI Description
                  A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding
                   protein
Seq. No.
                   164689
Seq. ID
                   LIB3177-079-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g2492514
BLAST score
                   542
E value
                   1.0e-55
Match length
                   125
% identity
                   86
NCBI Description
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
                  >gi 1483215 emb CAA68141 (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
Seq. No.
                  164690
Seq. ID
                  LIB3177-079-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  576
E value
                  1.0e-59
Match length
                  141
% identity
                  75
NCBI Description
                  (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  164691
Seq. ID
                  LIB3177-079-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  q4678705
BLAST score
                  55
E value
                  4.0e-22
Match length
                  225
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                  (ESSA project)
Seq. No.
                  164692
Seq. ID
                  LIB3177-079-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2244868
BLAST score
                  706
E value
                  7.0e-75
Match length
                  135
                  100
% identity
NCBI Description
                 (Z97337) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  164693
Seq. ID
                  LIB3177-079-P1-K1-G3
```

```
Method
                   BLASTX
NCBI GI
                   q464621
BLAST score
                   197
E value
                   9.0e-16
Match length
                   46
% identity
                   87
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
Seq. No.
                   164694
Seq. ID
                   LIB3177-079-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   775
E value
                   7.0e-83
Match length
                   147
                   100
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab16\overline{5} - Arabidopsis thaliana
                   >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   164695
Seq. ID
                   LIB3177-079-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g1575754
BLAST score
                   480
E value
                   3.0e-48
Match length
                   129
% identity
                   78
NCBI Description
                   (U70616) ADP glucose pyrophosphorylase small subunit
                   [Arabidopsis thaliana]
Seq. No.
                   164696
Seq. ID
                   LIB3177-079-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   g4468801
BLAST score
                   246
E value
                   1.0e-136
Match length
                   363
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
                   (ESSA project)
Seq. No.
                   164697
Seq. ID
                   LIB3177-079-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   678
E value
                   1.0e-71
Match length
                   125
% identity
                   99
```

```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   164698
Seq. ID
                   LIB3177-079-P1-K1-G9
Method
                   BLASTN
NCBI GI
                   q4757409
BLAST score
                   77
E value
                   4.0e-35
Match length
                   432
% identity
                   67
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MVC8, complete sequence
Seq. No.
                   164699
Seq. ID
                   LIB3177-079-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g3478700
BLAST score
                   508
E value
                   9.0e-52
Match length
                   113
% identity
                   88
NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]
Seq. No.
                   164700
Seq. ID
                   LIB3177-079-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g4263791
BLAST score
                   333
E value
                   4.0e-31
Match length
                   61
% identity
                   100
NCBI Description
                  (AC006068) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  164701
                  LIB3177-079-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                  400
E value
                  2.0e-39
Match length
                  87
% identity
                  95
NCBI Description
                  60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  164702
Seq. ID
                  LIB3177-079-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2894596
BLAST score
                  291
E value
                  2.0e-38
Match length
                  118
% identity
                  67
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
```

```
Seq. No.
                   164703
                   LIB3177-079-P1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2828267
BLAST score
                   521<sup>-</sup>
E value
                   4.0e-53
Match length
                   127
% identity
                   83
NCBI Description (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
Seq. No.
                   164704
Seq. ID
                   LIB3177-079-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   g2252848
BLAST score
                   151
E value
                   2.0e-79
Match length
                   302
% identity
                   97
NCBI Description Arabidopsis thaliana BAC TM018A10
Seq. No.
                   164705
Seq. ID
                  LIB3177-079-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g2264310
BLAST score
                   191
E value
                  1.0e-103
                   392
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKP11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164706
Seq. ID
                  LIB3177-079-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3913418
BLAST score
                  633
E value
                  2.0e-66
Match length
                  121
% identity
                  99
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >gi_1531763_emb_CAA69073_ (Y07765)
                  S-adenosylmethionine decarboxylase [Arabidopsis thaliana]
Seq. No.
                  164707
Seq. ID
                  LIB3177-079-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g3184098
BLAST score
                  416
E value
                  8.0e-41
Match length
                  141
% identity
                  (AL023777) coenzyme a synthetase [Schizosaccharomyces
NCBI Description
                  pombe]
                                                                      4
Seq. No.
                  164708
Seq. ID
                  LIB3177-079-P1-K1-H8
```

BLAST score

312

```
Method
                   BLASTN
NCBI GI
                   g4467094
BLAST score
                   312
E value
                   1.0e-175
Match length
                   320
                   99
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
                   (ESSA project)
Seq. No.
                   164709
Seq. ID
                   LIB3177-080-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   q4519191
BLAST score
                   120
E value
                   2.0e-61
Match length
                   141
                   95
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K9P8, complete sequence
Seq. No.
                   164710
Seq. ID
                   LIB3177-080-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q4417280
BLAST score
                   521
E value
                   3.0e-53
Match length
                   124
% identity
                   86
NCBI Description
                  (AC007019) putative ATP synthase [Arabidopsis thaliana]
Seq. No.
                   164711
Seq. ID
                   LIB3177-080-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   g3985934
BLAST score
                   115
E value
                   7.0e-58
Match length
                   309
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164712
Seq. ID
                  LIB3177-080-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q4539419
BLAST score
                   288
                  1.0e-27
E value
                  7:7
Match length
                  82
% identity
                  (AL049171) putative ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164713
Seq. ID
                  LIB3177-080-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q4678349
```

₩.

NCBI GI

```
E value
                  6.0e-29
Match length
                  91
% identity
                  30
NCBI Description
                  (AL049659) putative protein [Arabidopsis thaliana]
                  164714
Seq. No.
Seq. ID
                  LIB3177-080-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g3985952
BLAST score
                  274
                  1.0e-153
E value
                  290
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MRC8, complete sequence [Arabidopsis thaliana]
                  164715
Seq. No.
                  LIB3177-080-P1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4741959
BLAST score
                  56
                  2.0e-23
E value
Match length
                  56
                 - 100
% identity
NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
                  cds
                  164716
Seq. No.
                  LIB3177-080-P1-K1-A9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4581161
                  89
BLAST score
                  7.0e-43
E value
                  121
Match length
% identity
                  93
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
NCBI Description
                  sequence, complete sequence
                  164717
Seq. No.
Seq. ID
                  LIB3177-080-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1172872
BLAST score
                  414
E value
                  4.0e-41
                  76
Match length
                  100
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >qi 541856 pir JN0718
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi 435618 dbj BAA02373
                  (D13042) thiol protease [Arabidopsis thaliana]
                  >gi 4539328 emb CAB38829.1 (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                  164718
Seq. ID
                  LIB3177-080-P1-K1-B10
Method
                  BLASTN
```

g2244788

E value

5.0e-10

```
BLAST score
                  51
. E value
                  1.0e-20
 Match length
                  59
 % identity
                  97
 NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
 Seq. No.
                  164719
                  LIB3177-080-P1-K1-B11
 Seq. ID
Method
                  BLASTN
NCBI GI
                  g4510323
BLAST score
                  135
E value
                  4.0e-70
Match length
                  201
 % identity
                  54
NCBI Description Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
                  cM, complete sequence
Seq. No.
                  164720
Seq. ID
                  LIB3177-080-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g2656028
BLAST score
                  213
                1.0e-116
E value ·
Match length
                  243
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNF13
Seq. No.
                  164721
Seq. ID
                  LIB3177-080-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q4835233
BLAST score
                  344
E value
                  1.0e-32 .
Match length
                  70
% identity
                  99
NCBI Description
                 (AL049862) putative protein 1 photosystem II
                  oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                  164722
Seq. ID
                  LIB3177-080-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g3252804
BLAST score
                  82
E value
                  6.0e-39
Match length
                  82
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F26C24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                 164723
Seq. ID
                 LIB3177-080-P1-K1-B5
Method
                 BLASTX
NCBI GI
                 g1732570
BLAST score
                 148
```

```
Match length
                   28
% identity
                   100
NCBI Description
                  (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                   164724
Seq. ID
                   LIB3177-080-P1-K1-B6
Method
                   BLASTN
NCBI GI
                   q1769904
BLAST score
                   87
E value
                   1.0e-41
Match length
                   139
% identity
                   91
NCBI Description A.thaliana psbP gene
Seq. No.
                   164725
Seq. ID
                   LIB3177-080-P1-K1-B8
Method
                   BLASTN
NCBI GI
                   g3355463
BLAST score
                   124
E value
                   1.0e-63
Match length
                   164
% identity
                   95
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164726
Seq. ID
                   LIB3177-080-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g4204285
BLAST score
                   282
E value
                   9.0e-26
Match length
                   63
% identity
                  81
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  164727
Seq. ID
                  LIB3177-080-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1169201
BLAST score
                  286
E value
                  7.0e-26
Match length
                  87
% identity
                  72
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
NCBI Description
                  >gi_421830_pir__S33707 DRT112 protein - Arabidopsis
                  thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  164728
Seq. ID
                  LIB3177-080-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  g4691223
BLAST score
                  133
E value
                  6.0e-69
Match length
                  197
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
```

NCBI GI

BLAST score

BLASTN

148

g2618601

(ESSA project) Seq. No. 164729 Seq. ID LIB3177-080-P1-K1-C3 Method BLASTN NCBI GI g4691223 BLAST score 131 E value 6.0e-68 Match length 135 % identity 99 NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project) Seq. No. 164730 Seq. ID LIB3177-080-P1-K1-C4 Method BLASTX NCBI GI g730645 BLAST score 229 E value 1.0e-19 Match length 52 % identity 90 NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679 (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 🚁 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449 (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis ·thaliana] Seq. No. 164731 Seq. ID LIB3177-080-P1-K1-C5 Method BLASTX NCBI GI q2738248 BLAST score 491 E value 6.0e-50Match length 92 % identity 99 NCBI Description (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana] Seq. No. 164732 Seq. ID LIB3177-080-P1-K1-C6 Method BLASTN NCBI GI g2264316 BLAST score 52 E value 2.0e-20 Match length 304 % identity 40 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MRO11, complete sequence [Arabidopsis thaliana] Seq. No. 164733 LIB3177-080-P1-K1-C7 Seq. ID

```
5.0e-78
E value
Match length
                   160
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164734
Seq. ID
                  LIB3177-080-P1-K1-C8
Method
                  BLASTX
                  g3023857
NCBI GI
BLAST score
                  238
                  1.0e-20
E value
                  49
Match length
                  53
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi 629591 pir S48839 guanine nucleotide
                  regulatory protein - rape >gi 563335 emb CAA83924 (Z33643)
                  guanine nucleotide regulatory protein [Brassica napus]
Seq. No.
                  164735
Seq. ID
                  LIB3177-080-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2570338
BLAST score
                  432
E value
                  7.0e-43
                  87
Match length
                  100
% identity
                  (U90927) glyoxalase II isozyme [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164736
Seq. ID
                  LIB3177-080-P1-K1-D1
                  BLASTX
Method
NCBI GI
                  q4454036
BLAST score
                  427
                  2.0e-42
E value
Match length
                  79
                  99
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164737
Seq. ID
                  LIB3177-080-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q99759
BLAST score
                  415
                  4.0e-4.1
E value
                  82
Match length
% identity
                  superoxide dismutase (EC 1.15.1.1) (Fe) - Arabidopsis
NCBI Description
                  thaliana (fragment)
                  164738
Seq. No.
Seq. ID
                  LIB3177-080-P1-K1-D11
                  BLASTX
Method
NCBI GI
                  g3157924
BLAST score
                  190
```

2.0e-14

E value

Seq. No.

Seq. ID

Method

164743

BLASTX

LIB3177-080-P1-K1-D7

```
Match length
                     58
% identity
                     71
NCBI Description
                     (AC002131) Contains homology to extensin-like protein
                     gb D83227 from Populus nigra. ESTs gb_H76425, gb_T13883,
                     gb_T45348, gb_H37743, gb_AA042634, gb \(\overline{Z}\)26960 and \(\overline{g}\)b \(\overline{Z}\)25951
                    come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like
                     protein [Arabidopsis thaliana]
Seq. No.
                    164739
Seq. ID
                    LIB3177-080-P1-K1-D12
Method
                    BLASTX
NCBI GI
                    q4406814
BLAST score
                     429
E value
                    2.0e-42
Match length
                    88
% identity
                    98
NCBI Description
                     (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
                    thaliana]
Seq. No.
                    164740
Seq. ID
                    LIB3177-080-P1-K1-D2
Method
                    BLASTX ·
NCBI GI
                    g1363489
BLAST score
                    289
E value
                    1.0e-26
Match length
                    54
                    100
% identity
                    thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                    thaliana >gi_984052_emb CAA61592 (X89413) thioglucoside
                    glucohydrolase [Arabidopsis thaliana]
                    164741
Seq. No.
Seq. ID
                    LIB3177-080-P1-K1-D3
Method
                    BLASTX
NCBI GI
                    q4741952
BLAST score
                    270
E value
                    2.0e-24
Match length
                    56
% identity
                    93
NCBI Description
                    (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                    164742
                    LIB3177-080-P1-K1-D4
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2129630
BLAST score
                    654
E value
                    9.0e-69
Match length
                    118
% identity
                    99
NCBI Description
                    lamin - Arabidopsis thaliana >qi 1262754 emb CAA65750
                    (X97023) lamin [Arabidopsis thal\overline{i}ana] >g\overline{i} 33\overline{9}5760 (U7\overline{7}721)
                    unknown [Arabidopsis thaliana]
```

```
NCBI GI
                    q2262164
 BLAST score
                    201
 E value
                    3.0e-16
 Match length
                    64
 % identity
                    66
 NCBI Description
                    (AC002329) putative obtusifoliol 14-alpha demethylase
                    [Arabidopsis thaliana]
 Seq. No.
                   164744
 Seq. ID
                   LIB3177-080-P1-K1-D8
 Method
                   BLASTX
 NCBI GI
                   g4725950
 BLAST score
                   237
 E value
                   5.0e-20
 Match length
                   92
 % identity
                   58
 NCBI Description
                   (ALO49730) putative Phospholipase D [Arabidopsis thaliana]
                   >gi_4725951_emb_CAB41722.1_ (AL049730) putative
                   proline-rich protein [Arabidopsis thaliana]
 Seq. No.
                   164745
 Seq. ID
                   LIB3177-080-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   q4335711
BLAST score
                   178
E value
                   1.0e-95
Match length
                   202
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F9013 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164746
Seq. ID
                   LIB3177-080-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   630
E value
                   6.0e-66
Match length
                   123
% identity
                   98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372 emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No. Seq. ID
                  164747
                  LIB3177-080-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3193323
BLAST score
                  584
E value
                  1.0e-60
Match length
                  116
% identity
                  99
                  (AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm,
NCBI Description
                  score: 78.35); identical to Arabidopsis 40S ribosomal
```

BLAST score

38

```
Seq. No.
                    164748
Seq. ID
                    LIB3177-080-P1-K1-E11
Method
                    BLASTX
NCBI GI
                    g1169201
BLAST score
                    328
E value
                    1.0e-30
Match length
                    95
% identity
                    76
NCBI Description
                    DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                    >gi_421830_pir__S33707 DRT112 protein - Arabidopsis
                    thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                    164749
Seq. ID
                    LIB3177-080-P1-K1-E12
Method
                   BLASTX
NCBI GI
                    g133872
BLAST score
                    235
E value
                    1.0e-19
Match length
                   71
% identity
                    62
NCBI Description
                   30S RÍBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
                   >gi_282838_pir__S26494 ribosomal protein S1, chloroplast -
                   spinach >gi_322404 pir_ A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060 emb_CAA46927_
                    (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >gi_170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
Seq. No.
                   164750
Seq. ID
                   LIB3177-080-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g1732570
BLAST score
                   47
E value
                   3.0e-27
Match length
                   80
% identity
                   81
NCBI Description
                  (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                   164751
Seq. ID
                   LIB3177-080-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   g3985931
BLAST score
                   132
E value
                   3.0e-68
Match length
                   234
% identity
                   97
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K21H1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164752
                   LIB3177-080-P1-K1-E4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3193311
```

protein S13 (fragment) (SW: P49203A) except the first 32

amino acids are different [Arabidopsis thaliana]

% identity

86

```
E value
                   2.0e-12
Match length
                   58
                   91
% identity
NCBI Description Arabidopsis thaliana BAC F6N15
Seq. No.
                   164753
Seq. ID
                  -LIB3177-080-P1-K1-E5
Method
                   BLASTN
NCBI GI
                   q4589410
BLAST score
                   25
                   4.0e-05
E value
                   59
Match length
% identity
                   49
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   F2015, complete sequence
Seq. No.
                   164754
Seq. ID
                   LIB3177-080-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   g58298
BLAST score
                   138
E value
                   5.0e-72
Match length
                   166
                   96
% identity
NCBI Description
                   Synthetic DNA for A.thaliana ats1A leader spliced to
                   B.thuringiensis CryIA(c)
Seq. No.
                   164755
Seq. ID
                  LIB3177-080-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   g4585918
BLAST score
                   48
E value
                   2.0e-18
Match length
                  120
% identity
                  85
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F1013 genomic
                  sequence, complete sequence
Seq. No.
                  164756
Seq. ID
                  LIB3177-080-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g4309683
BLAST score
                  84
E value
                  7.0e-40
Match length
                  92
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  164757
Seq. ID
                  LIB3177-080-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g4704613
BLAST score
                  305
E value
                  4.0e-28
Match length
                  72
```

Match length

71

```
NCBI Description (AF109695) monodehydroascorbate reductase [Brassica juncea]
   Seq. No.
                      164758
   Seq. ID
                      LIB3177-080-P1-K1-F10
   Method
                      BLASTX
   NCBI GI
                      g4220485
   BLAST score
                      255
🛌 E value
                      5.0e-22
   Match length
                      49
   % identity
                      98
                      (AC006069) putative beta-1,3-glucanase [Arabidopsis
   NCBI Description
                      thaliana)
                      164759
   Seq. No.
   Seq. ID
                      LIB3177-080-P1-K1-F11
   Method
                      BLASTN
   NCBI GI
                      g4678291
   BLAST score
                      212
   E value
                      1.0e-116
   Match length
                      358
   % identity
                      98
   NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10
                      (ESSA project)
   Seq. No.
                      164760
   Seq. ID
                      LIB3177-080-P1-K1-F3
   Method
                      BLASTX
   NCBI GI
                      g132110
   BLAST score
                      394
   E value
                      2.0e-38
   Match length
                      78
   % identity
                      99
                      RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
   NCBI Description
                      (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                      B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                      (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                      thaliana]
   Seq. No.
                      164761
   Seq. ID
                      LIB3177-080-P1-K1-F5
  Method
                      BLASTN
  NCBI GI
                      q3449329
  BLAST score
                      190
  E value
                      1.0e-102
  Match length
                      397
                      98
  % identity
  NCBI Description
                      Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                      MDH9, complete sequence [Arabidopsis thaliana]
  Seq. No.
                      164762
  Seq. ID
                      LIB3177-080-P1-K1-F6
  Method
                      BLASTN
  NCBI GI
                      q2970638
  BLAST score
                      35
  E value
                      2.0e-10
```

```
% identity
                   87
NCBI Description Brassica napus unknown gene, complete cds
Seq. No.
                   164763
Seq. ID
                   LIB3177-080-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g1871577
BLAST score
                   188
                   2.0e-14
E value
Match length
                   52
% identity
                   65
NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]
Seq. No.
                   164764
Seq. ID
                   LIB3177-080-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q421826
BLAST score
                   240
E value
                   8.0e-21
Match length
                   71
% identity
                   65
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                   >gi_298036_emb CAA50712 (X71878) CP29 [Arabidopsis
                   thaliana]
Seq. No.
                   164765
Seq. ID
                   LIB3177-080-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g282865
BLAST score
                   812
E value
                   3.0e-87
                   150
Match length
% identity
                   78
NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                   protein [Arabidopsis thaliana] >gi_166644 (M85150)
                   chlorophyll a/b-binding protein [Arabidopsis thaliana]
                   >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                   a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                   164766
Seq. ID
                   LIB3177-080-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g4539009
BLAST score
                   643
E value
                   2.0e-67
Match length
                   140
% identity
                   82
NCBI Description (ALO49481) putative protein [Arabidopsis thaliana]
Seq. No.
                   164767
Seq. ID
                   LIB3177-080-P1-K1-G2
Method
                   BLASTX .
NCBI GI
                   g3600055
BLAST score
                   330
E value
                   6.0e-31
Match length
                   103
```

NCBI GI

BLASTN

g3402671

```
% identity
                   63
NCBI Description
                   (AF080120) contains similarity to Pisum sativum disease
                  resistance response protein 206-d (GB:U11716) [Arabidopsis
                  thaliana]
Seq. No.
                  164768
Seq. ID
                  LIB3177-080-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q132110
BLAST score
                  423
E value
                  5.0e-46
                  98
Match length
% identity
                  97
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana
Seq. No.
                  164769
Seq. ID
                  LIB3177-080-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  g2264317
BLAST score
                  110
E value
                  2.0e-55
Match length
                  118
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164770
Seq. ID
                  LIB3177-080-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  g21142
BLAST score
                  39
E value
                  5.0e-13
Match length
                  55
                  93
% identity
                  Mustard mRNA for cytosolic glyceraldehyde-3-phosphate
NCBI Description
                  dehydrogenase (GAPDH, NAD-specific; EC 1.2.1.12)
Seq. No.
                  164771
                  LIB3177-080-P1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264317
BLAST score
                  246
                  1.0e-136
E value
                  246
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUG13, complete sequence [Arabidopsis thaliana]
                  164772
Seq. No.
Seq. ID
                  LIB3177-080-P1-K1-G8
```

•

```
BLAST score
                   50
                   1.0e-19
E value
Match length
                   54
% identity
                   60
                  Arabidopsis thaliana chromosome II BAC T16B24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   164773
Seq. No.
Seq. ID
                  LIB3177-080-P1-K1-H1
Method
                  BLASTX
NCBI GI
                   g2118220
BLAST score
                   164
                  1.0e-11
E value
                   47
Match length
% identity
                  72
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                   (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581)
                   vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16
                   kDa proteolipid [Arabidopsis thaliana]
                  >gi 3096941 emb CAA18851.1_ (AL023094) vacuolar
                   H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                  >gi_4539311_emb_CAB38812.1 (AL035679) H+-transporting
                  ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
                  >gi_4589976_gb_AAD26493.1 AC007195 7 (AC007195) vacuolar
                  H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
                  164774
Seq. No.
Seq. ID
                  LIB3177-080-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g4220635
BLAST score
                  437
                  0.0e+00
E value
Match length
                  461
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164775
Seq. ID
                  LIB3177-080-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g3882273
BLAST score
                  155
E value
                  2.0e-10
Match length
                  97
% identity
                  30
                  (AB018319) KIAA0776 protein [Homo sapiens]
NCBI Description
                  164776
Seq. No.
Seq. ID
                  LIB3177-080-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2914700
BLAST score
                  556
                  3.0e-57
E value
Match length
                  151
% identity
                  77
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
```

```
thaliana]
Seq. No.
                   164777
Seq. ID
                   LIB3177-080-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g2398679
BLAST score
                   408
E value
                   6.0e-40
Match length
                   84
% identity
                   90
NCBI Description
                   (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
                   synthase [Morinda citrifolia]
Seq. No.
                   164778
Seq. ID
                  LIB3177-080-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g1171770
BLAST score
                   106
E value
                   6.0e-23
Match length
                   61
% identity
                   97
NCBI Description
                  NITRILASE 3 >gi_508735 (U09959) nitrilase [Arabidopsis
                  thaliana]
                  164779
Seq. No.
Seq. ID
                  LIB3177-080-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g3953458
BLAST score
                  532
E value
                  2.0e-54
Match length
                  132
% identity
                  83
                  (AC002328) F20N2.3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164780
Seq. ID
                  LIB3177-080-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g4490734
BLAST score
                  416
E value
                  0.0e + 00
Match length
                  416
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
                  project)
Seq. No.
                  164781
Seq. ID
                  LIB3177-080-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q1170191
BLAST score
                  516
E value
                  1.0e-52
Match length
                  116
% identity
                  91
NCBI Description
                  HOMEOBOX PROTEIN HD1 >gi 1076449 pir $47535
                  homeodomain-containing protein - rape
                  >gi_453949_emb_CAA82314 (Z29073) homeodomain-containing
                  protein [Brassica napus] >gi 1090522 prf 2019252A homeobox
```

protein [Brassica napus] Seq. No. 164782 Seq. ID LIB3177-080-P1-K1-H7 Method BLASTX NCBI GI g115767 BLAST score 656

E value 5.0e-69 Match length 127 % identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164783

Seq. ID LIB3177-080-P1-K1-H8

Method BLASTN
NCBI GI g1877523
BLAST score 54
E value 1.0e-21
Match length 234

Match length 234 % identity 92

NCBI Description Arabidopsis thaliana BAC T7I23, complete sequence

[Arabidopsis thaliana]

Seq. No. 164784

Seq. ID LIB3177-080-P1-K1-H9

Method BLASTX
NCBI GI g541858
BLAST score 441
E value 5.0e-44
Match length 86
% identity 97

NCBI Description

escription endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921 (D16454) endo-xyloglucan

transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)

endo-xyloglucan transferase [Arabidopsis thaliana] .

Seq. No. 164785

Seq. ID LIB3177-081-P1-K1-A1

Method BLASTX
NCBI GI g4741960
BLAST score 365
E value 4.0e-35
Match length 90
% identity 80

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 164786

Seq. ID LIB3177-081-P1-K1-A10

Method BLASTX NCBI GI g131187 BLAST score 304

NCBI GI

```
E value
                     3.0e-28
Match length
                    60
% identity
                    87
NCBI Description
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
                     (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                    >gi_72681_pir__F1SP3 photosystem I chain III precursor -
                    spinach >gi_21303_emb_CAA31523_ (X13133) PSI subunit IV preprotein (AA -77 to 154) [Spinacia oleracea] >gi_226166_prf__1413236A photosystem I reaction center IV
                    [Spinacia oleracea]
Seq. No.
                    164787
Seq. ID
                    LIB3177-081-P1-K1-A11
Method
                    BLASTX
NCBI GI
                    q4531434
BLAST score
                    503
E value
                    4.0e-51
Match length
                    132
% identity
                    77
NCBI Description (AC006224) unknown protein [Arabidopsis thaliana]
Seq. No.
                    164788
Seq. ID
                    LIB3177-081-P1-K1-A12
Method
                    BLASTN
NCBI GI
                    g4309683
BLAST score
                    163
E value
                    9.0e-87
Match length
                    234
                    97
% identity
NCBI Description
                    Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,
                    complete sequence [Arabidopsis thaliana]
Seq. No.
                    164789
Seq. ID
                    LIB3177-081-P1-K1-A2
Method
                    BLASTX
NCBI GI
                    g4741962
BLAST score
                    198
                    7.0e-16
E value
Match length
                    53
                    74
% identity
NCBI Description
                   (AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.
                    164790
Seq. ID
                    LIB3177-081-P1-K1-A3
                    BLASTN
Method
NCBI GI
                    g4741953
BLAST score
                    42
E value
                    4.0e-15
Match length
                    58
% identity
                    93
NCBI Description
                   Arabidopsis thaliana Lhcb4.2 protein (Lhcb4.2) mRNA,
                    complete cds
Seq. No.
                    164791
Seq. ID
                   LIB3177-081-P1-K1-A5
Method
                   BLASTX
```

g2911078

BLAST score

181

```
BLAST score
                   590
E value
                   2.0e-61
Match length
                   117
% identity
                   99
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
Seq. No.
                   164792
Seq. ID
                   LIB3177-081-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g2501812
BLAST score
                   500
E value
                   8.0e-51
Match length
                   117
% identity
                   84
NCBI Description (U91509) glycolate oxidase [Arabidopsis thaliana]
Seq. No.
                   164793
Seq. ID
                   LIB3177-081-P1-K1-A9
Method
                  BLASTX
NCBI GI
                   g2213595
BLAST score
                   493
E value
                   5.0e-50
                   107
Match length
% identity
                   90
NCBI Description (AC000348) T7N9.15 [Arabidopsis thaliana]
Seq. No.
                  164794
Seq. ID
                  LIB3177-081-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g3985958
BLAST score
                  209
E value
                  1.0e-114
Match length
                  456
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164795
Seq. ID
                  LIB3177-081-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  342
E value
                  2.0e-32
Match length
                  73
                  88
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  164796
Seq. ID
                  LIB3177-081-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4827050
```

```
6.0e-14
E value
Match length
                   58
                   60
% identity
NCBI Description
                   ubiquitin specific protease 14 (tRNA-guanine
                   transglycosylase) >gi 1729927 sp P54578 TGT HUMAN QUEUINE
                   TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE)
                   (GUANINE INSERTION ENZYME) >gi_940182 (U30888) tRNA-Guanine
                   Transglycosylase [Homo sapiens]
Seq. No.
                   164797
Seq. ID
                   LIB3177-081-P1-K1-B2
                   BLASTX
Method
                   q3548810
NCBI GI
                   169
BLAST score
E value
                   3.0e-12
                   78
Match length
                   42
% identity
                   (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   164798
Seq. ID
                   LIB3177-081-P1-K1-B3
                   BLASTX
Method
NCBI GI
                   q2246621
                   218
BLAST score
E value
                   8.0e-18
Match length
                   57
% identity -
                   82
                   (AF004393) salt-stress induced tonoplast intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   164799
Seq. ID
                   LIB3177-081-P1-K1-B4
Method
                  .BLASTX
NCBI GI
                   g2119846
BLAST score
                   700
E value
                   4.0e-74
                   136
Match length
                   98
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364_emb_CAA45790 (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi 3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   164800
Seq. ID
                   LIB3177-081-P1-K1-B5
Method
                   BLASTN
NCBI GI
                   q3386593
BLAST score
                   40
E value
                   2.0e-13
Match length
                   120
% identity
                   83
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
NCBI Description
```

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   164801
 Seq. ID
                   LIB3177-081-P1-K1-B6
 Method
                   BLASTX
 NCBI GI
                   q2559012
 BLAST score
                   £26
 E value
                   5.0e-18
Match length
                   75
 % identity
                   65
 NCBI Description
                   (AF026293) chaperonin containing t-complex polypeptide 1,
                   beta subunit; CCT-beta [Homo sapiens] >gi_4090929
                   (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                   [Homo sapiens]
Seq. No.
                   164802
Seq. ID
                   LIB3177-081-P1-K1-B7
Method
                   BLASTN
NCBI GI
                   g4220640
BLAST score
                   53
E value
                   1.0e-21
Match length
                   73
% identity
                   95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                  MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164803
Seq. ID
                  LIB3177-081-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g4585952
BLAST score
                  163
E value
                  1.0e-86
Match length
                  336
% identity
                  99
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F26F24,
                  complete sequence
Seq. No.
                  164804
Seq. ID
                  LIB3177-081-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1706772
BLAST score
                  449
E value
                  5.0e-47
Match length
                  99
% identity
                  95
NCBI Description
                  FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE
                  SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE)
                  >gi_1076324_pir__S54251 farnesyl-diphosphate
                  farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana
                  >gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate
                  farnesyltransferase [Arabidopsis thaliana]
                  >gi_806325_dbj_BAA06103_ (D29017) squalene synthase
                  [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene
                  synthase 1 [Arabidopsis thaliana]
                  >gi_3096933_emb_CAA18843.1 (AL023094) farnesyl-diphosphate
                  farnesyltransferase [Arabidopsis thaliana] >gi_4098519
                  (U79159) squalene synthase [Arabidopsis thaliana]
```

```
Seq. No.
                   164805
 Seq. ID
                   LIB3177-081-P1-K1-C11
 Method
                   BLASTX
 NCBI GI
                   g1169278
 BLAST score
                   340
 E value
                   3.0e~32
Match length
                   81
 % identity
                   DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14
 NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   164806
Seq. ID
                   LIB3177-081-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g2911085
BLAST score
                   345
E value
                   7.0e-33
Match length
                   90
% identity
                   83
NCBI Description
                   (AL021960) photosystem II oxygen-evolving complex protein
                   3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_
                   (AL031187) photosystem II oxygen-evolving complex protein 3
                   - like [Arabidopsis thaliana]
Seq. No.
                   164807 -
Seq. ID
                   LIB3177-081-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g4539329
BLAST score
                   322
E value
                   2.0e-30
Match length
                   63
% identity
                   100
NCBI Description
                  (AL035679) ES43 like protein [Arabidopsis thaliana]
Seq. No.
                  164808
                  LIB3177-081-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                  q3983125
BLAST score
                  235
E value
                  3.0e-20
Match length
                  58
% identity
NCBI Description
                  (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  164809
Seq. ID
                  LIB3177-081-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3413700
BLAST score
                  350
E value
                  2.0e-33
Match length
                  89
% identity
                  82
NCBI Description
                 (AC004747) putative YME1 protein [Arabidopsis thaliana]
Seq. No.
                  164810
Seq. ID
                  LIB3177-081-P1-K1-C6
```

BLASTX

```
Method
                    BLASTN
 NCBI GI
                    q4567259
 BLAST score
                    40
 E value
                    1.0e-13
 Match length
                    56
 % identity
                    93
 NCBI Description Arabidopsis thaliana chromosome II BAC F3K23 genomic
                    sequence, complete sequence
 Seq. No.
                    164811
 Seq. ID
                    LIB3177-081-P1-K1-C8
Method
                    BLASTX
NCBI GI
                    q115470
 BLAST score
                    363
E value
                    1.0e-34
Match length
                    150
% identity
                    53
                    CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                    DEHYDRATASE) >gi_320554_pir__$28412 carbonate dehydratase
                    (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                    [Arabidopsis thaliana]
Seq. No.
                   164812
Seq. ID
                   LIB3177-081-P1-K1-C9
Method
                   BLASTN
NCBI GI
                   g2245031
BLAST score
                   442
E value
                   0.0e+00
Match length
                   446
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   164813
                   LIB3177-081-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4469003
BLAST score
                   590
E value
                   3.0e-61
Match length
                   133
% identity
NCBI Description
                   (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   164814
Seq. ID
                   LIB3177-081-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g2282584
BLAST score
                   428
E value
                   2.0e-42
Match length
                   115
% identity
                   75
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]
Seq. No.
                   164815
Seq. ID
                   LIB3177-081-P1-K1-D12
```

```
NCBI GI
                   q282865
 BLAST score
                   607
 E value
                   3.0e-63
 Match length
                   123
 % identity
                   69
 NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana
                   >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                   protein [Arabidopsis thaliana] >gi 166644 (M85150)
                   chlorophyll a/b-binding protein [Arabidopsis thaliana]
                   >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                   a/b-binding protein [Arabidopsis thaliana]
 Seq. No.
                   164816
 Seq. ID
                   LIB3177-081-P1-K1-D2
 Method
                   BLASTX
 NCBI GI
                   g3184100
 BLAST score
                   179
 E value
                   4.0e-13
Match length
                   52
 % identity
                   60
NCBI Description (AL023777) rna binding protein [Schizosaccharomyces pombe]
Seq. No.
                   164817
Seq. ID
                   LIB3177-081-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g4406807
BLAST score
                   477
E value
                   4.0e-48
Match length
                   107
% identity
                  (AC006201) putative elongation factor beta-1 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164818
Seq. ID
                  LIB3177-081-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g4454447
BLAST score
                  76
E value
                  2.0e-35
Match length
                  88
% identity
                  97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164819
Seq. ID
                  LIB3177-081-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  734
                  4.0e-78
E value
Match length
                  141
% identity
                  99
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
```

Match length

```
>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
 Seq. No.
                   164820
 Seq. ID
                   LIB3177-081-P1-K1-D7
 Method
                   BLASTX
 NCBI GI
                   g4544456
 BLAST score
                   117
 E value
                   1.0e-25
 Match length
                   69
 % identity
                   84
 NCBI Description (AC006592) putative cytochrome P450 [Arabidopsis thaliana]
 Seq. No.
                   164821
 Seq. ID
                   LIB3177-081-P1-K1-D8
 Method
                   BLASTX
 NCBI GI
                   g4406775
 BLAST score
                   297
 E value
                   6.0e-27
 Match length
                   121
 % identity
                   45
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
Seq. No.
                   164822
Seq. ID
                  LIB3177-081-P1-K1-E1
Method
                  BLASTX
NCBI GI
                   g4538963
BLAST score
                   476
E value
                   5.0e-48
Match length
                  110
% identity
                  83
NCBI Description (AL049488) chlorophyll a/b-binding protein-like
                  [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                  164823
Seq. ID
                  LIB3177-081-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  719
E value
                  3.0e-76
Match length
                  141
% identity
                  73
NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  164824
Seq. ID
                  LIB3177-081-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q2497733
BLAST score
                  230
E value
                  2.0e-19
```

% identity

```
% identity
                   82
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
                  >gi_1177796 (M80567) non-specific lipid transfer protein
                   [Arabidopsis thaliana] >gi 3786018 (AC005499) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  164825
                  LIB3177-081-P1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618601
BLAST score
                  111
E value
                  5.0e-56
Match length
                  115
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164826
Seq. ID
                  LIB3177-081-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  g3299824
BLAST score
                  115
                  2.0e-58
E value
Match length
                  143
% identity
                  95
NCBI Description
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
                  near 17 cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164827
Seq. ID
                  LIB3177-081-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g4544435
BLAST score
                  103
E value
                  2.0e-51
Match length
                  103
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14M13 genomic
                  sequence, complete sequence
Seq. No.
                  164828
                  LIB3177-081-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538897
BLAST score
                  164
E value
                  6.0e-12
Match length
                  59
                  49
% identity
NCBI Description
                 (AL049482) AX110P-like protein [Arabidopsis thaliana]
Seq. No.
                  164829
Seq. ID
                  LIB3177-081-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  439
E value
                  2.0e-43
                  95
Match length
```

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
Seq. No.
                   164830
Seq. ID
                   LIB3177-081-P1-K1-F11
Method
                   BLASTN
NCBI GI
                   g3688798
BLAST score
                   222
E value
                   1.0e-122
Match length
                   222
% identity
                   100
NCBI Description
                  Arabidopsis thaliana gamma tonoplast intrinsic protein 2
                   (TIP2) mRNA, complete cds
Seq. No.
                   164831
Seq. ID
                  LIB3177-081-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2199574
BLAST score
                  288
E value
                   3.0e-26
Match length
                   53
% identity
                  100
NCBI Description
                  (AF004293) aquaporin [Brassica rapa]
Seq. No.
                  164832
Seq. ID
                  LIB3177-081-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  g4558521
BLAST score
                  92
E value
                  2.0e-44
Match length
                  238
% identity
                  96
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T10024,
                  complete sequence
Seq. No.
                  164833
Seq. ID
                  LIB3177-081-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  g16367
BLAST score
                  37
                  3.0e-12
E value
Match length
                  57
                  91
% identity
NCBI Description A.thaliana gene (LHCP AB 165) for chlorophyll a/b binding
                  protein
Seq. No.
                  164834
Seq. ID
                  LIB3177-081-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g2764940
BLAST score
                  45
E value
                  4.0e-17
Match length
                  53
% identity
                  96
NCBI Description A.thaliana GASA4 gene
```

Method

BLASTN

```
Seq. No.
                   164835
Seq. ID
                   LIB3177-081-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g1769905
BLAST score
                   512
E value
                   5.0e-52
Match length
                   143
% identity
                   70
NCBI Description
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                   164836
Seq. ID
                   LIB3177-081-P1-K1-G10
Method
                   BLASTN
NCBI GI
                   g1916349
BLAST score
                   97
E value
                   2.0e-47
Match length
                   169
% identity
                   89
NCBI Description
                  Brassica rapa PSI-H subunit (psaH) mRNA, complete cds
Seq. No.
                   164837
Seq. ID
                   LIB3177-081-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   q21142
BLAST score
                   51
E value
                   3.0e-20
Match length
                   67
% identity
                   94
NCBI Description
                  Mustard mRNA for cytosolic glyceraldehyde-3-phosphate
                   dehydrogenase (GAPDH, NAD-specific; EC 1.2.1.12)
Seq. No.
                   164838
                  LIB3177-081-P1-K1-G12
Seq. ID
Method
                   BLASTN
NCBI GI
                  g2764940
BLAST score
                   66
E value
                   5.0e-29
Match length
                  127
                  94
% identity
NCBI Description A.thaliana GASA4 gene
Seq. No.
                  164839
Seq. ID
                  LIB3177-081-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  q4741953
BLAST score
                  135
E value
                  3.0e-70
Match length
                  163
% identity
                  96
NCBI Description
                  Arabidopsis thaliana Lhcb4.2 protein (Lhcb4.2) mRNA,
                  complete cds
Seq. No.
                  164840
Seq. ID
                  LIB3177-081-P1-K1-G3
```

```
NCBI GI
                   g4580454
BLAST score
                   92
E value
                   1.0e-44
Match length
                   120
% identity
                   95
                  Arabidopsis thaliana chromosome II BAC T2G17 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   164841
                   LIB3177-081-P1-K1-G4
Seq. ID
Method
                   BLASTX
                   g3775987
NCBI GI
BLAST score
                   504
E value
                   2.0e-51
Match length
                   98
% identity
                   100
NCBI Description
                  (AJ010457) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   164842
Seq. ID
                  LIB3177-081-P1-K1-G5
Method
                   BLASTN
NCBI GI
                   q4584351
BLAST score
                  154
E value
                   2.0e-81
Match length
                  198
% identity
                   95
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T12H3 genomic
                  sequence, complete sequence
Seq. No.
                  164843
Seq. ID
                  LIB3177-081-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q2809242
BLAST score
                   518
E value
                   6.0e - 53
Match length
                  108
% identity
                  99
NCBI Description
                  (AC002560) F21B7.11 [Arabidopsis thaliana]
Seq. No.
                  164844
Seq. ID
                  LIB3177-081-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q3149952
BLAST score
                  222
E value
                  1.0e-18
Match length
                  52
% identity
                  83
NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]
Seq. No.
                  164845
Seq. ID
                  LIB3177-081-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q4558661
BLAST score
                  298
                  1.0e-27
E value
Match length
                  61
% identity
                  95
```

```
NCBI Description
                   (AC007063) putative malate oxidoreductase (NAD)
                   [Arabidopsis thaliana]
Seq. No.
                  164846
Seq. ID
                  LIB3177-081-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  q769742
BLAST score
                  40
                  5.0e-14
E value
Match length
                  68
% identity
                  90
NCBI Description A.thaliana mRNA for phosphoinositide-specific phospholipase
Seq. No.
                  164847
Seq. ID
                  LIB3177-081-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g2828182
                  37
BLAST score
                  1.0e-11
E value
Match length
                  73
% identity
                  92
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164848
Seq. ID
                  LIB3177-081-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g1345594
BLAST score
                  384
E value
                  2.0e-37
Match length
                  84
                  93
% identity
                  14-3-3-LIKE PROTEIN GF14 KAPPA >gi 1022780 (U36447) GF14
NCBI Description
                  Kappa isoform [Arabidopsis thaliana]
Seq. No.
                  164849
Seq. ID
                  LIB3177-081-P1-K1-H2
Method
                  BLASTN
                  g4733961
NCBI GI
BLAST score
                  105
E value
                  2.0e-52
Match length
                  113
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F16G22 genomic
                  sequence, complete sequence
Seq. No.
                  164850
Seq. ID
                  LIB3177-081-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q4741960
BLAST score
                  294
E value
                  1.0e-26
                  75
Match length
                  79
% identity
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
```

```
Seq. No.
                   164851
Seq. ID
                   LIB3177-081-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g1402904
BLAST score
                   434
E value
                   4.0e-43
Match length
                   .86
% identity
                   97
NCBI Description
                  (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                   164852
Seq. ID
                   LIB3177-081-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q2894574
BLAST score
                   352
E value
                   1.0e-33
Match length
                   73
                   92
% identity
NCBI Description
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
                   >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
Seq. No.
                   164853
Seq. ID
                   LIB3177-081-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q1053047
BLAST score
                   357
E value
                   4.0e-34
Match length
                   90
                   84
% identity
NCBI Description
                   (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
                   histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                   [Glycine max]
Seq. No.
                   164854
                  LIB3177-082-P1-K1-A1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2062153
BLAST score
                   74
E value
                   6.0e-34
Match length
                   126
% identity
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164855
Seq. ID
                  LIB3177-082-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g119975
BLAST score
                  308
E value
                  8.0e-29
Match length
                  68
% identity
                  96
NCBI Description
                  FERREDOXIN PRECURSOR >gi_99692_pir S09979 ferredoxin
                  [2Fe-2S] precursor - Arabidopsis thaliana
                  >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
                  [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
```

[Arabidopsis thaliana]

```
Seq. No.
                   164856
Seq. ID
                   LIB3177-082-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g115385
BLAST score
                   203
E value
                   2.0e-16
Match length
                   41
% identity
                   98
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   164857
Seq. ID
                   LIB3177-082-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   g3510347
BLAST score
                   166
E value
                   2.0e-88
Match length
                   194 .
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164858
Seq. ID
                  LIB3177-082-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  214
E value
                   9.0e-18
Match length
                   48
                   92
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir_ RKMUA1
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                  Al precursor - Arabidopsis thaliana
                  164859
Seq. No.
                  LIB3177-082-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062153
BLAST score
                  36
E value
                  2.0e-11
Match length
                  75
% identity
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164860
Seq. ID
                  LIB3177-082-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g240069
BLAST score
                  49
E value
                  2.0e-19
Match length
                  65
% identity
                  94
```

```
NCBI Description light-regulated glutamine synthetase isoenzyme [Arabidopsis
                  thaliana, mRNA, 1548 nt]
                  164861
Seq. No.
Seq. ID
                  LIB3177-082-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  g3510347
BLAST score
                  162
E value
                  3.0e-86
                  182
Match length
                  97
% identity
                 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164862
Seq. ID
                  LIB3177-082-P1-K1-B1
Method
                  BLASTN
                  g4490324
NCBI GI
                  95
BLAST score
E value
                  1.0e-46
Match length
                  99
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
                  (ESSA project)
Seq. No.
                  164863
Seq. ID
                  LIB3177-082-P1-K1-B11
Method
                  BLASTN
                  g4559344
NCBI GI
BLAST score
                  79
E value
                  2.0e-36
Match length
                  163
                  88
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F27C12 genomic
                  sequence, complete sequence
Seq. No.
                  164864
Seq. ID
                  LIB3177-082-P1-K1-B12
                  BLASTX
Method
NCBI GI
                  g416681
BLAST score
                  242
                  2.0e-20
E value
                  112
Match length
                  41
% identity
                 ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_280404_pir S26198 H+-transporting ATP synthase (EC
                  3.6.1.34) delta chain precursor, chloroplast - common
                  tobacco >gi 19787 emb CAA45153 (X63607) chloroplast ATP
                  synthase (delta subunit) [Nicotiana tabacum]
                  164865
Seq. No.
Seq. ID
                  LIB3177-082-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  g2641637
                  101
BLAST score
                  9.0e-50
E value
```

183

Match length

NCBI GI ·

g3676296

```
% identity
                   96
NCBI Description
                  Arabidopsis thaliana DnaJ homolog AtJ3 (ATJ3) gene,
                  complete cds
Seq. No.
                  164866
                  LIB3177-082-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                   545
                   6.0e-56
E value
                  140
Match length
                   80
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372 emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  164867
Seq. No.
                  LIB3177-082-P1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4115370
BLAST score
                  36
E value
                  1.0e-11
Match length
                   65
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F27D4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164868
Seq. ID
                  LIB3177-082-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q464849
BLAST score
                  175
                  3.0e-13
E value
Match length
                  31
                  100
% identity
                  TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
NCBI Description
                  chain - almond >gi 20\overline{4}\overline{13} emb \overline{CAA47635} (X67162)
                  alpha-tubulin [Prunus dulcis]
Seq. No.
                  164869
Seq. ID
                  LIB3177-082-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g16436
BLAST score
                  58
                  3.0e-24
E value
Match length
                  170
                  84
% identity
NCBI Description A.thaliana gene for pre-ferredoxin
Seq. No.
                  164870
Seq. ID
                  LIB3177-082-P1-K1-B8
Method
                  BLASTX
```

Method

BLASTN

```
BLAST score
                     244
  E value
                     3.0e-21
  Match length
                     60
  % identity
                     77
  NCBI Description
                     (U96497) mitochondrial ATPase beta subunit [Nicotiana
                     sylvestris]
                     164871
  Seq. No.
  Seq. ID
                     LIB3177-082-P1-K1-B9
  Method
                     BLASTX
  NCBI GI
                     q416681
  BLAST score
                     203
  E value
                     5.0e-16
                     99
  Match length
                     37
  % identity
  NCBI Description
                     ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
                     >gi_280404_pir__S26198 H+-transporting ATP synthase (EC
                     3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP
                     synthase (delta subunit) [Nicotiana tabacum]
  Seq. No.
                     164872
  Seq. ID
                     LIB3177-082-P1-K1-C1
 Method
                     BLASTN
NCBI_GI
                     q1732569
  BLAST score
                     113
  E value
                     7.0e-57
 Match length
                     125
  % identity
                     98
 NCBI Description
                     Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA,
                     complete cds
  Seq. No.
                     164873
  Seq. ID
                     LIB3177-082-P1-K1-C10
 Method
                     BLASTN
 NCBI GI
                     g3176701
 BLAST score
                     210
 E value
                     1.0e-115
 Match length
                     242
  % identity
                     90
                     Arabidopsis thaliana chromosome II BAC T20K24 genomic
  NCBI Description
                     sequence, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     164874
  Seq. ID
                     LIB3177-082-P1-K1-C11
 Method
                     BLASTN
 NCBI GI
                     g3449323
 BLAST score
                     185
 E value
                     1.0e-100
 Match length
                     197
  % identity
                     98
 NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                     MZA15, complete sequence [Arabidopsis thaliana]
 Seq. No.
                     164875
 Seq. ID
                     LIB3177-082-P1-K1-C12
```

Method

BLASTX

```
NCBI GI
                    q3738088
BLAST score
                    76
E value
                    6.0e-35
Match length
                    159
% identity.
                    88
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T30L20 genomic
                    sequence, complete sequence [Arabidopsis_thaliana]
Seq. No.
                    164876
Seq. ID
                   LIB3177-082-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   q541858
BLAST score
                   805
E value
                   2.0e-86
Match length
                   161
                   94
% identity
NCBI Description
                   endoxyloglucan transferase - Arabidopsis thaliana
                   >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.
                   164877
Seq. ID
                   LIB3177-082-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g4678259
BLAST score
                   267
E value
                   5.0e-24
Match length
                   63
                   87
% identity
NCBI Description
                   (ALO49657) putative protein [Arabidopsis thaliana]
Seq. No.
                   164878
Seq. ID
                   LIB3177-082-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q4587542
BLAST score
                   264
                   1.0e-23
E value
Match length
                   51
% identity
                   92
NCBI Description
                   (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase
                   with GDSL-motif family. ESTs gb_T45815, gb_T45130 and
                   gb_Z38046 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   164879
Seq. ID
                   LIB3177-082-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q1172977
BLAST score
                   166
E value
                   4.0e-12
Match length
                   37
% identity
                   92
NCBI Description
                   60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
                   ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                   164880
Seq. ID
                   LIB3177-082-P1-K1-C9
```

BLAST score

```
NCBI GI
                   g3738091
BLAST score
                   430
E value
                   1.0e-42
Match length
                   117
                   74
% identity
NCBI Description
                   (AC005617) similar to symbiotic ammonium transporter, SAT1
                   [Arabidopsis thaliana]
Seq. No.
                   164881
Seq. ID
                   LIB3177-082-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   q99735
                   575
BLAST score
                   1.0e-59
E value
Match length
                   110
% identity
                   99
NCBI Description
                  L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                   Arabidopsis thaliana (fragment)
Seq. No.
                   164882
Seq. ID
                   LIB3177-082-P1-K1-D10
Method .
                  BLASTN
NCBI GI
                   q2341023
BLAST score
                   56
                                                           ÷ .
E value
                   2.0e-23
Match length
                   88
% identity.
                   92
                  Sequence of BAC F19P19 from Arabidopsis thaliana chromosome
NCBI Description

    complete sequence [Arabidopsis thaliana]

Seq. No.
                  164883
Seq. ID
                  LIB3177-082-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  g2815519
BLAST score
                  232
E value
                  1.0e-128
Match length
                  236
% identity
                  100
                  Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  164884
Seq. ID
                  LIB3177-082-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g3885511
BLAST score
                  229
E value
                  3.0e-19
Match length
                  66
% identity
                  71
NCBI Description
                   (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
Seq. No.
                  164885
Seq. ID
                  LIB3177-082-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g166631
```

```
E value
                   1.0e-128
 Match length
                   248
 % identity
                   98 -
NCBI Description A.thaliana chloroplast ATP synthase gamma subunit (atpCl)
                   gene, complete cds
 Seq. No.
                   164886
 Seq. ID
                   LIB3177-082-P1-K1-D8
                                                               ĕ .
 Method
                   BLASTN
NCBI GI
                   g12219
 BLAST score
                   48
E value
                   2.0e-18
Match length
                   125
 % identity
                   84
NCBI Description Mustard chloroplast trnk gene for tRNA-Lys(UUU)
Seq. No.
                   164887
Seq. ID
                   LIB3177-082-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   q2815519
BLAST score
                   360
E value
                   0.0e+00
Match length
                   428
% identity.
                   96
NCBI Description Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   164888
Seq. ID
                   LIB3177-082-P1-K1-E10
Method
                   BLASTN
NCBI GI
                   g4008005
BLAST score
                   82
E value
                   1.0e-38
Match length
                  150
% identity
                   89
NCBI Description Arabidopsis thaliana receptor-like protein kinase (RKL1)
                  gene, complete cds
Seq. No.
                  164889
Seq. ID
                  LIB3177-082-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  q1871173
BLAST score
                  109
E value
                  1.0e-54
Match length
                  154
% identity
                  92
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T06D20 genomic
                  sequence, complete sequence
Seq. No.
                  164890
Seq. ID
                  LIB3177-082-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g4093154
BLAST score
                  44
E value
                  3.0e-16
Match length
                  44
% identity
                  100
```

```
NCBI Description Arabidopsis thaliana phytochrome-associated protein 1
                   (PAP1) mRNA, complete cds
Seq. No.
                   164891
Seq. ID
                   LIB3177-082-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q3913727
BLAST score
                   143
E value
                   2.0e-09
Match length
                   28
% identity
                   100
                   GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                   (G6PD) >gi_1174336_emb_CAA59012_ (X84230)
                   glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   164892
Seq. ID
                   LIB3177-082-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g4567268
BLAST score
                   253
E value
                   4.0e-22
Match length
                   56
                   95--
% identity
NCBI Description
                   (AC006841) putative fructose biphosphate aldolase
                   [Arabidopsis thaliana]
Seq. No.
                   164893
Seq. ID
                  LIB3177-082-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2459926
BLAST score
                   154
E value
                  1.0e-10
Match length
                  51
% identity
                  63
NCBI Description
                  (AF006197) annexin [Lavatera thuringiaca]
Seq. No.
                  164894
Seq. ID
                  LIB3177-082-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g2583106
BLAST score
                  166
E value
                  1.0e-88
Match length
                  215
% identity
                  93
                  Arabidopsis thaliana chromosome II BAC F4L23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164895
Seq. ID
                  LIB3177-082-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g4093154
BLAST score
                  59
E value
                  4.0e-25
Match length
                  71
% identity
                  96
NCBI Description
                  Arabidopsis thaliana phytochrome-associated protein 1
                  (PAP1) mRNA, complete cds
```

Seq. ID

```
Seq. No.
                   164896
 Seq. ID
                   LIB3177-082-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   g4689466
BLAST score
                   219
E value
                   1.0e-120
Match length
                   231
 % identity
                   99
NCBI Description Arabidopsis thaliana chromosome II BAC T23015 genomic
                   sequence, complete sequence
Seq. No.
                   164897
Seq. ID
                   LIB3177-082-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   g297877
BLAST score
                   54
E value
                   3.0e-22
Match length
                   66
% identity
                   95
NCBI Description
                  A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme
                  homolog >gi_349212_gb_L00640_ATHUBCC Arabidopsis thaliana
                  ubiquitin conjugating enzyme mRNA, complete cds
Seq. No.
                  164898
Seq. ID
                  LIB3177-082-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  g887938
BLAST score
                  152
E value
                  3.0e-80
Match length
                  160
% identity
NCBI Description
                  Arabidopsis thaliana clone YAP317 GAST1 protein homolog
                  mRNA, complete cds
Seq. No.
                  164899
Seq. ID
                  LIB3177-082-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1755156
BLAST score
                  296
E value
                  2.0e-28
Match length
                  92
% identity
                  76
NCBI Description
                  (U75189) germin-like protein [Arabidopsis thaliana]
                  >gi_1755158 (U75190) germin-like protein [Arabidopsis
                  thaliana] >gi 1755170 (U75196) germin-like protein
                  [Arabidopsis thaliana] >gi_1755172 (U75197) germin-like
                  protein [Arabidopsis thaliana] >gi_1755180 (U75201)
                  germin-like protein [Arabidopsis thaliana] >gi 1755190
                  (U75206) germin-like protein [Arabidopsis thaliana]
                  >gi_1934728 (U95035) germin-like protein [Arabidopsis
                  thaliana] >gi 4154285 (AF090733) germin-like protein 1
                  [Arabidopsis thaliana] >gi_4666248_dbj BAA77207.1 (D89055)
                  germin-like protein precursor [Arabidopsis thaliana]
Seq. No.
                  164900
```

LIB3177-082-P1-K1-F2

```
Method
                    BLASTN
 NCBI GI
                    q2213606
 BLAST score
                    294
 E value
                    1.0e-165
 Match length
                    298
 % identity.
                   100
 NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F21J9,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   164901
 Seq. ID
                   LIB3177-082-P1-K1-F4
Method
                   BLASTN
NCBI GI
                   g2564050
BLAST score
                   90
E value
                   1.0e-43
Match length
                   98
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUA22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164902
Seq. ID
                   LIB3177-082-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g231700
BLAST score
                   202
E value
                   2.0e-16
Match length
                   44
% identity
                   93
NCBI Description
                   22 KD CALMODULIN-LIKE CALCIUM-BINDING PROTEIN (CABP-22)
                   >gi_479694_pir__S35188 calmodulin-related protein (clone
                   CaBP-22) - Arabidopsis thaliana >gi_16209_emb_CAA78124
                   (Z12136) calcium binding protein [Arabidopsis thaliana]
                   >gi_3402708 (AC004261) calcium binding protein [Arabidopsis
                   thalianal
Seq. No.
                   164903
Seq. ID
                   LIB3177-082-P1-K1-F9
Method
                   BLASTX
NCBI GI ·
                   g1592672
BLAST score
                   363
E value
                   8.0e-35
Match length
                  102
% identity
                  71
NCBI Description
                  (X91921) germin1 [Arabidopsis thaliana]
Seq. No.
                  164904
Seq. ID
                  LIB3177-082-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  623
E value
                  4.0e-65
Match length
                  115
% identity
                  99
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
```

B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702

```
(X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana]
 Seq. No.
                    164905
 Seq. ID
                   LIB3177-082-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g4689386
BLAST score
                   380
E value
                   1.0e-36
Match length
                   144
 % identity
                   56
NCBI Description
                    (AF139468) photosystem I reaction center subunit III [Vigna
                   radiata]
Seq. No.
                   164906
Seq. ID
                   LIB3177-082-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   g3046849
BLAST score
                   209
E value
                   1.0e-114
Match length
                   249
% identity
                   96
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   164907
Seq. ID
                   LIB3177-082-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g3123712
BLAST score
                   275
E value
                   3.0e-24
Match length
                   79
% identity
                   54
NCBI Description
                  (D89051) ERD6 protein [Arabidopsis thaliana]
Seq. No.
                   164908
                   LIB3177-082-P1-K1-G3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4519195
BLAST score
                   218
E value
                   1.0e-119
Match length
                   360
% identity
                   61
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
Seq. No.
                  164909
Seq. ID
                  LIB3177-082-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1592679
BLAST score
                  261
E value
                  9.0e-23
Match length
                  71
% identity
                  77
NCBI Description
                  (X91915) LEA D113 homologue typel [Arabidopsis thaliana]
Seq. No.
                  164910
```

```
LIB3177-082-P1-K1-G5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4757394
BLAST score
                   192
E value
                   1.0e-104
Match length
                   192
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K1904, complete sequence
Seq. No.
                   164911
                   LIB3177-082-P1-K1-G8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4586241
BLAST score
                   44
E value
                   4.0e-16
Match length
                   95
% identity
                   96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                   (ESSA project)
Seq. No.
                  164912
Seq. ID
                  LIB3177-082-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  g3046849
BLAST score
                   334
E value
                  0.0e+00
Match length
                  409
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164913
Seq. ID
                  LIB3177-082-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  575
E value
                  2.0e-59
Match length
                  108
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  164914
Seq. ID
                  LIB3177-082-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g16192
BLAST score
                  61
E value
                  6.0e-26
Match length
                  200
% identity
                  60
                  A.thaliana ats1B, ats2B and ats3B gene for
NCBI Description
                  ribulose-1,5-biphosphate carboxylase small subunit (rbcS)
```

(EC 4.1.1.39)

Seq. No.

```
Seq. No.
                   164915
Seg. ID
                   LIB3177-082-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   280
E value
                   2.0e-25
Match length
                   60
% identity
                   92
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                    (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   164916
Seq. ID
                   LIB3177-082-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g464621
BLAST score
                   332
E value
                   3.0e - 31
Match length
                   110
                   64
% identity
                   60S RIBOSOMAL PROTEIN, L6 (YL16-LIKE) >gi 280374 pir S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
Seq. No.
                   164917
Seq. ID
                   LIB3177-082-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g118619
BLAST score
                   160
E value
                   3.0e-11
Match length
                   51
% identity
                   59
NCBI Description
                   SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN
                   PRECURSOR (IP) >gi 66072 pir RDBYIS succinate
                   dehydrogenase (ubiquinone) (EC 1.3.5.1) iron-sulfur protein
                   precursor - yeast (Saccharomyces cerevisiae) >qi 172549
                   (J05487) succinate dehydrogenase iron-protein subunit (SDH)
                   (EC 1.3.99.1) [Saccharomyces cerevisiae]
                   >gi_1360235_emb_CAA97492_ (Z73146) ORF YLL041c
                   [Saccharomyces cerevisiae]
Seq. No.
                   164918
Seq. ID
                   LIB3177-082-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q4455342
BLAST score
                   820
E value
                   4.0e-88
                   160
Match length
% identity
                   100
                   (AL035522) O-methyltransferase-like protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No.

```
LIB3177-082-P1-K1-H5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2494276
 BLAST score
                    176
 E value
                    2.0e-13
Match length
                    63
 % identity
                    52
NCBI Description
                   ELONGATION FACTOR P (EF-P) >gi_1001112_dbj BAA10251
                    (D64001) elongation factor P [Synechocystis sp.]
 Seq. No.
                   164920
 Seq. ID
                   LIB3177-082-P1-K1-H7
Method
                   BLASTN
NCBI GI
                   g4734003
BLAST score
                   109
E value
                   2.0e-54
Match length
                   220
% identity
                   97
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F3L12 genomic
                   sequence, complete sequence
Seq. No.
                   164921
Seq. ID
                   LIB3177-082-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q464621
BLAST score
                   385
E value
                   3.0e-37
Match length
                   119
% identity
                   67
NCBI Description
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir S28586
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
Seq. No.
                   164922
Seq. ID
                   LIB3177-083-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q475719
BLAST score
                   334
E value
                   2.0e-31
Match length
                   119
% identity
                   45
                   (U08467) RNA-binding protein 2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   164923
Seq. ID
                   LIB3177-083-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q166835
BLAST score
                   183
E value
                   4.0e-14
Match length
                   41
% identity
                   88
NCBI Description
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
                   activase [Arabidopsis thaliana] >gi 2642170 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
```

Method

BLASTX

```
LIB3177-083-P1-K1-A12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4741939
BLAST score
                   123
E value
                   4.0e-63
Match length
                   139
% identity
                   97
NCBI Description
                   Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete
Seq. No.
                   164925
Seq. ID
                   LIB3177-083-P1-K1-A2
Method
                   BLASTN
NCBI GI
                   g3434970
BLAST score
                   137
E value
                   3.0e-71
Match length
                   153
% identity
                   97
NCBI Description
                   Arabidopsis thaliana AtERF-3 mRNA for ethylene responsive
                   element binding factor 3, complete cds
Seq. No.
                   164926
Seq. ID
                   LIB3177-083-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   g99735
BLAST score
                   252
E value
                   3.0e-22
Match length
                   59
% identity
                   86
NCBI Description
                  L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                   Arabidopsis thaliana (fragment)
Seq. No.
                   164927
Seq. ID
                   LIB3177-083-P1-K1-B1
Method
                   BLASTN
NCBI GI
                   g3859658
BLAST score
                   268
E value
                   1.0e-149
Match length
                   296
% identity
                   98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
                   (ESSAII project)
Seq. No.
                  164928
Seq. ID
                  LIB3177-083-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4741929
BLAST score
                  321
E value
                  9.0e-30
Match length
                  95
% identity
                  65
                  (AF130253) membrane related protein CP5 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  164929
Seq. ID
                  LIB3177-083-P1-K1-B12
```

Seq. ID

```
NCBI GI
                   q2062158
BLAST score
                   672
E value
                   8.0e-71
Match length
                  139
% identity
                   47
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
Seq. No.
                   164930
Seq. ID
                  LIB3177-083-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q4741959
BLAST score
                  166
E value
                  2.0e-88
Match length
                  228
% identity
                  93
                  Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
NCBI Description
                  cds
Seq. No.
                  164931
Seq. ID
                  LIB3177-083-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  147
E value
                  6.0e-10
Match length
                  42
% identity
                  79
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  164932
Seq. ID
                  LIB3177-083-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g4220510
BLAST score
                  246
E value
                  1.0e-136
Match length
                  254
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                  (ESSAII project)
Seq. No.
                  164933
Seq. ID
                  LIB3177-083-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q417381
BLAST score
                  362
E value
                  3.0e-80
Match length
                  155
% identity
                  99
NCBI Description
                  NITRILASE 1 >gi 99738 pir S22398 nitrilase (EC 3.5.5.1) -
                  Arabidopsis thaliana >gi 16400 emb CAA45041 (X63445)
                  nitrilase I [Arabidopsis thaliana]
Seq. No.
                  164934
```

LIB3177-083-P1-K1-C10

Seq. ID

```
Method
                  BLASTN
NCBI GI
                  q4741939
BLAST score
                   112
E value
                  1.0e-56
Match length
                   124
% identity
                   98
NCBI Description
                  Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete
                  cds
Seq. No.
                  164935
Seq. ID
                  LIB3177-083-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  q1532162
BLAST score
                  407
E value
                  0.0e + 00
Match length
                  441
% identity
                  100
NCBI Description
                  Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,
                  AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14
                  genes, partial cds, AT.I.24-7, ascorbate peroxidase
                   (ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I
Seq. No.
                  164936
Seq. ID
                  LIB3177-083-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  q1490552
BLAST score
                  85
E value
                  1.0e-40
Match length
                  97
                  97
% identity
NCBI Description
                  Arabidopsis thaliana S-adenosylmethionine decarboxylase
                  (SAMdc) mRNA, complete cds
Seq. No.
                  164937
Seq. ID
                  LIB3177-083-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q629518
BLAST score
                  551
E value
                  9.0e-57
Match length
                  116
% identity
                  91
NCBI Description
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small
                  chain - Arabidopsis thaliana (fragment)
Seq. No.
                  164938
Seq. ID
                  LIB3177-083-P1-K1-C3
                  BLASTN
Method
NCBI GI
                  q2264305
BLAST score
                  94
                  7.0e-46
E value
Match length
                  121
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBK23, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164939
```

LIB3177-083-P1-K1-C5

BLAST score

```
Method
                    BLASTX
 NCBI GI
                    q125576
 BLAST score
                    528
 E value
                    7.0e-54
Match length
                    123
 % identity
 NCBI Description
                    PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
                    (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC
                    2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate
                    kinase [Arabidopsis thaliana]
 Seq. No.
                    164940
 Seq. ID
                    LIB3177-083-P1-K1-D1
Method
                    BLASTX
NCBI GI
                    g1172441
BLAST score
                    180
E value
                    3.0e-13
Match length
                    49
% identity
                    78
                    POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi_99685_pir__S21883
NCBI Description
                    DNA-binding protein POSF21 - Arabidopsis thaliana
                    >gi_16429_emb_CAA43366_ (X61031) posF21 [Arabidopsis
thaliana] >gi_4589968_gb_AAD26486.1_AC007169_18 (AC007169)
                    DNA-binding protein POSF21 [Arabidopsis thaliana]
Seq. No.
                    164941
Seq. ID
                    LIB3177-083-P1-K1-D12
Method
                    BLASTX
NCBI GI
                    g1170939
BLAST score
                    668
E value
                    2.0e-70
Match length
                    133
% identity
                    94
NCBI Description
                    S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
                    ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                    >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                    2.5.1.6) - tomato >gi 429108 emb_CAA80867 (Z24743)
                    S-adenosyl-L-methionine synthetase [Lycopersicon
                    esculentum]
Seq. No.
                    164942
                   LIB3177-083-P1-K1-D5
Seq. ID
Method
                    BLASTN
NCBI GI
                    g3688798
BLAST score
                    107
E value
                    1.0e-53
Match length
                   127
% identity
                    96
NCBI Description
                   Arabidopsis thaliana gamma tonoplast intrinsic protein 2
                    (TIP2) mRNA, complete cds
Seq. No.
                   164943
Seq.: ID
                   LIB3177-083-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g2832625
```

Match length

```
3.0e-17
E value
Match length
                  73
% identity
                  55
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  164944
                  LIB3177-083-P1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4741959
BLAST score
                  189
E value
                  1.0e-102
                  263
Match length
                  93
% identity
NCBI Description
                  Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
                  164945
Seq. No.
Seq. ID
                  LIB3177-083-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g129817
                  530
BLAST score
E value
                  2.0e-54
                  106
Match length
                  97
% identity
                  BASIC PEROXIDASE E PRECURSOR >gi 81653 pir JU0458
NCBI Description
                  peroxidase (EC 1.11.1.7) E - Arabidopsis thaliana
                  >gi_166807 (M58381) peroxidase [Arabidopsis thaliana]
                  164946
Seq. No.
Seq. ID
                  LIB3177-083-P1-K1-E11
                  BLASTX
Method
NCBI GI
                  g3929651
BLAST score
                  458
E value
                  6.0e-46
                  90
Match length
                  100
% identity
                   (AJ131206) microbody NAD-dependent malate dehydrogenase
NCBI Description
                  [Arabidopsis thaliana]
                  164947
Seq. No.
Seq. ID
                  LIB3177-083-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g4757410
BLAST score
                  200
                  1.0e-109
E value
                  271
Match length
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MVE11, complete sequence
                  164948
Seq. No.
Seq. ID
                  LIB3177-083-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g322577
BLAST score
                  665
                  4.0e-70
E value
```

```
% identity
                   98
NCBI Description Raf protein kinase homolog CTR1 - Arabidopsis thaliana
Seq. No.
                   164949
Seq. ID
                   LIB3177-083-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   g4741945
BLAST score
                   82
E value
                   1.0e-38
Match length
                   122
% identity
                   92
                   Arabidopsis thaliana Lhcb2 protein (Lhcb2.2) mRNA, complete
NCBI Description
Seq. No.
                   164950
Seq. ID
                   LIB3177-083-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g4583542
BLAST score
                   614
                   5.0e-64
E value
Match length
                   152
% identity
                   86
NCBI Description
                   (Y16847) 16 kDa polypeptide of oxygen-evolving complex
                   [Arabidopsis thaliana]
Seq. No.
                   164951
Seq. ID
                   LIB3177-083-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   g166705
BLAST score
                   70
E value
                   1.0e-31
Match length
                   70
                   100
% identity
NCBI Description
                  Arabidopsis thaliana glyceraldehyde-3-phosphate
                  dehydrogenase C subunit (GapC) gene, complete cds
Seq. No.
                   164952
Seq. ID
                  LIB3177-083-P1-K1-F1
                  BLASTX
Method
NCBI GI
                  g1332579
BLAST score
                   502
E value
                  5.0e-51
Match length
                  103
% identity
                  10
NCBI Description
                  (X98063) polyubiquitin [Pinus sylvestris]
                  164953
Seq. No.
                  LIB3177-083-P1-K1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2506443
BLAST score
                  337
E value
                  4.0e-32
Match length
                  69
                  100
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi 2117520 pir JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
```

```
3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130)
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) [Arabidopsis thaliana]
Seq. No.
                   164954
Seq. ID
                   LIB3177-083-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   q2956689
BLAST score
                   46
E value
                   4.0e-17
Match length
                   124
% identity
                   88
NCBI Description
                   Arabidopsis thaliana mRNA for PSBY (Ycf32-related
                   chloroplast thylakoid membrane proteins)
Seq. No.
                   164955
Seq. ID
                   LIB3177-083-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q1617270
BLAST score
                   69
E value
                   2.0e-48
Match length
                   133
% identity
                   80
NCBI Description
                  (X94624) acyl-CoA synthetase [Brassica napus]
                   164956
Seq. No.
Seq. ID
                   LIB3177-083-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   g4585890
BLAST score
                   89
E value
                   7.0e-43
Match length
                   93
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T3G21 genomic
                   sequence, complete sequence
Seq. No.
                   164957
Seq. ID
                   LIB3177-083-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g4454037
BLAST score
                   370
E value
                   6.0e-36
Match length
                   65
% identity
                   100
                   (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   164958
Seq. ID
                   LIB3177-083-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g2245118
BLAST score
                   323
E value
                   6.0e-30
Match length
                   110
```

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde

```
% identity
                   65
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   164959
Seq. ID
                  LIB3177-083-P1-K1-G3
Method
                   BLASTX
NCBI GI
                  g1399380
BLAST score
                  176
E value
                   3.0e-13
Match length
                   45
% identity
                  71
                  (U43683) S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                  methyltransferase [Glycine max]
Seq. No.
                  164960
Seq. ID
                  LIB3177-083-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  g4741959
BLAST score
                  84
E value
                  9.0e-40
Match length
                  141
% identity
                  94
NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
                  cds
Seq. No.
                  164961
Seq. ID
                  LIB3177-083-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g3212846
BLAST score
                  253
                                                              -----
E value
                  1.0e-140
Match length
                  317
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164962
Seq. ID
                  LIB3177-083-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q3450889
BLAST score
                  447
E value
                  2.0e-44
Match length
                  96
% identity
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.
                  164963
Seq. ID
                  LIB3177-083-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  g3869072
BLAST score
                  138
                  7.0e-72
E value
Match length
                  162
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MJB24, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                       164964
     Seq. ID
                       LIB3177-083-P1-K1-H12
     Method
                       BLASTX
     NCBI GI
                       g115783 ·
     BLAST score
                       380
     E value
                       7.0e-37
     Match length
                       73
                       97
     % identify
     NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                       (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                       chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                       thaliana]
                       164965
     Seq. No.
     Seq. ID
                       LIB3177-083-P1-K1-H2
     Method
                       BLASTX
     NCBI GI
                       g4741948
     BLAST score
                       475
     E value
                       6.0e-48
    Match length
                       94
     % identity
                       96
    NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana]
    Seq. No.
                      164966
    Seq. ID
                      LIB3177-083-P1-K1-H3
                                                                        • 3
    Method
                      BLASTN
    NCBI GI
                      g3046856
    BLAST score
                      40
    E value
                       5.0e-14
    Match length
                       60
                       92
    % identity
    NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                      MXI22, complete sequence [Arabidopsis thaliana]
    Seq. No.
                      164967
    Seq. ID
                      LIB3177-083-P1-K1-H4
    Method
                      BLASTX
    NCBI GI
                      q2499327
    BLAST score
                      359
    E value
                      3.0e - 34
    Match length
                      119
    % identity
                      NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
    NCBI Description
                      (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH
                      dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
                      >gi_643090_emb_CAA58887.1 (X84078) NADH dehydrogenase
                      [Arabidopsis thaliana]
    Seq. No.
                      164968
    Seq. ID
                      LIB3177-083-P1-K1-H5
    Method
                      BLASTX
    NCBI GI
                      g4056497
BLAST score
                      199
    E value
                      1.0e-15
    Match length
                      52
    % identity
                      79
    NCBI Description (AC005896) putative histone H2B [Arabidopsis thaliana]
```

E value

3.0e-29

```
Seq. No.
                    164969
 Seq. ID
                    LIB3177-083-P1-K1-H6
 Method
                    BLASTX
 NCBI GI
                    g115767
 BLAST score
                    477
 E value
                    3.0e-48
 Match length
                    95
                    96
 % identity
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana
                    >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                    protein (LHCP AB 65) [Arabidopsis thaliana]
                    >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                    protein (LHCP AB 180) [Arabidopsis thaliana]
 Seq. No.
                    164970
 Seq. ID
                    LIB3177-083-P1-K1-H7
 Method
                    BLASTN
 NCBI GI
                    g16446
 BLAST score
                    50
 E value
                    9.0e-20 .
Match length
                    86
                    90
 % identity
NCBI Description A.thaliana gene for photosystem II 10 kDa polypeptide
 Seq. No.
                    164971
 Seq. ID
                   LIB3177-083-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g1769905
BLAST score
                    519
                   7.0e-53
E value
Match length
                   142
                   71
 % identity
NCBI Description
                    (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                    [Arabidopsis thaliana]
Seq. No.
                 . 164972
Seq. ID
                   LIB3177-083-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   378
E value
                   9.0e-37
Match length
                   74
% identity
                   99
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   164973
                   LIB3177-084-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3075398
BLAST score
                   315
```

```
Match length
                  88
% identity
                  76
NCBI Description
                  (AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.
                  164974
Seq. ID
                  LIB3177-084-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q4512683
BLAST score
                  766
E value
                  7.0e-82
Match length
                  145
                  100
% identity
NCBI Description
                  (AC006931) putative lipase [Arabidopsis thaliana]
                  >gi_4559323_gb_AAD22985.1 AC007087 4 (AC007087) putative
                  lipase [Arabidopsis thaliana]
Seq. No.
                  164975
Seq. ID
                  LIB3177-084-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q3128195
BLAST score
                  577
                  7.0e-60
E value
Match length
                  119
% identity
                  98
NCBI Description
                  (AC004521) putative phosphoribosyl pyrophosphate synthetase
                  [Arabidopsis thaliana] >gi_3341673 (AC003672) putative
                  phosphoribosyl pyrophosphate synthetase [Arabidopsis
                  thaliana]
Seq. No.
                  164976
Seq. ID
                  LIB3177-084-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2829133
BLAST score
                  489
                  1.0e-49
E value
Match length
                  95
% identity
                  98
NCBI Description
                  (AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis
                  thaliana] >gi 4490745 emb CAB38907.1 (AL035708)
                  adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]
Seq. No.
                  164977
Seq. ID
                  LIB3177-084-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q2119848
BLAST score
                  395
E value
                  1.0e-38
Match length
                  84
                  89
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B1 -
                  Arabidopsis thaliana >gi 16366 emb CAA45789 (X64459)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128229 (AC004077) putative
                  photosystem II type I chlorophyll a/b binding protein
                  [Arabidopsis thaliana] >gi_3337372 (AC004481) putative
                  photosystem II type I chlorophyll a/b binding protein
                  [Arabidopsis thaliana]
```

```
Seq. No.
                    164978
 Seq. ID
                    LIB3177-084-P1-K1-A5
 Method
                    BLASTX
 NCBI GI
                    q4539292
 BLAST score
                    470
 E value
                    4.0e-47
Match length
                    87
 % identity
                    100
 NCBI Description
                    (AL049480) putative ribosomal protein S10 [Arabidopsis
                    thalianal
Seq. No.
                    164979
Seq. ID
                    LIB3177-084-P1-K1-A6
Method
                    BLASTX
NCBI GI
                    g115470
BLAST score
                    492
E value
                    7.0e-50
Match length
                    116
% identity
                    84
NCBI Description
                   CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                   DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase
                   (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                    [Arabidopsis thaliana]
Seq. No.
                   164980
Seq. ID
                   LIB3177-084-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g2062161
BLAST score
                   559
E value
                   1.0e-57
Match length
                   111
% identity
NCBI Description
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   164981
Seq. ID
                   LIB3177-084-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g99772
BLAST score
                   521
E value
                   3.0e-53
Match length
                   130
% identity
                   82
NCBI Description
                   ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana
                   >gi_166936 (J05540) ubiquitin extension protein (UBQ6)
                   [Arabidopsis thaliana] >gi 3522953 (AC004411) ubiquitin
                   extension protein (UBQ6) [Arabidopsis thaliana]
Seq. No.
                   164982
Seq. ID
                   LIB3177-084-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g4455271
BLAST score
                   386
E value
                   2.0e-37
Match length
                  129
```

% identity

```
% identity
                     55
 NCBI Description
                     (AL035527) serine protease-like protein [Arabidopsis
                     thaliana]
 Seq. No.
                     164983
 Seq. ID
                    LIB3177-084-P1-K1-B12
 Method
                    BLASTX
 NCBI GI
                    g417381
 BLAST score
                     414
 E value
                     5.0e-41
 Match length
                    83
 % identity
                    99
                    NITRILASE 1 >gi_99738_pir_S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_(X63445)
 NCBI Description
                    nitrilase I [Arabidopsis thaliana]
 Seq. No.
                    164984
 Seq. ID
                    LIB3177-084-P1-K1-B2
 Method
                    BLASTX
 NCBI GI
                    g3914740
 BLAST score
                    272
 E value
                    1.0e-24
 Match length
                    64
 % identity
                    86
                    60S RIBOSOMAL PROTEIN L26 >gi_2160300 dbj_BAA18941
NCBI Description
                    (D78495) ribosomal protein [Brassica rapa]
 Seq. No.
                    164985
 Seq. ID
                    LIB3177-084-P1-K1-B3
 Method
                    BLASTN
 NCBI GI
                    g2264316
 BLAST score
                    92
 E value
                    3.0e-44
 Match length
                    349
 % identity
                    38
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MRO11, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    164986
 Seq. ID
                    LIB3177-084-P1-K1-B4
Method
                    BLASTX
 NCBI GI
                    g4371282
 BLAST score
                    569
E value
                    8.0e-59
Match length
                    122
% identity
NCBI Description
                    (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
                    thaliana]
Seq. No.
                   164987
Seq. ID
                   LIB3177-084-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g2435604
BLAST score
                   82
E value
                   9.0e-11
Match length
                   69
```

```
NCBI Description
                  (AF026213) strong similarity to Saccharomyces cerevisiae
                   endosomal P24A protein (SP:P32802) [Caenorhabditis elegans]
Seq. No.
                   164988
Seq. ID
                   LIB3177-084-P1-K1-B6
Method
                   BLASTN ·
NCBI GI
                   g4589440
BLAST score
                   171
E value
                   2.0e-91
Match length
                   210
% identity
                   94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSD21, complete sequence
Seq. No.
                   164989
Seq. ID
                   LIB3177-084-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g3850573
BLAST score
                   723
E value
                   8.0e-77
Match length
                   146
                   97
% identity
NCBI Description
                   (AC005278) Similar to gi 1652733 glycogen operon protein
                  GlgX from Synechocystis sp. genome gb D90908. ESTs
                   gb H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from
                  this gene. [Arabidopsis thaliana]
                  164990
Seq. No.
Seq. ID
                  LIB3177-084-P1-K1-B9
                                                   à.
Method
                  BLASTX
NCBI · GI
                  g1363489
BLAST score
                  745
                  2.0e-79
E value
                  144
Match length
                  98
% identity
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                  thaliana >gi 984052 emb CAA61592 (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  164991
                  LIB3177-084-P1-K1-C1
Seq. ID
Method
                  BLASTX
                  g1170247
NCBI GI
BLAST score
                  445
E value
                  2.0e-44
Match length
                  104
% identity
                  78
                  HEVEIN-LIKE PROTEIN PRECURSOR >qi 407248 (U01880)
NCBI Description
                  pre-hevein-like protein [Arabidopsis thaliana]
Seq. No.
                  164992
Seq. ID
                  LIB3177-084-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q4587564
BLAST score
                  581
E value
                  3.0e-60
Match length
                  119
```

```
% identity
 NCBI Description
                   (AC006550) Strong similarity to gb_X14017 photosystem I
                   reaction centre subunit II precursor (psaD) from Spinacia
                   oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,
                   gb_N65521, gb_T42498, gb_T41918, gb_N38024
Seq. No.
                   164993
Seq. ID
                   LIB3177-084-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g3882356
BLAST score
                   255
E value
                   6.0e-22
Match length
                   97
% identity
                   54
                   (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   164994
Seq. ID
                   LIB3177-084-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3478700
BLAST score
                   517
E value
                   1.0e-52
Match length
                   118
% identity
                   86
NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]
Seq. No.
                   164995
Seq. ID
                   LIB3177-084-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g3136336
BLAST score
                   152
E value
                   4.0e-10
Match length
                   99
% identity
                 · 28
NCBI Description (AF064552) calmodulin; Cam [Apium graveolens]
Seq. No.
                   164996
Seq. ID
                   LIB3177-084-P1-K1-C6
Method
                  BLASTX
NCBI GI
                   g4585935
BLAST score
                   537
E value
                   3.0e-55
Match length
                  104
% identity
                   97
NCBI Description
                   (AC007211) putative chlorophyll A/B binding protein
                   [Arabidopsis thaliana] >gi_4741946 gb_AAD28770.1 AF134123 1
                   (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  164997
                  LIB3177-084-P1-K1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g166645
BLAST score
                  69
                  5.0e-31
E value
Match length
                  113
% identity
```

```
NCBI Description Arabidopsis thaliana light-harvesting chlorophyll
                      a/b-binding protein (Cab4) mRNA, complete cds
   Seq. No.
                      164998
   Seq. ID
                      LIB3177-084-P1-K1-C8
   Method
                      BLASTX
   NCBI GI
                      g520478
   BLAST score
                      541
   E value
                      2.0e-55
   Match length
                      111
   % identity
                      98
   NCBI Description
                      (U09137) pyruvate dehydrogenase E1 beta subunit
                      [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate
                     dehydrogenase [Arabidopsis thaliana]
   Seq. No.
                     164999
   Seq. ID
                     LIB3177-084-P1-K1-C9
   Method
                     BLASTX
   NCBI GI
                     g1082054
   BLAST score
                     301
   E value
                     2.0e-27
   Match length
                     56
   % identity
                     100
   NCBI Description (Z49859) copper transporter protein [Arabidopsis thaliana]
   Seq. No.
                     165000
   Seq. ID
                     LIB3177-084-P1-K1-D1
   Method
                     BLASTN
   NCBI GI
                     -g4531433
   BLAST score
                     187
   E value
                     1.0e-101
   Match length
                     251
   % identity
                     94
: NCBI Description Arabidopsis thaliana chromosome II P1 MFL8 genomic
                     sequence, complete sequence
  Seq. No.
                     165001
  Seq. ID
                     LIB3177-084-P1-K1-D10
  Method
                     BLASTX
  NCBI GI
                     g115778
  BLAST score
                     114
  E value
                     4.0e-48
  Match length
                     103
  % identity
                     90
  NCBI Description
                     CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                     (CAB-1) (LHCP) >gi_282896_pir__S22511 chlorophyll
                     a/b-binding protein (cab-\overline{1}) - white mustard
                     >gi_21138_emb_CAA34459_ (X16436) chlorophyll a/b-binding
                     protein (AA 1-266) [Sinapis alba] >gi 21140 emb CAA33903
                     (X15894) chlorophyll a/b-binding polypeptide [Sinapis alba]
  Seq. No.
                    165002
  Seq. ID
                    LIB3177-084-P1-K1-D11
 . Method
                    BLASTX
  NCBI GI
                    g3914442
  BLAST score
                    419
  E value
                    3.0e-41
```

Seq. ID

```
Match length
                   105
 % identity
                   78
 NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                   >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
 Seq. No.
                   165003
Seq. ID
                   LIB3177-084-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q461550
BLAST score
                   352
E value
                   1.0e-33
Match length
                   89
% identity
                   84
                   ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_81635_pir__B39732 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma-1 chain precursor, chloroplast -
                   Arabidopsis thaliana >gi_166632 (M61741) ATP synthase
                   gamma-subunit [Arabidopsīs thaliana]
Seq. No.
                   165004
Seq. ID
                   LIB3177-084-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q416758
BLAST score
                   340
E value
                   4.0e-32
Match length
                   110
% identity
                   61
                  SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130)
NCBI Description
                   carboxypeptidase Y-like protein [Arabidopsis thaliana]
                   >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis
                   thaliana]
Seq. No.
                  165005
                  LIB3177-084-P1-K1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2656028
BLAST score
                 349
E value
                  0.0e+00
Match length
                  357
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
Seq. No.
                  165006
Seq. ID
                  LIB3177-084-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g166645
BLAST score
                  178
E value
                  8.0e-96
Match length
                  178
% identity
                  100
NCBI Description
                  Arabidopsis thaliana light-harvesting chlorophyll
                  a/b-binding protein (Cab4) mRNA, complete cds
Seq. No.
                  165007
```

LIB3177-084-P1-K1-D8

```
Method
                   BLASTN
NCBI GI
                   g1657620
BLAST score
                   287
E value
                   1.0e-160
Match length
                   291
% identity
                   100
                   Arabidopsis thaliana putative acyl-coA dehydrogenase G6p
NCBI Description
                   (AtG6) mRNA, complete cds
Seq. No.
                   165008
Seq. ID
                   LIB3177-084-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g1408473
BLAST score
                   431
E value
                   5.0e-47
Match length
                   100
                   96
% identity
                   (U48939) actin depolymerizing factor 2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   165009
Seq. ID
                   LIB3177-084-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g4585882
BLAST score
                   239
E value
                   3.0e-20
Match length
                   46
% identity
                   100
NCBI Description
                   (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   165010
                   LIB3177-084-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132102
BLAST score
                   718
                   3.0e-76
E value
Match length
                   136
                   99
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir RKMUB2
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  165011
Seq. ID
                  LIB3177-084-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g3869075
BLAST score
                  49
E value
                  2.0e-19
Match length
                  57
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MXK3, complete sequence [Arabidopsis thaliana]

BLAST score

312

```
Seq. No.
                   165012
 Seq. ID
                   LIB3177-084-P1-K1-E3
 Method
                   BLASTX
 NCBI GI
                   g3915865
BLAST score
                   292
 E value
                   1.0e-26
 Match length
                   59
% identity
                   93
NCBI Description 40S RIBOSOMAL PROTEIN S4
 Seq. No.
                   165013
 Seq. ID
                   LIB3177-084-P1-K1-E5
Method
                  BLASTX
NCBI GI
                   g2832355
BLAST score
                   497
E value
                   3.0e-50
Match length
                   113
% identity
                   87
NCBI Description (Y14074) HMG protein [Arabidopsis thaliana]
Seq. No.
                  165014
Seq. ID
                  LIB3177-084-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q430947
BLAST score
                  275
E value
                  1.0e-24
Match length
                  85
% identity
                  67
NCBI Description
                  (U01103) PSI type III chlorophyll a/b-binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  165015
Seq. ID
                  LIB3177-084-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g457403
BLAST score
                  161
E value ·
                  3.0e-85
Match length
                  161
% identity
                  100
NCBI Description Arabidopsis thaliana mRNA for MAP kinase, complete cds
Seq. No.
                  165016
                  LIB3177-084-P1-K1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4678705 °
BLAST score
                  448
E value
                  0.0e+00
Match length
                  456
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                  (ESSA project)
Seq. No.
                  165017
Seq. ID
                  LIB3177-084-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g4454447
```

E value

7.0e-61

```
E value
                   1.0e-175
Match length
                   316
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165018
Seq. ID
                  LIB3177-084-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1172969
BLAST score
                  534
E value
                  1.0e-54
Match length
                  112
% identity
                  95
NCBI Description
                  60S RIBOSOMAL PROTEIN L11 (L16) >gi 629552 pir $49033
                  ribosomal protein L11.e - Arabidopsis thaliana
                  >gi_550544_emb_CAA57394_ (X81798) ribosomal protein L16
                   [Arabidopsis thaliana]
Seq. No.
                  165019
Seq. ID
                  LIB3177-084-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  q3047074
BLAST score
                  455
E value
                  0.0e + 00
Match length
                  455
% identity
                  100
NCBI Description Arabidopsis thaliana BAC F21E10
Seq. No.
                  165020
Seq. ID
                  LIB3177-084-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g2477521
                  29
BLAST score
E value
                  2.0e-06
Match length
                  412
                  18
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165021
Seq. ID
                  LIB3177-084-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  g3063690
BLAST score
                  301
E value
                  1.0e-169
                  364
Match length
% identity
                  96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
                  (ESSAII project)
Seq. No.
                  165022
Seq. ID
                  LIB3177-084-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1350956
BLAST score
                  587
```

```
Match length
                  117
% identity
                  98
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
Seq. No.
                  165023
Seq. ID
                  LIB3177-084-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3043414
BLAST score
                  77
E value
                  2.0e-35
Match length
                  179
% identity
                  93
NCBI Description Arabidopsis thaliana mRNA for At-hsc70-3 protein
Seq. No.
                  165024
Seq. ID
                  LIB3177-084-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g4741962
BLAST score
                  532
E value
                  2.0e-54
Match length
                  144
% identity
                  57
NCBI Description (AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.
                  165025
                  LIB3177-084-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498731
BLAST score
                  197
E value
                  4.0e-15
Match length
                  45
% identity
                  80
                 PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi_1362013 pir S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886428 emb_CAA89838 (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                  165026
                  LIB3177-084-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406774
BLAST score
                  754
E value
                  2.0e-80
Match length
                  149
% identity
                  98
NCBI Description (AC006836) putative nonsense-mediated mRNA decay protein,
                  5' partial [Arabidopsis thaliana]
Seq. No.
                  165027
Seq. ID
                  LIB3177-084-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  665
E value
                  4.0e-70
Match length
                  122
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
```

BLAST score

Match length

E value

297

462

1.0e-166

```
(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain Al precursor - Arabidopsis thaliana
```

```
Seq. No.
                  165028
Seq. ID
                  LIB3177-084-P1-K1-G11
Method ...
                  BLASTX
NCBI GI
                  g3885511
BLAST score
                  420
E value
                  3.0e-41
Match length
                  103
% identity
                  82
NCBI Description
                  (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
                  165029
Seq. No.
Seq. ID
                  LIB3177-084-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2811028
BLAST score
                  660
                  2.0e-69
E value
                  149
Match length
                  89
% identity
NCBI Description HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >qi 2191188
                   (AF007271) similar to S. cerevisiae SIK1P (PID:q984964)
                   [Arabidopsis thaliana]
Seq. No.
                  165030
Seq. ID
                  LIB3177-084-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  589
                  3.0e-61
E value
                  110
Match length
                  99
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  165031
                  LIB3177-084-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4678941
BLAST score
                  443
E value
                  6.0e-44
Match length
                  89
                  99
% identity
NCBI Description (AL049711) gamma response I protein [Arabidopsis thaliana]
Seq. No.
                  165032
Seq. ID
                  LIB3177-084-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  g4314374
```

.

```
% identity
                   100
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F10A12 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165033
Seq. ID
                   LIB3177-084-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g1173218
BLAST score
                   616
E value
                   3.0e-64
Match length
                   122
                   99
% identity
                   40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
NCBI Description
                   protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                   cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                   165034
Seq. ID
                   LIB3177-084-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   g2264316
BLAST score
                   91
E value
                   2.0e-43
Match length
                   404
% identity
                   36
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165035
Seq. ID
                  LIB3177-084-P1-K1-G8
Method
                  BLASTX
NCBI GI
                   g2330797
BLAST score
                   226
E value
                  1.0e-18
Match length
                  114
% identity
                  43
NCBI Description
                  (Z98601) zinc finger protein [Schizosaccharomyces pombe]
Seq. No.
                  165036
Seq. ID
                  LIB3177-084-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  358
E value
                  3.0e - 34
Match length
                  76
% identity
                  93
NCBI Description
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  165037
Seq. ID
                  LIB3177-084-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q115385
BLAST score
                  555
E value
                  4.0e-57
Match length
                  111
% identity
                  97
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
```

chlorophyll a/b binding protein [Arabidopsis thaliana]

```
Seq. No.
                  165038
Seq. ID
                  LIB3177-084-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q3983125
BLAST score
                  645
E value
                  9.0e-68
Match length
                  126
% identity
                  100
NCBI Description
                  (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  165039
Seq. ID
                  LIB3177-084-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  75
E value
                  2.0e-56
Match length
                  107
% identity
                  87
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir_ RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                 Al precursor - Arabidopsis thaliana
Seq. No.
                  165040
Seq. ID
                  LIB3177-084-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g2576362
BLAST score
                  115
E value
                  2.0e-58
Match length
                  123
% identity
NCBI Description
                  Arabidopsis thaliana amino acid transport protein mRNA,
                  complete cds
Seq. No.
                  165041
Seq. ID
                  LIB3177-084-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g115385
BLAST score
                  475
E value
                  9.0e-48
Match length
                  91
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165042
Seq. ID
                  LIB3177-084-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q1145697
BLAST score
                  316
E value
                  2.0e-29
Match length
                  68
```

94

% identity

```
NCBI Description (U39485) delta tonoplast integral protein [Arabidopsis
                  thaliana]
Seq. No.
                  165043
Seq. ID
                  LIB3177-084-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q282833
BLAST score
                  344
E value
                  7.0e-33
Match length
                  78
% identity
                  91
NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
                  165044
Seq. No.
Seq. ID
                  LIB3177-085-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  g3337347
BLAST score
                  185
                  1.0e-99
E value
Match length
                  445
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F13P17 genomic
                sequence, complete sequence [Arabidopsis thaliana]
                  165045
Seq. No.
Seq. ID
                  LIB3177-085-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g4662640
BLAST score
                  446
E value
                  0.0e+00
Match length
                  458
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K19 genomic
                  sequence, complete sequence
Seq. No.
                  165046
                  LIB3177-085-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928758
BLAST score
                  555
E value
                  3.0e-57
Match length
                  116
% identity
                  91
NCBI Description
                  (AB007987) Lipoic acid synthase [Arabidopsis thaliana]
                  >gi 4454462_gb_AAD20909_ (AC006234) putative lipoic acid
                  synthase [Arabidopsis thaliana]
                  165047
Seq. No.
Seq. ID
                  LIB3177-085-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4512615
BLAST score
                  164
E value
                  3.0e-55
Match length
                  116
% identity
                  100
NCBI Description
                  (ACO04793) Strong similarity to gb X59970 3-isopropylmalate
                  dehydrogenase (IMDH) from Brassica napus. EST gb F14478
```

comes from this gene. [Arabidopsis thaliana]

```
Seq. No.
                   165048
Seq. ID
                   LIB3177-085-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g2832625
BLAST score
                   693
                   3.0e-73
E value
Match length
                   128
                   100
% identity
NCBI Description
                  (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                   165049
Seq. ID
                   LIB3177-085-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g4263771
BLAST score
                   515
E value
                   2.0e-52
Match length
                   152
% identity
                   70
NCBI Description
                  (AC006218) putative nonspecific lipid-transfer protein
                  precursor [Arabidopsis thaliana]
                  >gi_4726121 gb AAD28321.1 AC006436 12 (AC006436) putative
                  nonspecific lipid-transfer protein precursor [Arabidopsis
                  thaliana]
Seq. No.
                  165050
Seq. ID
                  LIB3177-085-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g4204285
BLAST score
                  505
E value
                  2.0e-51
Match length
                  125
                  75
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  165051
                  LIB3177-085-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2358139
BLAST score
                  306
E value
                  1.0e-172
Match length
                  306
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
                  sequence [Arabidopsis thaliana]
Seq. No.
                  165052
Seq. ID
                  LIB3177-085-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2501188
BLAST score
                  608
E value
                  3.0e-63
Match length
                  146
% identity
                  84
NCBI Description
                  THIAZOLE BIOSYNTHETIC ENZYME >gi 2129750 pir S71191 TH14
```

```
Seq. No.
                  165053
Seq. ID
                  LIB3177-085-P1-K1-A7-
Method
                  BLASTN
NCBI GI
                  g3420042
BLAST score
                  136
E value
                  2.0e-70
                  429
Match length
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC T13E15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165054
Seq. ID
                  LIB3177-085-P1-K1-A8
                  BLASTN
Method
NCBI GI
                  g4589419
BLAST score
                  373
E value
                  0.0e + 00
                  429
Match length
% identity
                  48
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2I5, complete sequence
Seq. No.
                  165055
Seq. ID
                  LIB3177-085-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  g2760316
BLAST score
                  303
E value
                  1.0e-170
                  373
Match length
                  97
% identity
                  The sequence of BAC F1N21 from Arabidopsis thaliana
NCBI Description
                  chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165056
Seq. ID
                  LIB3177-085-P1-K1-B1 .
Method
                  BLASTX
                                                                       الأحاج أسامي
NCBI GI
                  g3885511
BLAST score
                  420
E value
                  3.0e-41
Match length
                  103
% identity
                  82
                  (AF084200) similar to PSI-K subunit of photosystem I from
NCBI Description
                  barley [Medicago sativa]
                  165057
Seq. No.
Seq. ID
                  LIB3177-085-P1-K1-B10
                  BLASTX
Method
NCBI GI
                  g132102
BLAST score
                  729
                  2.0e-77
E value
                  138
Match length
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
```

Thil protein [Arabidopsis thaliana]

protein homolog - Arabidopsis thaliana >gi 1113783 (U17589)

(RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2

```
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_(X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
```

```
Seq. No.
                     165058
 Seq. ID
                    LIB3177-085-P1-K1-B11
 Method
                    BLASTX
 NCBI GI
                    g3914826
 BLAST score
                    498
 E value
                    1.0e-50
 Match length
                    98
 % identity
                    100
 NCBI Description
                    DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR
                    >gi_2330560_emb_CAA69972_ (Y08722) chloroplast
                    single-subunit DNA-dependent RNA polymerase [Arabidopsis
                    thaliana] >gi_2330564_emb_CAA69717_ (Y08463) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis
                    thaliana] >gi_4115372 (AC005967) chloroplast single subunit
                    DNA-dependent RNA polymerase [Arabidopsis thaliana]
 Seq. No.
                    165059
 Seq. ID
                    LIB3177-085-P1-K1-B2
Method
                    BLASTX
NCBI GI
                    g4455248
BLAST score
                    363
E value
                    1.0e-34
Match length
                    77
% identity
                    100
                   (AL035523) acyl carrier-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    165060
Seq. ID
                    LIB3177-085-P1-K1-B3
Method
                    BLASTX
NCBI GI
                    g4337175
BLAST score
                    668
E value
                    2.0e-70
Match length
                   148
% identity
                    90
                   (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                   gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   165061
Seq. ID
                   LIB3177-085-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   q4454447
BLAST score
                   24
E value
                   5.0e-04
Match length
                   159
% identity
                   76
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F5H14 genomic
```

Seq. No. 165062

Seq. ID LIB3177-085-P1-K1-B5

sequence, complete sequence [Arabidopsis thaliana]

NCBI GI

```
Method
                    BLASTN
 NCBI GI
                    g16407
 BLAST score
                   207
 E value
                   1.0e-112
 Match length
                   207
 % identity
                   100
 NCBI Description Arabidopsis thaliana PIP1b gene
 Seq. No.
                   165063
 Seq. ID
                   LIB3177-085-P1-K1-B6
 Method
                   BLASTX
 NCBI GI
                   g3142289
 BLAST score
                   48
 E value
                   2.0e-53
 Match length
                   118
 % identity
                   92
 NCBI Description
                   (AC002411) Strong similarity to beta-keto-Coa synthase
                   gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
Seq. No.
                   165064
Seq. ID
                   LIB3177-085-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g2497733
BLAST score
                   591
E value
                   2.0e-61
Match length
                   117
% identity
                   97
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
                   >gi_1177796 (M80567) non-specific lipid transfer protein
                   [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   165065
Seq. ID
                   LIB3177-085-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   g4263655
BLAST score
                   205
E value
                   6.0e-26
Match length
                  74
% identity
                   76
NCBI Description
                  (AC006136) putative reverse transcriptase [Arabidopsis
                  thaliana]
Seq. No.
                  165066
Seq. ID
                  LIB3177-085-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g4336756
BLAST score
                  688
E value
                  1.0e-72
Match length
                  134
% identity
                  97
NCBI Description
                  (AF104453) catalase [Brassica juncea]
Seq. No.
                  165067
Seq. ID
                  LIB3177-085-P1-K1-C10
Method
                  BLASTX
```

g3688799

```
BLAST score
                   168
 E value
                   1.0e-11
 Match length
                   53
 % identity
                   68
 NCBI Description
                   (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
                   thaliana]
 Seq. No.
                   165068
 Seq. ID
                   LIB3177-085-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q1769905
BLAST score
                   49
E value
                   1.0e-21
Match length
                   86
 % identity
                   69
NCBI Description
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                   165069
Seq. ID
                   LIB3177-085-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   g4835223
BLAST score
                   4,37
E value
                   0.0e+00
Match length
                   462
% identity
                   98
                   Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3
NCBI Description
                   (ESSA project)
Seq. No.
                   165070
Seq. ID
                   LIB3177-085-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g4454036
BLAST score
                   642
E value
                   2.0e-75
Match length
                   139
% identity
                   99
NCBI Description
                  (AL035394) putative major latex protein [Arabidopsis
                   thaliana]
Seq. No.
                   165071
                  LIB3177-085-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4538963
BLAST score
                   523
E value
                  2.0e-53
Match length
                  136
% identity
                   (AL049488) chlorophyll a/b-binding protein-like
NCBI Description
                   [Arabidopsis thaliana] >gi_4741958 gb AAD28776.1 AF134129 1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                  165072
Seq. ID
                  LIB3177-085-P1-K1-C5
Method
                  BLASTN
NCBI GI
                  q3236234
BLAST score
```

244

BLAST score

268

```
E value
                    1.0e-135
 Match length
                    324
 % identity
                    93
 NCBI Description
                    Arabidopsis thaliana chromosome II BAC F13M22 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    165073
 Seq. ID
                    LIB3177-085-P1-K1-C6
 Method
                    BLASTX
 NCBI GI
                    g4415907
 BLAST score
                    538
 E value
                    4.0e-55
 Match length
                    108
 % identity
                    97
 NCBI Description
                    (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]
                   >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative
                    60S ribosomal protein L24 [Arabidopsis thaliana]
 Seq. No.
                    165074
 Seq. ID
                   LIB3177-085-P1-K1-C7
 Method
                   BLASTN
 NCBI GI
                   g4220627
 BLAST score
                   128
 E value
                   1.0e-65
 Match length
                   468
 % identity
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K20J1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165075
Seq. ID
                   LIB3177-085-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g4741960
BLAST score
                   589
E value
                   4.0e-61
Match length
                   126
% identity
                   89
NCBI Description
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                   165076
Seq. ID
                   LIB3177-085-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g2160168
BLAST score
                   752
E value
                   3.0e-80
Match length
                   151
% identity
                   97
NCBI Description
                  (AC000132) Strong similarity to R. communis
                  phosphoglycerate mutase (gb X70652). ESTs
                  gb_T41853,gb_T76648 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                  165077
Seq. ID
                  LIB3177-085-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g4102703
```

Method

BLASTX

```
E value
                    1.0e-23
 Match length
                    56
  % identity
                    98
 NCBI Description
                    (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis
                    thalianal
 Seq. No.
                    165078
 Seq. ID
                    LIB3177-085-P1-K1-D12
 Method
                    BLASTX
 NCBI GI
                    q132102
 BLAST score
                    767
 E value
                    6.0e-82
 Match length
                    140
 % identity
                    99
 NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                    (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
 Seq. No.
                   165079
Seq. ID
                   LIB3177-085-P1-K1-D2
 Method
                   BLASTN
 NCBI Gİ
                   g2828185
 BLAST score
                   166
 E value
                   2.0e-88
 Match length
                   317
 % identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MUD21, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   165080
 Seq. ID
                   LIB3177-085-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g3123271
BLAST score
                   517
E value
                   9.0e-53
Match length
                   100
% identity
                   97
NCBI Description
                  40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052)
                   ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                   165081
Seq. ID
                  LIB3177-085-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g4455251 ··
BLAST score
                   443
E value
                   6.0e-44
Match length
                  132
% identity
                   67
NCBI Description
                  (AL035523) magnesium-protoporphyrin IX
                  methyltransferase-like protein [Arabidopsis thaliana]
Seq. No.
                  165082
Seq. ID
                  LIB3177-085-P1-K1-D5
```

```
NCBI GI
                     g1657621
   BLAST score
                     774
   E value
                     9.0e-83
   Match length
                     159
   % identity
                     92
NCBI Description
                     (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
                     putative acyl-coA dehydrogenase [Arabidopsis thaliana]
   Seq. No.
                     165083
  Seq. ID
                     LIB3177-085-P1-K1-D8
  Method
                     BLASTN
  NCBI GI
                     g2564046
  BLAST score
                     178
  E value
                     2.0e-95
  Match length
                     471
  % identity
  NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                     MGI19, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     165084
  Seq. ID
                     LIB3177-085-P1-K1-D9
  Method
                     BLASTX
  NCBI GI
                     g2894564
  BLAST score
                     127
  E value
                     9.0e-28
  Match length
                     65
  % identity
                     98
  NCBI Description
                     (AL021890) putative protein [Arabidopsis thaliana]
  Seq. No.
                    165085
  Seq. ID
                    LIB3177-085-P1-K1-E1
  Method
                    BLASTX
  NCBI GI
                    g4741960
  BLAST score
                    472
  E value
                    2.0e-47
  Match length
                    109
  % identity
                    83
  NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
  Seq. No.
                    165086
  Seq. ID
                    LIB3177-085-P1-K1-E11
 Method
                    BLASTX
 NCBI GI
                    g4741940
 BLAST score
                    637
 E value
                    1.0e-66
 Match length
                    119
 % identity
                    68
 NCBI Description
                   (AF134120) Lhca2 protein [Arabidopsis thaliana]
 Seq. No.
                    165087
 Seq. ID
                    LIB3177-085-P1-K1-E12
 Method
                    BLASTN
 NCBI GI
                    g2618601
 BLAST score
                    301
 E value
                    1.0e-169
 Match length
                    341
 % identity
```

97

Seq. ID

•

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                     MHJ24, complete sequence [Arabidopsis thaliana]
 Seq. No.
                     165088
 Seq. ID
                     LIB3177-085-P1-K1-E2
-Method
                     BLASTX
 NCBI GI
                     q4539459
 BLAST score
                     165
E value
                     8.0e-12
Match length
                     58
 % identity
                     57
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                    165089
Seq. ID
                    LIB3177-085-P1-K1-E3
Method
                    BLASTX
NCBI GI
                    g1175012
BLAST score
                    149
E value
                    3.0e-39
Match length
                    87
% identity
                    99
NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
                    B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane
                    protein TMP-B [Arabidopsis thaliana]
Seq. No.
                    165090
Seq. ID
                    LIB3177-085-P1-K1-E5
Method
                    BLASTX
NCBI GI
                    g133709
BLAST score
                    149
E value
                    2.0e-09
Match length
                    45
% identity
                    60
NCBI Description CYANELLE 30S RIBOSOMAL PROTEIN S10 >gi_70927_pir__R3KT10
                    ribosomal protein S10 - Cyanophora paradoxa cyanelle >gi_11391_emb_CAA36388_ (X52143) ribosomal protein S10 (AA 1-105) [Cyanophora paradoxa] >gi_336632 (M35206) ribosomal
                    protein S10 (rps10; rpsJ) [Cyanophora paradoxa] >gi 1016150
                    (U30821) ribosomal protein S10 [Cyanophora paradoxa]
Seq. No.
                    165091
Seq. ID
                    LIB3177-085-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q282865
BLAST score
                    616
E value
                    3.0e-64
Match length
                   123
% identity
                   70
NCBI Description
                   chlorophyll a/b-binding protein - Arabidopsis thaliana
                   >gi_16207_emb_CAA39534 (X56062) chlorophyll A/B-binding
                   protein [Arabidopsis thaliana] >gi_166644 (M85150)
                   chlorophyll a/b-binding protein [Arabidopsis thaliana]
                   >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                   a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                   165092
```

LIB3177-085-P1-K1-E7

```
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  145
                  9.0e-76
E value
                  201
Match length
% identity
                  93
                 Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  165093
Seq. ID
                  LIB3177-085-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2970036
BLAST score
                  145
                  6.0e-09
E value
                  35
Match length
                  83
% identity
NCBI Description (D88537) delta 9 desaturase [Arabidopsis thaliana]
Seq. No.
                  165094
Seq. ID
                  LIB3177-085-P1-K1-E9
                  BLASTX
Method
NCBI GI
                  g4544443
                  167
BLAST score
E value
                  9.0e-12
Match length
                  33
                  100
% identity
                 (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  165095
Seq. ID
                  LIB3177-085-P1-K1-F10
Method
                  BLASTX
                  g4741952
NCBI GI
BLAST score
                  366
E value
                  4.0e-35
                  108
Match length
% identity
                  68
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  165096
Seq. ID
                  LIB3177-085-P1-K1-F11
                  BLASTX
Method
NCBI GI
                  g3249100
BLAST score
                  516
                  9.0e~53
E value
Match length
                  103
                  94
% identity
                  (ACO03114) Match to calreticulin (AtCRTL) mRNA gb U27698
NCBI Description
                  and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323
                  and gb AA042519 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  165097
Seq. ID
                  LIB3177-085-P1-K1-F12
Method
                  BLASTX
```

g417381

668

NCBI GI

BLAST score

Method

BLASTX

```
E value
                        2.0e-70
     Match length
                        150
     % identity
                       88
     NCBI Description
                       NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) -
                       Arabidopsis thaliana >gi 16400 emb CAA45041 (X63445)
                       nitrilase I [Arabidopsis thaliana]
772 .
     Seq. No.
                       165098
     Seq. ID
                       LIB3177-085-P1-K1-F2
     Method
                       BLASTX
    NCBI GI
                       g115767
    BLAST score
                       706
    E value
                       7.0e-75
    Match length
                       132
     % identity
                       99
     NCBI Description
                       CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                       (CAB-165/180) (LHCP) >gi_81603_pir_ A29280_chlorophyll
                       a/b-binding protein ab16\overline{5} - Arabidopsis thaliana
                       >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                       protein (LHCP AB 65) [Arabidopsis thaliana]
                       >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                       protein (LHCP AB 180) [Arabidopsis thaliana]
    Seq. No.
                       165099
    Seq. ID
                       LIB3177-085-P1-K1-F4
    Method
                       BLASTX
    NCBI GI
                       g4741952
    BLAST score
                       552
    E value
                       7.0e-57
    Match length
                       108
                       97
    % identity
                      (AF134126) Lhcb3 protein [Arabidopsis thaliana]
    NCBI Description
    Seq. No.
                       165100
    Seq. ID
                       LIB3177-085-P1-K1-F5
    Method
                       BLASTN
    NCBI GI
                       q2462264
    BLAST score
                       33
    E value
                       7.0e-09
    Match length
                       53
    % identity
                       91
    NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
    Seq. No.
                       165101
    Seq. ID
                       LIB3177-085-P1-K1-F6
    Method
                       BLASTX
    NCBI GI
                       g2583125
    BLAST score
                       368
    E value
                       4.0e-35
    Match length
                       108
    % identity
                       73
    NCBI Description
                       (AC002387) putative transketolase precursor [Arabidopsis
                       thaliana]
    Seq. No.
                       165102
    Seq. ID
                       LIB3177-085-P1-K1-F7
```

```
NCBI GI
                        q417103
BLAST score
                        453
E value
                        3.0e-45
Match length
                        92
                        100
% identity
                        HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone
NCBI Description
                        H3.3-like protein - Arabidopsis thaliana
                       >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                        (U09458) histone H3.2 [Medicago sativa] >gi 488567 (\overline{\text{U}}09460)
                       histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157 emb_CAA58445 (X83422)
                        histone H3 variant H3.3 [Lycopersicon esculentum]
                        >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
                        >gi 3273350 dbj_BAA31218 (AB015760) histone H3 [Nicotiana
                        tabacum] >gi_3885890 (AFO93633) histone H3 [Oryza sativa]
                        >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
                       coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone
                       H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
                        (AL035708) Histon H3 [Arabidopsis thaliana]
Seq. No.
                       165103
Seq. ID
                       LIB3177-085-P1-K1-F8
Method
                       BLASTN
NCBI GI
                       g2262135
BLAST score
                        340
E value
                       0.0e+00
Match length
                       456
                       100
% identity
NCBI Description
                       Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                       cM, complete sequence
Seq. No.
                       165104
                       LIB3177-085-P1-K1-F9
Seq. ID
Method
                       BLASTX
NCBI GI
                       g320558
BLAST score
                       511
E value
                       4.0e-52
Match length
                       117
% identity
                       DNA-binding protein - Arabidopsis thaliana >gi 601843
NCBI Description
                       (M25268) DNA-binding protein [Arabidopsis thaliana]
Seq. No.
                       165105
Seq. ID
                       LIB3177-085-P1-K1-G1
Method
                       BLASTX
NCBI GI
                       g1755160
BLAST score
                       526
E value
                       1.0e-53
Match length
                       114
% identity
                       89
NCBI Description
                       (U75191) germin-like protein [Arabidopsis thaliana]
```

>gi_1755174 (U75198) germin-like protein [Arabidopsis

Seq. No.

165110

thaliana]

```
Seq. No.
                    165106
Seq. ID
                    LIB3177-085-P1-K1-G10
Method
                    BLASTX
NCBI GI
                    g3915847
BLAST score
                    650
E value
                    2.0e-68
Match length
                    131
% identity
NCBI Description
                    40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
                    40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                    165107
Seq. ID
                    LIB3177-085-P1-K1-G11
Method
                    BLASTX
NCBI GI
                    g113026
BLAST score
                    729
E value
                    2.0e-77
Match length
                    151
% identity
                    91
                   ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                   >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
                    S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
                   napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
                    isocitrate lyase [Brassica napus] >gi_447142 prf 1913424A
                    isocitrate lyase [Brassica napus]
Seq. No.
                   165108
Seq. ID
                   LIB3177-085-P1-K1-G12
                   BLASTX
Method
NCBI GI
                   g1922944
BLAST score
                   244
E value
                   7.0e-21 ..
Match length
                   69
% identity
                   74
NCBI Description
                   (AC000106) Strong similarity to Picea histone H2A
                    (gb X67819). ESTs gb_ATTS3874,gb_T46627,gb_T14194 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   165109
Seq. ID
                   LIB3177-085-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   q132110
BLAST score
                   657
                   4.0e-69
E value
Match length
                   122
% identity
                   98
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
```

```
Seq. ID
                   LIB3177-085-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q4510385
BLAST score
                   571
E value
                   5.0e-59
Match length
                   142
% identity
                   75
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   165111
Seq. ID
                   LIB3177-085-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   g2191126
BLAST score
                   208
E value
                   1.0e-113
Match length
                   208
% identity
                   100
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                  165112
Seq. ID
                  LIB3177-085-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3912997
BLAST score
                  509
                                      æ.,
E value
                   9.0e-52
Match length
                  113
% identity
                  94
NCBI Description
                  FLORAL HOMEOTIC PROTEIN AGL15 >gi 2129535 pir S71200 AGL15
                  protein - Arabidopsis thaliana >gi_790635 (U22528) AGL15
                   [Arabidopsis thaliana]
Seq. No.
                  165113
Seq. ID
                  LIB3177-085-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1161926
BLAST score
                  326
E value
                  3.0e-30
Match length
                  161
% identity
                  46
                  (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
NCBI Description
Seq. No.
                  165114
Seq. ID
                  LIB3177-085-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g4586021
BLAST score
                  719
E value
                  2.0e-76
Match length
                  138
% identity
                  100
NCBI Description
                  (AC007170) putative cytoplasmic aconitate hydratase
                  [Arabidopsis thaliana]
Seq. No.
                  165115
Seq. ID.
                  LIB3177-085-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g282865
```

NCBI GI

q541858

```
BLAST score
                   594
E value
                   1.0e-61
Match length
                   120
% identity
                   69
NCBI Description
                   chlorophyll a/b-binding protein - Arabidopsis thaliana
                   >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                   protein [Arabidopsis thaliana] >gi_166644 (M85150)
                   chlorophyll a/b-binding protein [Arabidopsis thaliana]
                   >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                   a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                   165116
Seq. ID
                   LIB3177-085-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g4263525
BLAST score
                   617
E value
                   2.0e-64
Match length
                   143
                   85
% identity
NCBI Description
                   (AC004044) putative photosystem I reaction center subunit
                   II precursor [Arabidopsis thaliana]
Seq. No.
                   165117
Seq. ID
                  LIB3177-085-P1-K1-H10
Method
                   BLASTX
NCBI GI
                  g2160151
BLAST score
                   601
E value
                   2.0e-62
Match length
                  129
% identity
                  89
NCBI Description
                  (AC000375) Strong similarity to Brassica aspartic protease
                   (gb_X77260). [Arabidopsis thaliana]
Seq. No.
                  165118
Seq. ID
                  LIB3177-085-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q4741952
BLAST score
                  533
E value
                  9.0e-55
Match length
                  101
% identity
                  99
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  165119
Seq. ID
                  LIB3177-085-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q1550740
BLAST score
                  436
                  8.0e-49
E value
                  99
Match length
% identity
                  99
NCBI Description
                  (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
Seq. No.
                  165120
Seq. ID
                  LIB3177-085-P1-K1-H2
Method
                  BLASTX
```

NCBI GI

```
BLAST score
                   657
E value
                   4.0e-69
Match length
                   126
% identity
                   99
NCBI Description
                   endoxyloglucan transferase - Arabidopsis thaliana
                   >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
                   transferase [Arabidopsis thaliana] >gi 4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.
                   165121
Seq. ID
                   LIB3177-085-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g2654122
BLAST score
                   321
                   9.0e-30
E value
Match length
                   102
% identity
                   66
NCBI Description
                  (AF034694) ribosomal protein L23a [Arabidopsis thaliana]
Seq. No.
                  165122
                  LIB3177-085-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                  q115783
BLAST score
                  - 589·
                   3.0e-61
E value
Match length
                  112
                   99
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  165123
Seq. No.
Seq. ID
                  LIB3177-085-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g336392
BLAST score
                  336
E value
                  7.0e-40
Match length
                  129
% identity
                  75
NCBI Description
                  (J05215) ribosomal protein S17 [Arabidopsis thaliana]
Seq. No.
                  165124
Seq. ID
                  LIB3177-085-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  q3228389
BLAST score
                  253
E value
                  1.0e-140
Match length
                  473
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  165125
Seq. ID
                  LIB3177-085-P1-K1-H7
Method
                  BLASTX
```

g4586256

```
D9684016 .10100
```

Seq. No.

165130

```
BLAST score
                         598
     .E value
                         3.0e-62
     Match length
                         144
      % identity
                         82
      NCBI Description
                         (AL049640) probable photosystem I chain XI precursor
                         [Arabidopsis thaliana]
. ....
     Seq. No.
                         165126
     Seq. ID
                         LIB3177-085-P1-K1-H8
     Method
                        BLASTX
     NCBI GI
                         g2618723
     BLAST score .
                         650
     E value
                         3.0e-68
     Match length
                         130
     % identity
                         96
     NCBI Description
                         (U49073) IAA17 [Arabidopsis thaliana] >gi_2921756
                         (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]
                        >gi_4389514_gb_AAB70451_ (AC000104) Identical to
Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs
                        gb_H36782 and gb_F14074 come from this gene. [Arabidopsis
                        thaliana]
     Seq. No.
                        165127
     Seq. ID
                        LIB3177-085-P1-K1-H9
     Method
                        BLASTN
     NCBI GI
                        g2191126
     BLAST score
                        355
     E value
                        0.0e+00
     Match length
                        371
     % identity
                        99
     NCBI Description Arabidopsis thaliana BAC IG002N01
     Seq. No.
                        165128
     Seq. ID
                        LIB3177-086-P1-K1-A1
     Method
                        BLASTX
     NCBI GI
                        g4585966
     BLAST score
                        547
     E value
                        2.0e-56
     Match, length
                        110
     % identity
     NCBI Description
                        (AC005287) Putative dihyrdolipoamide acetyltransferase
                        [Arabidopsis thaliana]
     Seq. No.
                        165129
     Seq. ID
                        LIB3177-086-P1-K1-A11
     Method
                        BLASTX
     NCBI GI
                        g2581783
     BLAST score
                        410
    E value
                        3.0e-40
    Match length
                        89
     % identity
                        92
    NCBI Description
                       (U94998) class 1 non-symbiotic hemoglobin [Arabidopsis
                       thaliana] >gi_4678203_gb_AAD26949.1_AC007134_7 (AC007134)
                       class 1 non-symbiotic hemoglobin (AHB1) [Arabidopsis
                        thalianal
```

```
Seq. ID
                   LIB3177-086-P1-K1-A12
 Method
                   BLASTX
 NCBI GI
                   g2829891
 BLAST score
                   396
 E value
                   9.0e-39
 Match length
                   91
 % identity
                   87
 NCBI Description
                   (AC002311) Unknown protein [Arabidopsis thaliana]
 Seq. No.
                   165131
 Seq. ID
                   LIB3177-086-P1-K1-A2
 Method
                   BLASTN
 NCBI GI
                   q4220644
 BLAST score
                   155
 E value
                   9.0e-82
 Match length
                   395
 % identity
                   98
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MXL8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165132
Seg. ID
                   LIB3177-086-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q543841
BLAST score
                   543
                   9.0e-56
E value
Match length
                   108
% identity
                   97
NCBI Description
                  ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir___S28875
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                   165133
Seq. ID
                   LIB3177-086-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g1175013
BLAST score
                  531
E value
                   2.0e-54
Match length
                  119
% identity
                  87
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir_ S44084
                  plasma membrane intrinsic protein 2a - Arabidopsis Thaliana
                  >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
Seq. No.
                  165134
Seq. ID
                  LIB3177-086-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g928931
BLAST score
                  203
E value
                  1.0e-110
Match length
                  227
% identity
                  97
NCBI Description A.thaliana mRNA for putative dTDP-glucose 4-6-dehydratases
```

```
Seq. No.
                    165135
 Seq. ID
                    LIB3177-086-P1-K1-A8
Method
                    BLASTX
NCBI GI
                    g132677
BLAST score
                    71
E value
                    8.0e-36
Match length
                    112
 % identity
                    75
NCBI Description
                    50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
                    >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor,
chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_
                    (Z11508) Plastid ribosomal protein CL15 [Arabidopsis
                    thaliana]
Seq. No.
                    165136
                    LIB3177-086-P1-K1-B1.
Seq. ID
Method
                    BLASTX
NCBI GI
                    q99696
BLAST score
                    314
E value
                    4.0e-29
Match length
                    84
% identity
                    76
NCBI Description
                   glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                   chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                   >gi_240070_bbs_69728 (S69727) light-regulated glutamine
                   Synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                   aa] [Arabidopsis thaliana] >gi 228453 prf 1804333A Gln
                   synthetase [Arabidopsis thaliana]
Seq. No.
                   165137
                   LIB3177-086-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1402908
BLAST score
                   197
E value
                   5.0e-65
Match length
                   132
% identity
                   93
                   (X98315) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
                   [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)
                   peroxidase [Arabidopsis thaliana]
Seq. No.
                   165138
Seq. ID
                   LIB3177-086-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2062161
BLAST score
                   668
E value
                   2.0e-70
Match length
                   126
% identity
                   50
NCBI Description
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   165139
Seq. ID
                   LIB3177-086-P1-K1-B12
Method
                   BLASTX
```

NCBI GI

```
NCBI GI
                  g3450842
BLAST score
                   403
E value
                  1.0e-39
Match length
                  86
% identity
                  87
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  165140
Seq. ID
                  LIB3177-086-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q4587641
BLAST score
                  212
E value
                  1.0e-115
                  373
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                  165141
Seq. ID
                  LIB3177-086-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  557
E value
                  2.0e-57
Match length
                  103
                  100
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                  165142
Seq. No.
Seq. ID
                  LIB3177-086-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g4584110
BLAST score
                  299
                  4.0e-27
E value
Match length
                  111
                  53
% identity
NCBI Description
                 (AJ133639) SAH7 protein [Arabidopsis thaliana]
Seq. No.
                  165143
Seq. ID
                  LIB3177-086-P1-K1-B9
                  BLASTN
Method
NCBI GI
                  g3510336
BLAST score
                  47
E value
                  3.0e-17
                  146
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18J17, complete sequence [Arabidopsis thaliana]
                  165144
Seq. No.
                  LIB3177-086-P1-K1-C1
Seq. ID
Method
                  BLASTX
```

g3242722

Seq. ID

```
BLAST score
                  778
E value
                  3.0e-83
Match length
                  147
% identity
                  100
NCBI Description
                   (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
                  thaliana]
Seq. No.
                  165145
Sea. ID
                  LIB3177-086-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q4582787
                  473
BLAST score
E value
                  1.0e-47
                  109
Match length
                  82
% identity
                  (AJ012281) adenosine kinase [Zea mays]
NCBI Description
Seq. No.
                  165146
Seq. ID
                  LIB3177-086-P1-K1-C11
Method
                  BLASTX
                  q3273743
NCBI GI
                  281
BLAST score
                  2.0e-49
E value
Match length
                  118
% identity
                  80
                  (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi 3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
Seq. No.
                  165147
                  LIB3177-086-P1-K1-C12
Seq. ID
Method
                  BLASTX
                  a399013
NCBI GI
                  294
BLAST score
E value
                  2.0e-26
                  105
Match length
% identity
                  61
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi 16175 emb CAA46518 (X65549)
                  adenylate translocator [Arabidopsis thaliana]
                  >gi 445607 prf 1909354A adenylate translocator
                   [Arabidopsis thaliana]
Seq. No.
                  165148
Seq. ID
                  LIB3177-086-P1-K1-C2
Method
                  BLASTX
                  g2058282
NCBI GI
BLAST score
                  371
                  1.0e-35
E value
Match length
                  101
                  76
% identity
                  (X97377) atranbpla [Arabidopsis thaliana]
NCBI Description
                  165149
Seq. No.
```

LIB3177-086-P1-K1-C4

```
Method
                   BLASTN
 NCBI GI
                   g4757409
 BLAST score
                    414
 E value
                   0.0e+00
 Match length
                   443
 % identity
                   99
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MVC8, complete sequence
 Seq. No.
                   165150
 Seq. ID
                   LIB3177-086-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g2832363
BLAST score
                   656
E value
                   6.0e-69
Match length
                   125
% identity
                   100
                   (Y14075) HMG protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3367575_emb_CAA20027_ (AL031135) HMG delta protein
                   [Arabidopsis thaliana]
Seq. No.
                   165151
Seq. ID
                   LIB3177-086-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   g4490324
BLAST score
                   320
E value
                   1.0e-180
Match length
                   340.
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
                   (ESSA project)
Seq. No.
                   165152
Seq. ID
                   LIB3177-086-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g2246621
BLAST score
                   342
E value
                   1.0e-32
Match length
                   71
% identity
                   96
NCBI Description
                   (AF004393) salt-stress induced tonoplast intrinsic protein
                   [Arabidopsis thaliana]
Seq. No.
                   165153
Seq. ID
                  LIB3177-086-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g3914740
BLAST score
                   491
E value
                   9.0e-50
Match length
                  106
% identity
                   91
NCBI Description
                  60S RIBOSOMAL PROTEIN L26 >gi 2160300 dbj BAA18941
                   (D78495) ribosomal protein [Brassica rapa]
Seq. No.
                  165154
Seq. ID
                  LIB3177-086-P1-K1-C9
Method
                  BLASTX
```

```
NCBI GI
                  g421826
BLAST score
                  284
                  1.0e-25
E value
                  73
Match length
                  74
% identity
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis
                  thaliana]
Seq. No.
                  165155
Seq. ID
                  LIB3177-086-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  q4309683
BLAST score
                  132
                  2.0e-68
E value
                  152
Match length
                  97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  165156
Seq. ID
                  LIB3177-086-P1-K1-D10
                  BLASTX
Method
NCBI GI
                  q115767
BLAST score
                  626
E value
                  2.0e-65
                  119
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165157
                  LIB3177-086-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585935
BLAST score
                  499
E value
                  4.0e-58
Match length
                  114
% identity
                  100
                  (AC007211) putative chlorophyll A/B binding protein
NCBI Description
                  [Arabidopsis thaliana] >gi 4741946 gb AAD28770.1 AF134123 1
                  (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  165158
Seq. ID
                  LIB3177-086-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  g2584827
BLAST score
                  173
                  2.0e-92
E value
                  339
Match length
% identity
```

NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,

Match length

120

complete sequence [Arabidopsis thaliana]

```
Seq. No.
                    165159
 Seq. ID
                    LIB3177-086-P1-K1-D2
 Method
                    BLASTX
 NCBI GI
                    g4587541
 BLAST score
                    653
 E value
                    1.0e-68
Match length
                    132
 % identity
                    97
NCBI Description
                    (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase
                    with GDSL-motif family. ESTs gb T44453, gb T04815,
                    gb_T45993, gb_R30138, gb_AI099570 and gb_T22281 come from
                    this gene. [Arabidopsis thaliana]
Seq. No.
                    165160
Seq. ID
                   LIB3177-086-P1-K1-D3
Method
                    BLASTN
NCBI GI
                    g3510347
BLAST score
                    229
E value
                    1.0e-126
Match length
                    373
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, Placlone:
                   MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165161
Seq. ID
                   LIB3177-086-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g3157944
BLAST score
                   308
                   4.0e-59
E value
Match length
                   122
% identity
NCBI Description
                   (AC002131) Very strong similarity to aminomethyltransferase
                   precursor gb_U79769 from Mesembryanthemum crystallinum.
                   ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773,
                   gb_N380\overline{3}8, gb_T137\overline{4}2, gb_Z265\overline{4}5, gb_T2075\overline{3} and gb_W43123
                   come from this ge
Seq. No.
                   165162
Seq. ID
                   LIB3177-086-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g4741962
BLAST score
                   280
E value
                   2.0e-50
Match length
                   145
% identity
                   54
NCBI Description
                   (AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.
                   165163
Seq. ID
                   LIB3177-086-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g2119846
BLAST score
                   323
E value
                   6.0e-58
```

Seq. ID

```
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  165164
Seq. No.
                  LIB3177-086-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2695965
BLAST score
                  171
                  3.0e-12
E value
                  126
Match length
                  31
% identity
NCBI Description (AL010186) pks4 [Mycobacterium tuberculosis]
Seq. No.
                  165165
Seq. ID
                  LIB3177-086-P1-K1-D9
Method
                  BLASTX
                  g3157944
NCBI GI
BLAST score
                  356
E value
                  2.0e-34
                  75
Match length
                  95
% identity
                 (AC002131) Very strong similarity to aminomethyltransferase
NCBI Description
                  precursor gb U79769 from Mesembryanthemum crystallinum.
                  ESTs gb T43167, gb T21076, gb H36999, gb T22773,
                  gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123
                  come from this ge
                  165166
Seq. No.
Seq. ID
                  LIB3177-086-P1-K1-E10
Method
                  BLASTN
                  g3702732
NCBI GI
BLAST score
                  199
                  1.0e-108
E value
Match length
                  290
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGF10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165167
Seq. ID
                  LIB3177-086-P1-K1-E2
Method ·
                  BLASTN
NCBI GI
                  q4581084
BLAST score
                  256
                  1.0e-142
E value
Match length
                  298
% identity
                  98
                 Arabidopsis thaliana chromosome I BAC T30F21 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  165168
```

LIB3177-086-P1-K1-E3

NCBI GI

```
Method
                   BLASTN
NCBI GI
                   g4159706
BLAST score
                   252
E value
                   1.0e-139
Match length
                   381
% identity
                   94
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MGL6, complete sequence
Seq. No.
                   165169
                   LIB3177-086-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2497733
BLAST score
                   143
                   1.0e-35
E value
Match length
                   79
                   99
% identity
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
                   >gi 1177796 (M80567) non-specific lipid transfer protein
                   [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  165170
Seq. ID
                  LIB3177-086-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  g598068
BLAST score
                  207
E value
                  1.0e-113
Match length
                  222
% identity
NCBI Description
                  Arabidopsis thaliana cinnamyl alcohol dehydrogenase (CAD1)
                  mRNA, cds 3' end
Seq. No.
                  165171
Seq. ID
                  LIB3177-086-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  g1465367
BLAST score
                  64
E välue
                  1.0e-27
Match length
                  128
% identity
                  88
NCBI Description A.thaliana mRNA for RAP-1 protein
Seq. No.
                  165172
Seq. ID
                  LIB3177-086-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4455244
BLAST score
                  514
E value
                  2.0e-52
Match length
                  102
% identity
                  100
NCBI Description (AL035523) MtN3-like protein [Arabidopsis thaliana]
Seq. No.
                  165173
Seq. ID
                  LIB3177-086-P1-K1-E9
Method
                  BLASTX
```

q4506635

```
BLAST score
                   267
E value
                   8.0e-37
Match length
                   109
% identity
                   65
                   ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S
NCBI Description
                   RIBOSOMAL PROTEIN L32 >gi_71335_pir__R5HU32 ribosomal
                   protein L32 - human >gi 71336_pir__R5MS32 ribosomal protein
                   L32 - mouse >gi_71337_pir_ R5RT32_ribosomal protein L32 - rat >gi_36132_emb_CAA27048_ (X03342) rpL32 (aa 1-135) [Homo
                   sapiens] >gi 57117 emb CAA29777 (X06483) ribosomal protein
                   L32 [Rattus norvegicus] >gi_200781 (K02060) ribosomal
                   protein L32-3A [Mus musculus] >gi 226004 prf 1405339A
                   ribosomal protein L32 [Rattus norvegicus]
Seq. No.
                   165174
Seq. ID
                   LIB3177-086-P1-K1-F10
                   BLASTX
Method
                   g3298443
NCBI GI
                   280
BLAST score
E value
                   7.0e-25
Match length
                   70
% identity
                   73
                   (AB010880) chloroplast ribosomal protein L17 [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   165175
Seq. ID
                   LIB3177-086-P1-K1-F11
                   BLASTX
Method
                   g3650028
NCBI GI
BLAST score
                   582
E value
                   3.0e-60
Match length
                   134
                   89
% identity
                   (AC005396) putative 22 kDa peroxisomal membrane protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   165176
                   LIB3177-086-P1-K1-F12
Seq. ID
Method ----
                   BLASTX
NCBI GI
                   g1168728
BLAST score
                   711
E value
                   2.0e-75
Match length
                   132
                   98
% identity
NCBI Description
                   CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi 598071 (L37883)
                   cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
                   165177
Seq. No.
Seq. ID
                   LIB3177-086-P1-K1-F2
                   BLASTN
Method
NCBI GI
                   q3980374
BLAST score
                   46
                   4.0e-17
E value
Match length
                   146
% identity
                   83
                  Arabidopsis thaliana chromosome II BAC F16P2 genomic
NCBI Description
```

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                    165178
Seq. ID
                    LIB3177-086-P1-K1-F3
Method
                    BLASTX
NCBI GI
                    g3096931
BLAST score
                    557
                    2.0e-57
E value
Match length
                    113
% identity
                    96
NCBI Description
                    (AL023094) putative ribosomal protein S16 [Arabidopsis
                    thaliana]
Seq. No.
                    165179
Seq. ID
                    LIB3177-086-P1-K1-F4
Method
                    BLASTX
NCBI GI
                    g282865
BLAST score
                    400
E value
                    6.0e-39
Match length
                    123
% identity
                    70
                   chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
NCBI Description
                    protein [Arabidopsis thaliana] >gi_166644 (M85150)
                    chlorophyll a/b-binding protein [Arabidopsis thaliana]
                    >gi 4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                    a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                    165180
Seq. ID
                   LIB3177-086-P1-K1-F5
Method
                    BLASTN
NCBI GI
                    g3738275
BLAST score
                    228
E value
                    1.0e-125
Match length
                    421
% identity
                    97
                   Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165181
Seq. ID
                   LIB3177-086-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   g2160716
BLAST score
                   430
E value
                   0.0e + 00
Match length
                   442
% identity
                   99
NCBI Description Arabidopsis thaliana GUT15 mRNA, complete cds
Seq. No.
                   165182
Seq. ID
                   LIB3177-086-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g3287695
BLAST score
                   396
E value
                   2.0e-38
Match length
                   107
% identity
NCBI Description
                   (AC003979) Similar to hypothetical protein C34B7.2
```

Seq. No.

```
gb 1729503 from C. elegans cosmid qb Z83220. [Arabidopsis
                   thaliana]
Seq. No.
                  165183
Seq. ID
                  LIB3177-086-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g16428
BLAST score
                  124
E value
                  3.0e-63
Match length
                  245
                  98
% identity
NCBI Description A.thaliana posF21 gene
                  165184
Seq. No.
Seq. ID
                  LIB3177-086-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2632059
BLAST score
                  655
E value
                  7.0e-69
Match length
                  145
% identity
                  88
                  (AJ002596) patatin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  165185
Seq. ID
                  LIB3177-086-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score
                  303
                  7.0e-28
E value
Match length
                  63
% identity
                  95
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
                  165186
Seq. No.
Seq. ID
                  LIB3177-086-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q4585935
BLAST score
                  714
E value
                  9.0e-76
Match length
                  134
% identity
                  100
NCBI Description
                  (AC007211) putative chlorophyll A/B binding protein
                  [Arabidopsis thaliana] >gi 4741946 gb AAD28770.1 AF134123 1
                  (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  165187
                  LIB3177-086-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2738248
BLAST score
                  745
E value
                  2.0e-79
Match length
                  144
% identity
                  97
NCBI Description
                  (U97200) cobalamin-independent methionine synthase
                  [Arabidopsis thaliana]
```

```
Seq. ID
                    LIB3177-086-P1-K1-G3
Method
                    BLASTN
NCBI GI
                    g3348076
BLAST score
                    189
E value
                    1.0e-102
Match length
                    241
                    95
% identity
NCBI Description
                    Arabidopsis thaliana isochorismate synthase mRNA, complete
Seq. No.
                    165189
Seq. ID
                    LIB3177-086-P1-K1-G4
Method
                    BLASTX
NCBI GI
                    g1363488
BLAST score
                    315
E value
                    3.0e-29
Match length
                    66
% identity
                    95
                    IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_
NCBI Description
                    (AC006340) auxin-induced IAA8 protein [Arabidopsis
                    thaliana]
Seq. No.
                    165190
Seq. ID
                    LIB3177-086-P1-K1-G5
Method
                    BLASTX
NCBI GI
                    g119975
BLAST score
                    408
E value
                    5.0e-40
Match length
                    92
% identity
                    90
NCBI Description
                    FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin
                    [2Fe-2S] precursor - Arabidopsis thaliana
                    >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                    [Arabidopsis thaliana]
Seq. No.
                    165191
Seq. ID
                    LIB3177-086-P1-K1-G6
Method
                    BLASTX
NCBI GI
                    g1363489
BLAST score
                    375
E value
                    3.0e-36
Match length
                    102
                    75
% identity
                    thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                    thaliana >gi 984052_emb CAA61592 (X89413) thioglucoside
                    glucohydrolase [Arabidopsis thaliana]
Seq. No.
                    165192
Seq. ID
                    LIB3177-086-P1-K1-G7
Method
                    BLASTX
NCBI GI
                    g3892709
BLAST score
                    448
E value
                    1.0e-44
Match length
                    90
% identity
                    98
```

```
NCBI Description (AL033545) putative protein [Arabidopsis thaliana]
Seq. No.
                   165193
Seq. ID
                   LIB3177-086-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1076440
BLAST score
                   374
E value
                   6.0e-36
Match length
% identity
                  acyl-CoA binding protein - rape >gi_1076441_pir__S49102
NCBI Description
                  acyl-CoA binding protein - rape >gi_509265 emb CAA54390
                   (X77134) acyl-CoA binding protein [Brassica napus]
Seq. No.
                  165194
Seq. ID
                  LIB3177-086-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2281089
BLAST score
                  55
E value
                  9.0e-32
Match length
                  74
% identity
                  82
NCBI Description
                  (AC002333) Sm protein F isolog [Arabidopsis thaliana]
Seq. No.
                  165195
Seq. ID
                  LIB3177-086-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  q3212846
BLAST score
                  139
E value
                  4.0e-72
Match length
                  390
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165196
Seq. ID
                  LIB3177-086-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  g2264311
BLAST score
                  91
E value
                  6.0e-44
Match length
                  176
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLN1, complete sequence [Arabidopsis thaliana]
                                                                      -# j.
Seq. No.
                  165197
Seq. ID
                  LIB3177-086-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  165
E value
                  7.0e-58
Match length
                  112
% identity
                  90
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
```

thaliana] Seq. No. 165198 Seq. ID LIB3177-086-P1-K1-H4 Method BLASTN NCBI GI g3510247 BLAST score 174 E value 5.0e-93 Match length 427 100 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 165199 Seq. ID LIB3177-086-P1-K1-H5

Seq. ID LIB3177-086-P1-K1-H5
Method BLASTX
NCBI GI g2493052
BLAST score 373
E value 8.0e-36
Match length 70
% identity 100

NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL

>gi_1655486_dbj_BAA13602_ (D88377) epsilon subunit of

mitochondrial F1-ATPase [Arabidopsis thaliana]

 Seq. No.
 165200

 Seq. ID
 LIB3177-086-P1-K1-H8

 Method
 BLASTX

 NCBI GI
 g3201618

 BLAST score
 464

 F value
 2.0e-46

BLAST score 464
E value 2.0e-46
Match length 87
% identity 99

NCBI Description (AC004669) Sop2p-like protein [Arabidopsis thaliana]

Seq. No. 165201

Seq. ID LIB3177-086-P1-K1-H9

Method BLASTX
NCBI GI 94455248
BLAST score 408
E value 7.0e-40
Match length 87
% identity 100

NCBI Description (AL035523) acyl carrier-like protein [Arabidopsis thaliana]

Seq. No. 165202

Seq. ID LIB3177-087-P1-K1-A1

Method BLASTX
NCBI GI g2760327
BLAST score 339
E value 2.0e-32
Match length 65
% identity 71

NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No. 165203

Seq. ID LIB3177-087-P1-K1-A10

Seq. No.

```
Method
                   BLASTN
NCBI GI
                   g4733953
BLAST score
                   270
E value
                   1.0e-150
Match length
                   274
                   100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
                   sequence, complete sequence
Seq. No.
                  165204
Seq. ID
                  LIB3177-087-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q99736
BLAST score
                   424
E value
                  5.0e-42
Match length
                  88
                  99
% identity
NCBI Description
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
                  Arabidopsis thaliana >gi_16187_emb_CAA46814_ (X66016)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
Seq. No.
                  165205
Seq. ID
                  LIB3177-087-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  576
                  1.0e-59
E value
                  107
Match length
                  96
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                  165206
Seq. No.
Seq. ID
                  LIB3177-087-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  g2760168
BLAST score
                  135
                  3.0e-70
E value
Match length
                  151
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MEE6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165207
Seq. ID
                  LIB3177-087-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2495365
BLAST score
                  461
E value
                  2.0e-46
Match length
                  105
                  87
% identity
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B
NCBI Description
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
```

```
Seq. ID
                  LIB3177-087-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g4559369
BLAST score
                  509
                , 1.0e-54
E value
Match length
                  114
% identity
                  94
NCBI Description
                  (AC006585) putative Rieske iron-sulfur protein [Arabidopsis
                  thaliana]
                  165209
Seq. No.
Seq. ID
                  LIB3177-087-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2464899
BLAST score
                  551
E value
                  1.0e-56
Match length
                  136
% identity
                  81
                  (Z99708) geranylgeranyl pyrophosphate synthase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165210
Seq. ID
                  LIB3177-087-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3273196
BLAST score
                  263
                  3.0e-23
E value
Match length
                  60
                  92
% identity
NCBI Description
                  (AB010915) responce regulator1 [Arabidopsis thaliana]
                  >gi 3323583 (AF057282) two-component response regulator
                  homolog [Arabidopsis thaliana] >gi_3953597_dbj_BAA34726_
                  (AB008487) response regulator 4 [Arabidopsis thaliana]
Seq. No.
                  165211
Seq. ID
                  LIB3177-087-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q466160
BLAST score
                  370
                  2.0e-35
E value
                  83
Match length
% identity
                  84
                  HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                  >gi 630771 pir S44903 ZK652.3 protein - Caenorhabditis
                  elegans >gi 289769 (L14429) putative [Caenorhabditis
                  elegans]
Seq. No.
                  165212
Seq. ID
                  LIB3177-087-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q464985
BLAST score
                  163
E value
                  8.0e-12
Match length
                  38
% identity
                  82
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN
NCBI Description
```

LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)

E value

9.0e-41

```
enzyme homolog [Arabidopsis thaliana]
Seq. No.
                     165213
Seq. ID
                    LIB3177-087-P1-K1-B10
                     BLASTX
Method
NCBI GI
                     g4337175
BLAST score
                     647
E value
                     6.0e-68
Match length
                     132
% identity
                     96
NCBI Description
                     (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
                     gb_T04111, gb_R841\overline{8}0, gb R654\overline{2}8, gb T444\overline{3}9, gb T76570,
                    gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
                    165214
Seq. No.
                    LIB3177-087-P1-K1-B12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g132110
BLAST score
                    631
                    4.0e-66
E value
Match length
                    118
                    98
% identity
NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                    (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                     (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana]
Seq. No.
                    165215
Seq. ID
                    LIB3177-087-P1-K1-B2
Method
                    BLASTX
NCBI GI
                    q1651828
BLAST score
                    443
E value
                    5.0e-44
Match length
                    136
% identity
                    67
NCBI Description
                    (D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]
Seq. No.
                    165216
Seq. ID
                    LIB3177-087-P1-K1-B3
Method
                    BLASTX
NCBI GI
                    a2677614
BLAST score
                    521
E value
                    3.0e-53
Match length
                    102
                    100
% identity
NCBI Description
                    (Y07625) NLM1 protein (NodLikeMip1) [Arabidopsis thaliana]
                    165217
Seq. No.
Seq. ID
                    LIB3177-087-P1-K1-B4
Method
                    BLASTX
NCBI GI
                    q2506443
BLAST score
                    412
```

>gi 398699 emb CAA78713 (Z14989) ubiquitin conjugating

```
Match length
                    81
% identity
                    100
NCBI Description
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                    CHLOROPLAST >gi_2117520_pir__JQ1285
                    glyceraldehyde-\overline{3}-phosphate \overline{de}hydrogenase (NADP+)
                    (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                    3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130)
                    glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                     (phosphorylating) [Arabidopsis thaliana]
Seq. No.
                    165218
Seq. ID
                    LIB3177-087-P1-K1-B6
Method
                    BLASTX
NCBI GI
                    g1709203
BLAST score
                    121
E value
                    3.0e-19
Match length
                    73
% identity
                    70
NCBI Description
                    MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (IMP 1) (INOSITOL
                    MONOPHOSPHATASE 1) >gi 1098977 (U39444) myo-inositol
                    monophosphatase 1 [Lycopersicon esculentum]
Seq. No.
                    165219
Seq. ID
                    LIB3177-087-P1-K1-B7
Method
                    BLASTX
NCBI GI
                    g4585882
BLAST score
                    517
                    9.0e-53
E value
Match length
                    104
% identity
                    (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    165220
Seq. ID
                    LIB3177-087-P1-K1-B8
Method
                    BLASTN
NCBI GI
                    g2477521
BLAST score
                    43
E value
                    8.0e-15
Match length
                    417
% identity
                    14
                    Arabidopsis thaliana chromosome I BAC F22K2O genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    165221
Seq. ID
                    LIB3177-087-P1-K1-C1
Method
                    BLASTX
NCBI GI
                    g3914740
BLAST score
                    555
E value
                    4.0e-57
Match length
                    138
% identity
NCBI Description
                    60S RIBOSOMAL PROTEIN L26 >gi 2160300 dbj_BAA18941
```

(D78495) ribosomal protein [Brassica rapa]

```
Seq. No.
                  165222
Seq. ID
                  LIB3177-087-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1914685
BLAST score
                  300
E value
                  2.0e-27
Match length
                  76
% identity
                  78
NCBI Description (Y12014) RAD23 protein, isoform II [Daucus carota]
Seq. No.
                  165223
Seq. ID
                  LIB3177-087-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3269293
BLAST score
                  269
E value
                  1.0e-23
Match length
                  101
% identity
                  56
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  165224
Seq. ID
                  LIB3177-087-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  q1769904
BLAST score
                  31
                  1.0e-08
E value
Match length
                  51
% identity
                  90
NCBI Description A.thaliana psbP gene
Seq. No.
                  165225
Seq. ID
                  LIB3177-087-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q121075
BLAST score
                  459
E value
                  7.0e-46
Match length
                  140
% identity
                  69
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725
NCBI Description
                  (M82921) H-Protein precursor [Arabidopsis thaliana]
                  >gi_861215 (U27144) glycine decarboxylase complex H-protein
                  precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                  glycine decarboxylase complex H-protein [Arabidopsis
                  thaliana] >gi 445119 prf 1908425A Gly
                  decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
Seq. No.
                  165226
Seq. ID
                  LIB3177-087-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2160694
BLAST score
                  509
E value
                  5.0e-52
Match length
                  101:
% identity
                  100
                  (U73528) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
```

thaliana]

```
Seq. No.
                   165227
 Seq. ID
                   LIB3177-087-P1-K1-C4
 Method
                   BLASTN
 NCBI GI
                   g555977
 BLAST score
                   239
 E value
                   1.0e-132
 Match length
                   251
 % identity
                   99
 NCBI Description
                   Arabidopsis thaliana metallothionein-like protein (AtMT-q)
                   mRNA, complete cds
 Seq. No.
                   165228
 Seq. ID
                   LIB3177-087-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   q1809305
BLAST score
                   348
E value
                   8.0e-34
Match length
                   86
                  • 95
% identity
NCBI Description
                   (U72241) histone H1-3 [Arabidopsis thaliana] >gi_1809315
                   (U73781) histone H1-3 [Arabidopsis thaliana]
                   >gi_4406813_gb_AAD20121_ (AC006201) Histone H1 [Arabidopsis
                   thalianal
Seq. No.
                   165229
Seq. ID
                   LIB3177-087-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g3023848
BLAST score
                   332
E value
                   4.0e-31
Match length
                   64
% identity
                   100
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                   >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis
                   thaliana]
Seq. No.
                   165230
Seq. ID
                   LIB3177-087-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q1769907
BLAST score
                   580
E value
                   5.0e-60
Match length
                   125
% identity
                  88
NCBI Description
                  (X92975) xyloglucan endo-transglycosylase [Arabidopsis
                  thaliana]
Seq. No.
                  165231
Seq. ID
                  LIB3177-087-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2129672
BLAST score
                  318
E value
                  2.0e-29
Match length
                  104
% identity
                  62
NCBI Description
                  photosystem II reaction center protein, 6.1K - Arabidopsis
```

thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No. 165232 Seq. ID LIB3177-087-P1-K1-D1 Method BLASTX NCBI GI g629562 BLAST score 454 E value 2.0e-45 Match length 107 87 % identity NCBI Description sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis thaliana >gi_2129743_pir__S68024 sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) -Arabidopsis thaliana >gi_487404 emb_CAA55799 (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana] >gi 1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana]

 Seq. No.
 165233

 Seq. ID
 LIB3177-087-P1-K1-D10

 Method
 BLASTX

 NCBI GI
 g2119848

 BLAST score
 587

 E value
 6.0e-61

E value 6.0eMatch length 109
% identity 100
NCRI Description ables

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459)
photosystem II type I chlorophyll a /b binding protein
[Arabidopsis thaliana] >gi_3128229 (AC004077) putative
photosystem II type I chlorophyll a/b binding protein
[Arabidopsis thaliana] >gi_3337372 (AC004481) putative
photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 165234

Seq. ID LIB3177-087-P1-K1-D11

Method BLASTN
NCBI GI g4490324
BLAST score 209
E value 1.0e-114
Match length 260
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 165235

Seq. ID LIB3177-087-P1-K1-D12

Method BLASTX
NCBI GI g1175010
BLAST score 89
E value 1.0e-36
Match length 98

BLAST score

```
% identity
                  84
NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi 629540 pir S44082
                  plasma membrane intrinsic protein 1a - Arabidopsis Thaliana
                  >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic
                  protein la [Arabidopsis thaliana]
  .: .
Seq. No.
                  165236
Seq. ID
                  LIB3177-087-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g121907
BLAST score
                  346
E value
                  1.0e-32
                  129
Match length
% identity
                  59
                  HISTONE H1.2 >gi 70682 pir HSMU12 histone H1.2 -
NCBI Description
                  Arabidopsis thaliana >gi 16320 emb CAA44316 (X62459)
                  Histone H1-2 [Arabidopsis thaliana] >gi_1946357 (U93215)
                  histone H1-2C [Arabidopsis thaliana]
Seq. No.
                  165237
Seq. ID
                  LIB3177-087-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4240122
BLAST score
                  409
E value
                  4.0e-40
Match length
                  86
                  97
% identity
                  (AB007802) cytochrome b5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  165238
Seq. ID
                  LIB3177-087-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g1769904
BLAST score
                  191
                  1.0e-103
E value
Match length
                  199
                  99
% identity
NCBI Description A.thaliana psbP gene
                  165239
Seq. No.
Seq. ID
                  LIB3177-087-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1363492
BLAST score
                  575
                  2.0e-59
E value
                  147
Match length
                  73
% identity
NCBI Description
                  outer envelope membrane protein OEP75 precursor - garden
                  pea >gi_576507 (L36858) outer membrane protein [Pisum
                  sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic
                  outer envelope membrane protein (OEP75) [Pisum sativum]
Seq. No...
                  165240
                  LIB3177-087-P1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3212846
```

```
E value
                    0.0e + 00
Match length
                    460
                    100
 % identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F6E13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165241
                   LIB3177-087-P1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2119846
BLAST score
                    680
E value
                    9.0e-72
                   133
Match length
                   97
% identity
NCBI Description
                   chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364 emb CAA45790 (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi 3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   165242
Seq. ID
                   LIB3177-087-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g1742963
BLAST score
                   538
E value
                   4.0e-55
Match length
                   104
% identity
                   100
NCBI Description
                   (Y09944) gamma-glutamylcysteine synthetase [Arabidopsis
                   thaliana]
Seq. No.
                   165243
Seq. ID
                   LIB3177-087-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1703108
BLAST score
                   670
E value
                   1:0e-70
Match length
                   129
% identity
                   100
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
NCBI Description
                   thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
Seq. No.
                   165244
                   LIB3177-087-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g481812
BLAST score
                   269
E value
                   8.0e-24
Match length
                   51
% identity
                   53
NCBI Description
                  DNA-binding protein GT-2 - Arabidopsis thaliana
```

>gi_416490_emb_CAA51289 (X72780) GT-2 factor [Arabidopsis

Seq. No. 165245

Seq. ID LIB3177-087-P1-K1-E2

Method BLASTX
NCBI GI g115767
BLAST score 622
E value 5.0e-65
Match length 118
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 165246

Seq. ID LIB3177-087-P1-K1-E3

Method BLASTN
NCBI GI 94220645
BLAST score 250
E value 1.0e-138
Match length 250
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:

MYA6, complete sequence [Arabidopsis thaliana]

Seq. No. 165247

Seq. ID LIB3177-087-P1-K1-E4

Method BLASTX
NCBI GI g132110
BLAST score 457
E value 9.0e-46
Match length 93
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 165248

Seq. ID LIB3177-087-P1-K1-E6

Method BLASTN
NCBI GI 94454587
BLAST score 128
E value 4.0e-66
Match length 140
% identity 98

NCBI Description Arabidopsis thaliana BAC F21A20 from chromosome V near 61

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 165249

Seq. ID LIB3177-087-P1-K1-E7

NCBI GI

```
Method
                   BLASTN
NCBI GI
                   q4558586
BLAST score
                   267
E value
                   1.0e-148
Match length
                   279
                                                       10 pt 1 "
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T518 sequence,
                  complete sequence
                  165250
Seq. No.
Seq. ID
                  LIB3177-087-P1-K1-E8
                  BLASTN
Method
NCBI GI
                  g1769904
BLAST score
                   36
                  1.0e-11
E value
Match length
                   40
                  97
% identity
NCBI Description A.thaliana psbP gene
Seq. No.
                  165251
                  LIB3177-087-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2959736
BLAST score
                   455
E value
                  2.0e-45
Match length
                  143
                   62
% identity
                   (Y13651) homologous to GATA-binding transcription factors
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  165252
                  LIB3177-087-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169278
BLAST score
                  305
                  9.0e-28
E value
Match length
                  83
% identity
                  DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  165253
Seq. ID
                  LIB3177-087-P1-K1-F11
Method
                  BLASTX
                  g2129637
NCBI GI
BLAST score
                  98
E value
                  5.0e-04
Match length
                  72
                  19
% identity
                  low temperature-induced protein cor47 - Arabidopsis
NCBI Description
                  thaliana >gi 975646 emb CAA62449 (X90959) dehydrin
                  [Arabidopsis thaliana]
                  165254
Seq. No.
Seq. ID
                  LIB3177-087-P1-K1-F12
                  BLASTX
Method
```

g2118220

E value

8.0e-75

```
BLAST score
                    403
 E value
                    3.0e-39
Match length
                  115
 % identity
                    51
NCBI Description
                    H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                    (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581)
                    vacuolar H+-pumping ATPase 16 kDa proteolipid (Arabidopsis
                    thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16
                    kDa proteolipid [Arabidopsis thaliana]
                    >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar
                    H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                    >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
                    ATPase 16K Chain P2, vacuolar [Arabidopsis thaliana] >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar
                    H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.
                    165255
Seq. ID
                    LIB3177-087-P1-K1-F2
Method
                    BLASTX
NCBI GI
                    g464621
BLAST score
                    666
E value
                    4.0e-70
Match length
                    157
% identity
                    82
                    60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__$28586
NCBI Description
                    ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
Seq. No.
                    165256
                    LIB3177-087-P1-K1-F3
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1145697
BLAST score
                    557
E value
                    2.0e-57
Match length
                    115
% identity
                    97
NCBI Description
                   (U39485) delta tonoplast integral protein [Arabidopsis
                    thaliana]
Seq. No.
                    165257
Seq. ID
                   LIB3177-087-P1-K1-F4
Method
                   BLASTN
NCBI GI
                   q2656024
BLAST score
                   61
E value
                   1.0e-25
Match length
                   243
% identity
                   87
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K15E6
Seq. No.
                   165258
Seq. ID
                   LIB3177-087-P1-K1-F5
Method
                   BLASTN
NCBI GI
                   q3805839
BLAST score
                   143
```

NCBI GI

```
Match length
                   232
% identity
                   97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14
                   (ESSAII project)
Seq. No.
                  165259
Seq. ID
                  LIB3177-087-P1-K1-F6
Method
                  BLASTN
NCBI GI
                   g3399678
BLAST score
                   208
E value
                   1.0e-113
Match length
                   432
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  165260
                  LIB3177-087-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  534
E value
                  9.0e-55
Match length
                  105
% identity
                  97
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  165261
                  LIB3177-087-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q399900
BLAST score
                  471
E value
                  2.0e-47
Match length
                  106
% identity
                  87
NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5)
                  (HD-ZIP PROTEIN ATHB-1) >gi 99659 pir S16325 homeotic
                  protein Athb-1 - Arabidopsis thaliana
                  >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein
                  [Arabidopsis thaliana]
Seq. No.
                  165262
Seq. ID
                  LIB3177-087-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2244759
BLAST score
                  504
E value
                  3.0e-51
Match length
                  112
% identity
                  85
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.
                  165263
                  LIB3177-087-P1-K1-G11
Seq. ID
Method
                  BLASTX
```

g2062164

Match length

```
BLAST score
                   535
E value
                  *5.0e-55
Match length
                   101
% identity
NCBI Description
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   165264
Seq. ID
                   LIB3177-087-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q421826
BLAST score
                   535
E value
                   7.0e-55
Match length
                   114
% identity
                   89
NCBI Description
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                   >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
Seq. No.
                   165265
Seq. ID
                   LIB3177-087-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g3341479
BLAST score
                   157
E value
                   2.0e-10
Match length
                   88
% identity
                   36
NCBI Description
                  (AJ000513) hypothetical protein [Pseudanabaena sp.]
Seq. No.
                   165266
Seq. ID
                   LIB3177-087-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q4678923
BLAST score
                   173
E value
                   2.0e-12
Match length
                  53
% identity
                   62
NCBI Description
                  (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
                  165267
                  LIB3177-087-P1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4757414
BLAST score
                  77
E value
                  2.0e-35
Match length
                  179
% identity
                  89
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYF24, complete sequence
Seq. No.
                  165268
Seq. ID
                  LIB3177-087-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  g4757407
BLAST score
                  265
E value
                  1.0e-147
```

```
100
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MQD19, complete sequence
Seq. No.
                    165269
Seq. ID
                   LIB3177-087-P1-K1-G6
Method
                   BLASTX
NCBI GI
                    g3386615
BLAST score
                    514
E value
                    4.0e-60
Match length
                    123
% identity
                    100
NCBI Description
                    (AC004665) putative phosphomannomutase [Arabidopsis
                   thaliana]
Seq. No.
                   165270
Seq. ID
                   LIB3177-087-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   570
E value
                   6.0e-59
Match length
                   107
                   99
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   165271
Seq. ID
                   LIB3177-087-P1-K1-G9
Method
                   BLASTN
NCBI GI
                   q4587641
BLAST score
                   212
E value
                   1.0e-116
Match length
                   266
% identity
                   100
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F20D21 genomic
                   sequence, complete sequence
Seq. No.
                   165272
Seq. ID
                   LIB3177-087-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g1435022
BLAST score
                   226
E value
                   2.0e-18
                   98
Match length
% identity
                   46
NCBI Description
                   (D26576) DNA-binding protein [Daucus carota]
Seq. No.
                   165273
Seq. ID
                   LIB3177-087-P1-K1-H10
Method
                  BLASTN
NCBI GI
                   g3335356
BLAST score
                   365
E value
                   0.0e + 00
```

```
Match length
                   386
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F16M14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165274
Seq. ID
                   LIB3177-087-P1-K1-H11
Method
                   BLASTN
NCBI GI
                   g3128138
BLAST score
                   408
                   0.0e + 00
E value
                   453
Match length
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFO20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165275
                  LIB3177-087-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4558661
BLAST score
                   622
                   4.0e-65
E value
Match length
                   121
                   99
% identity
NCBI Description
                   (AC007063) putative malate oxidoreductase (NAD)
                   [Arabidopsis thaliana]
Seq. No.
                  165276
Seq. ID
                  LIB3177-087-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4200249
BLAST score
                  232
E value
                  3.0e-19
Match length
                  115
% identity
                  42
NCBI Description
                  (AL035297) hypothetical protein [Homo sapiens]
Seq. No.
                  165277
Seq. ID
                  LIB3177-087-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q4589965
BLAST score
                  110
E value
                  6.0e-44
Match length
                  97
                  95
% identity
NCBI Description
                  (AC007169) putative glyoxalase II [Arabidopsis thaliana]
                  165278
Seq. No.
Seq. ID
                  LIB3177-087-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g4159709
BLAST score
                  254
E value
                  1.0e-141
Match length
                  275
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLN21, complete sequence
```

```
Seq. No.
                   165279
Seq. ID
                   LIB3177-087-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g113026
BLAST score
                   676
E value
                   2.0e-71
Match length
                   131
% identity
                   93
NCBI Description
                   ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                   >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
                   S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
                   napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
                   isocitrate lyase [Brassica napus] >gi 447142 prf 1913424A
                   isocitrate lyase [Brassica napus]
                   165280
Seq. No.
Seq. ID
                   LIB3177-087-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g4006934
                   473
BLAST score
E value
                   1.0e-47
Match length
                   112
                   79 .
% identity
NCBI Description
                  (AJ012571) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                   165281
Seq. ID
                   LIB3177-087-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g4538963
BLAST score
                   546
                   4.0e-56
E value
Match length
                   136
                   79
% identity
NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                   165282
Seq. ID
                   LIB3177-087-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g4582468
BLAST score
                   389
E value
                   5.0e-38
Match length
                   86
% identity
                   92
                  (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
Seq. No.
                   165283
Seq. ID
                  LIB3177-087-P1-K1-H9
Method
                   BLASTX
                  g2129672
NCBI GI
BLAST score
                  275
E value
                   2.0e-24
```

98

Match length

```
% identity
                    59
NCBI Description photosystem II reaction center protein, 6.1K - Arabidopsis
                   thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center
                    [Arabidopsis thaliana]
Seq. No.
                   165284
Seq. ID
                   LIB3177-088-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q1769905
BLAST score
                   523
E value
                   2.0e-53
Match length
                   141
% identity
                   72
NCBI Description
                    (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                    [Arabidopsis thaliana]
                   165285
Seq. No.
Seq. ID
                   LIB3177-088-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q4454049
BLAST score
                   336
E value
                   2.0e-31
                   122
Match length
% identity
                   61
NCBI Description
                   (AL035394) 98b like protein [Arabidopsis thaliana]
Seq. No.
                   165286
Seq. ID
                   LIB3177-088-P1-K1-A11
Method
                   {\tt BLASTX}
NCBI GI
                   g3868857
BLAST score
                   448
                   1.0e-44
E value
                   86
Match length
                   99
% identity
NCBI Description (AB013886) RAV1 [Arabidopsis thaliana]
Seq. No.
                   165287
                   LIB3177-088-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g421826
BLAST score
                   281
E value
                   2.0e-25
Match length
                   75
% identity
                   71
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                   >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
                   165288
Seq. No.
Seq. ID
                   LIB3177-088-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1755156
BLAST score
                   513
E value
                   3.0e-52
Match length
                   113
                   88
% identity
```

```
(U75189) germin-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi 1755158 (U75190) germin-like protein [Arabidopsis
                   thaliana] >gi 1755170 (U75196) germin-like protein
                   [Arabidopsis thaliana] >gi_1755172 (U75197) germin-like protein [Arabidopsis thaliana] >gi_1755180 (U75201)
                   germin-like protein [Arabidopsis thaliana] >gi 1755190
                   (U75206) germin-like protein [Arabidopsis thaliana]
                   >gi 1934728 (U95035) germin-like protein [Arabidopsis
                   thaliana] >gi 4154285 (AF090733) germin-like protein 1
                   [Arabidopsis thaliana] >gi 4666248 dbj BAA77207.1 (D89055)
                   germin-like protein precursor [Arabidopsis thaliana]
                   165289
Seq. No.
Seq. ID
                   LIB3177-088-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   g2244894
BLAST score
                   461
E value
                   3.0e-46
Match length
                   110
% identity
                   79
NCBI Description
                   (Z97338) similarity to cycloartenol synthase [Arabidopsis
                   thaliana]
Seq. No.
                   165290
Seq. ID
                   LIB3177-088-P1-K1-A5
Method
                   BLASTN
NCBI GI
                   g4388714
BLAST score
                   192
                   1.0e-104
E value
Match length
                   377
                   76
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F5K7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   165291
Seq. No.
Seq. ID
                   LIB3177-088-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g541858
BLAST score
                   662
                   1.0e-69
E value
Match length
                   130
% identity
NCBI Description
                   endoxyloglucan transferase - Arabidopsis thaliana
                   >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
                   transferase [Arabidopsis thaliana] >gi 4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
                   165292
Seq. No.
                  LIB3177-088-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4049348
BLAST score
                   266
E value
                   3.0e-23
Match length
                   60
% identity
                   82
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
```

```
Seq. No.
                  165293
Seq. ID
                  LIB3177-088-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  q2262135
BLAST score
                  340
                  0.0e + 00
E value
Match length
                  432
% identity
                  100
                  Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
NCBI Description
                  cM, complete sequence
                  165294
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  g3080352
BLAST score
                  87
E value
                  3.0e-41
Match length
                  101
% identity
                  97
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18
                  (ESSAII project)
                  165295
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g4586256
BLAST score
                  491
E value
                  1.0e-49
Match length
                  95
% identity
                  100
                  (AL049640) probable photosystem I chain XI precursor
NCBI Description
                  [Arabidopsis thaliana]
                  165296
Seq. No.
Seg. ID
                  LIB3177-088-P1-K1-B11
Method
                  BLASTX
                  q2119846
NCBI GI
BLAST score
                  618
                  1.0e-64
E value
Match length
                  127
                  94
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >qi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  165297
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  596
E value
                  5.0e-62
Match length
                  113
% identity
                  100
```

% identity

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   165298
Seq. No.
Seq. ID
                   LIB3177-088-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g4538963
BLAST score
                   642
E value
                   2.0e-67
                   118
Match length
                   77
% identity
NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                   165299
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-B4
Method
                  BLASTX
NCBI GI
                   q4262229
BLAST score
                   403
E value
                  1.0e-51
Match length
                  115
                   95
% identity
NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]
Seq. No.
                  165300
Seq. ID
                  LIB3177-088-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  g2584827
BLAST score
                  253
E value
                  1.0e-140
                  273
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  165301
Seq. ID
                  LIB3177-088-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g4512690
BLAST score
                  304
E value
                  1.0e-170
                  336
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F11A3 genomic
NCBI Description
                  sequence, complete sequence
                  165302
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-B7
                  BLASTX
Method
NCBI GI
                  g2149640
BLAST score
                  675
                  3.0e-71
E value
                  137
Match length
```

```
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                  165303
Seq. ID
                  LIB3177-088-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g1169476
                   654
BLAST score
E value
                   9.0e-69
                   125
Match length
                   100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
                  165304
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-C10
                  BLASTX
Method
                  g135449
NCBI GI
                  185
BLAST score
E value
                   4.0e-14
Match length
                  50
                  72
% identity
                  TUBULIN BETA-1 CHAIN >gi 100932 pir S14701 tubulin beta-1
NCBI Description
                  chain - maize >gi 295851 emb CAA37060 (X52878) beta 1
                  tubulin [Zea mays]
                  165305
Seq. No.
                  LIB3177-088-P1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129634
BLAST score
                  311
                  1.0e-28
E value
Match length
                  121
                  54
% identity
                  lectin-like protein - Arabidopsis thaliana
NCBI Description
                  >gi_995619_emb_CAA62665_ (X91259) lectin like protein
                   [Arabidopsis thaliana]
                  165306
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g4757409
BLAST score
                  32
E value
                  2.0e-08
                  384
Match length
                  71
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MVC8, complete sequence
Seq. No.
                  165307
Seq. ID
                  LIB3177-088-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3548803
BLAST score
                  285
                  2.0e-25
E value
Match length
                  129
% identity
                  44
```

```
NCBI Description (AC005313) putative DNA-binding protein [Arabidopsis
                  thaliana] >gi 4335770 qb AAD17447 (AC006284) putative
                  SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]
                  165308
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g166765
BLAST score
                  561
E value
                  6.0e-58
Match length
                  107
                  100
% identity
NCBI Description (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]
Seq. No.
                  165309
Seq. ID
                  LIB3177-088-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2062160
BLAST score
                  422
E value
                  1.0e-41
Match length
                  104
% identity
                  37
                 (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana].
Seq. No.
                  165310
Seq. ID
                  LIB3177-088-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g4455242
BLAST score
                  347
E value
                  7.0e-33
Match length
                  69
                  97
% identity
                 (AL035523) geranylgeranylated protein ATGP4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165311
                  LIB3177-088-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454036
BLAST score
                  543
E value
                  7.0e-56
Match length
                  100
% identity
                  100
                 (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
                  165312
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g136636
BLAST score
                  432
E value
                  1.0e-42
Match length
                  80
                  99
% identity
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                  LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
```

>gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

```
Seq. No.
                  165313
Seq. ID
                  LIB3177-088-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q1168748
BLAST score
                  652
E value
                  2.0e-68 -
Match length
                  128
% identity
                  63
NCBI Description
```

ICBI Description CALMODULIN-4 > gi_479693_pir__ S35185 calmodulin 4 Arabidopsis thaliana > gi_16223_emb_CAA78057_ (Z12022)
calmodulin [Arabidopsis thaliana]

 Seq. No.
 165314

 Seq. ID
 LIB3177-088-P1-K1-D1

 Method
 BLASTX

 NCBI GI
 g541799

 BLAST score
 54

 E value
 2.0e-09

Match length 35 % identity 100

NCBI Description light-harvesting chlorophyll a/b-binding protein - ginkgo

>gi_349443 (L23107) light-harvesting chlorophyll a/b
binding protein of photosystem II [Ginkgo biloba]

Seq. No. 165315

Seq. ID LIB3177-088-P1-K1-D10

Method BLASTN
NCBI GI g3738275
BLAST score 333
E value 0.0e+00
Match length 333
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165316

Seq. ID LIB3177-088-P1-K1-D11

Method BLASTN
NCBI GI g4662640
BLAST score 344
E value 0.0e+00
Match length 344
% identity 30

NCBI Description Arabidopsis thaliana chromosome II BAC F15K19 genomic

sequence, complete sequence

Seq. No. 165317

Seq. ID LIB3177-088-P1-K1-D12

Method BLASTX

```
NCBI GI
                  q115783
BLAST score
                   567
E value
                  1.0e-58
Match length
                  106
% identity
                  100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  165318
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g3913733
BLAST score
                  498
E value
                  1.0e-50
Match length
                  95
% identity
                  99
NCBI Description
                  HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME
                  (GLYOXALASE II) (GLX II) >gi 1924921 emb CAA69644 (Y08357)
                  hydroxyacylglutathione hydrolase [Arabidopsis thaliana]
                  165319
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2980768
BLAST score
                  545
E value
                  6.0e-56
Match length
                  148
% identity
                  70
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
Seq. No.
                  165320
Seq. ID
                  LIB3177-088-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3882081
BLAST score
                  594
E value
                  8.0e-62
Match length
                  123
% identity
NCBI Description (AJ012552) polyubiquitin [Vicia faba]
Seq. No.
                  165321
Seq. ID
                  LIB3177-088-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q131398
BLAST score
                  451
E value
                  4.0e-45
Match length
                  107
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi_16447_emb_CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi 3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb X55970. ESTs gb_Z17693, gb_N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
```

```
Seq. No.
                    165322
Seq. ID
                    LIB3177-088-P1-K1-D6
  Method
                    BLASTN
  NCBI GI
                    q3892698
  BLAST score
                    71
  E value
                    1.0e-31
  Match length
                    297
                    95
  % identity
  NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2
                     (ESSAII project)
                    165323
  Seq. No.
  Seq. ID
                    LIB3177-088-P1-K1-D7
  Method
                    BLASTX
                    g1575699
  NCBI GI
  BLAST score
                    510
                    7.0e-52
  E value
                    102
  Match length
                     98
  % identity
  NCBI Description
                     (U70478) putative leucoanthocyanidin dioxygenase
                     [Arabidopsis thaliana] >gi 3292813 emb CAA19803 (AL031018)
                    putative leucoanthocyanidin dioxygenase (LDOX) [Arabidopsis
                    thaliana]
  Seq. No.
                    165324
  Seq. ID
                    LIB3177-088-P1-K1-D8
  Method
                    BLASTN
  NCBI GI
                    q4587641
  BLAST score
                    229
                    1.0e-126
  E value
  Match length
                    422
  % identity
                    99
  NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic
                    sequence, complete sequence
                    165325
  Seq. No.
  Seq. ID
                    LIB3177-088-P1-K1-D9
  Method
                    BLASTN
  NCBI GI
                    g12219
  BLAST score
                    69
                    2.0e-30
  E value
  Match length
                    182
  % identity
                    93
  NCBI Description Mustard chloroplast trnk gene for tRNA-Lys(UUU)
  Seq. No.
                    165326
                    LIB3177-088-P1-K1-E1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g461899
  BLAST score
                    614
  E value
                    5.0e-64
  Match length
                    127
  % identity
                    98
  NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR
```

come from this gene. [Arabidopsis

gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

Seq. ID Method

```
PROTEIN) >gi 1076368 pir B53422 peptidylprolyl isomerase
                  (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi 405131
                  (L14845) cyclophilin [Arabidopsis thaliana] >gi 1322278
                  (U42724) cyclophilin [Arabidopsis thaliana]
                  165327
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q2583134
BLAST score
                  364
E value
                  1.0e-34
                  75
Match length
                  92
% identity
                  (AC002387) putative proline-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                  165328
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q3047077
BLAST score
                  714
                  9.0e-76
E value
                  145
Match length
                  99
% identity
                  (AF058914) contains similarity to the conserved C-terminal
NCBI Description
                  domain of helicases (Pfam: helicase C.hmm, score: 90.11),
                  similar to DEAD-box helicases [Arabidopsis thaliana]
                  165329
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-E12
                  BLASTX
Method
NCBI GI
                  q2129772
BLAST score
                  502
                  7.0e-51
E value
Match length
                  113
                  82
% identity
                  xyloglucan endotransglycosylase-related protein XTR-7 -
NCBI Description
                  Arabidopsis thaliana >qi 1244760 (U43489) xyloglucan
                  endotransglycosylase-related protein [Arabidopsis thaliana]
                  165330
Seq. No.
                  LIB3177-088-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  q1709006
NCBI GI
BLAST score
                  340
                  2.0e-32
E value
Match length
                  76
                  86
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi 726032
                  (U17241) S-adenosylmethionine synthetase [Actinidia
                  chinensis]
                  165331
Seq. No.
```

(PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING

LIB3177-088-P1-K1-E4

BLASTX

```
NCBI GI
                   g4105696
BLAST score
                   559
E value
                   1.0e-57
Match length
                   102
% identity
                   99
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]
Seq. No.
                  165332
Seq. ID
                  LIB3177-088-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4589964
BLAST score
                  178
E value
                  8.0e-13
Match length
                  38
% identity
                  89
NCBI Description
                  (AC007169) delta 9 desaturase [Arabidopsis thaliana]
Seq. No.
                  165333
Seq. ID
                  LIB3177-088-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q461550
BLAST score
                  302
E value
                  1.0e-27
Match length
                  97
% identity
                  66
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
                  >gi 81635 pir B39732 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma-1 chain precursor, chloroplast -
                  Arabidopsis thaliana >gi 166632 (M61741) ATP synthase
                  gamma-subunit [Arabidopsis thaliana]
Seq. No.
                  165334
Seq. ID
                  LIB3177-088-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3660187
BLAST score
                  217
E value
                  2.0e-17
Match length
                  72
% identity
                  54
NCBI Description
                  Chain A, E2-C, An Ubiquitin Conjugating Enzyme Required For
                  The Destruction Of Mitotic Cyclins >gi_3660188 pdb 1E2C B
                  Chain B, E2-C, An Ubiquitin Conjugating Enzyme Required For
                  The Destruction Of Mitotic Cyclins >gi 3660189 pdb 1E2C C
                  Chain C, E2-C, An Ubiquitin Conjugating Enzyme Required For
                  The Destruction Of Mitotic Cyclins >gi 4388942_pdb_2E2C
                  E2-C, An Ubiquitin Conjugating Enzyme Required For The
                  Destruction Of Mitotic Cyclins
Seq. No.
                  165335
Seq. ID
                  LIB3177-088-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3914442
BLAST score
                  226
E value
                  4.0e-19
Match length
                  77
% identity
                  61
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
```

NCBI GI

```
>gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                    165336
Seq. ID
                    LIB3177-088-P1-K1-E9
Method
                    BLASTX
NCBI GI
                    g120667
BLAST score
                    596
E value
                    5.0e-62
                    123
Match length
                    98
% identity
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                    >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                    thaliana >gi 166706 (M64116) cystolic
                    glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                    thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                    dehydrogenase [Arabidopsis thaliana]
Seq. No.
                    165337
Seq. ID
                    LIB3177-088-P1-K1-F1
                    BLASTX
Method
NCBI GI
                    q1402908
BLAST score
                    537
E value
                    4.0e-55
Match length
                   119
                    88
% identity
NCBI Description
                   (X98315) peroxidase [Arabidopsis thaliana]
                   >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
[Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)
                    peroxidase [Arabidopsis thaliana]
Seq. No.
                    165338
Seq. ID
                    LIB3177-088-P1-K1-F11
Method
                    BLASTN
NCBI GI
                    q3292807
BLAST score
                    233
E value
                    1.0e-128
Match length
                    379
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
                    (ESSAII project)
Seq. No.
                    165339
Seq. ID
                    LIB3177-088-P1-K1-F12
Method
                    BLASTX
NCBI GI
                   q4678948
BLAST score
                    461
E value
                    2.0e-46
Match length
                    93
                    95
% identity
NCBI Description (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
                    165340
Seq. ID
                   LIB3177-088-P1-K1-F2
Method
                   BLASTX
```

(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

g1171577

Seq. No.

```
BLAST score
                   167
E value
                   1.0e-11
Match length
                   100
% identity
                   39
NCBI Description
                  (X95343) hypersensitivity-related gene [Nicotiana tabacum]
Seq. No.
                   165341
Seq. ID
                   LIB3177-088-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   626
E value
                   2.0e-65
                   137
Match length
                   84
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372 emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  165342
Seq. No.
Seq. ID
                  LIB3177-088-P1-K1-F5
Method :
                  BLASTX
NCBI GI
                  g3128217
BLAST score
                   691
                   4.0e-73
E value
Match length
                  141
% identity
NCBI Description
                   (AC004077) hypothetical protein [Arabidopsis thaliana]
                  >gi_3337374 (AC004481) hypothetical protein [Arabidopsis
                  thaliana]
Seq. No.
                  165343
Seq. ID
                  LIB3177-088-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  g3785992
BLAST score
                  172
E value
                  5.0e-92
Match length
                  322
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T6A23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165344
Seq. ID
                  LIB3177-088-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2832661
BLAST score
                  343
E value
                  2.0e-32
Match length
                  115
% identity
                  66
NCBI Description
                  (AL021710) pherophorin - like protein [Arabidopsis
                  thaliana]
```

Seq. No.

```
Seq. ID
                  LIB3177-088-P1-K1-G1
Method
                  BLASTX
NCBI GI
                   q4566505
BLAST score
                   437
E value
                   3.0e-43
Match length
                  131
                   63
% identity
NCBI Description
                  (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI
                   [Hordeum vulgare]
Seq. No.
                  165346
Seq. ID
                  LIB3177-088-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2494144
BLAST score
                  189
                  3.0e-14
E value
Match length
                  64
% identity
                  69
NCBI Description
                  (AC002329) predicted leucine-rich protein [Arabidopsis
                  thaliana]
                  165347
Seq. No.
                  LIB3177-088-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432860
BLAST score
                  107
E value
                  1.0e-04
Match length
                  122
                  12
% identity
NCBI Description
                  (AC006300) putative glucose-induced repressor protein
                  [Arabidopsis thaliana]
                  165348
Seq. No.
                  LIB3177-088-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g114339
BLAST score
                  521
                  3.0e-53
E value
                  125
Match length
% identity
                  83
                  PLASMA MEMBRANE ATPASE 3 (PROTON PUMP)
NCBI Description
                  >gi 67974 pir PXMUP3 H+-transporting ATPase (EC 3.6.1.35)
                  type 3, plasma membrane - Arabidopsis thaliana >gi 166625
                  (J04737) ATPase [Arabidopsis thaliana]
Seq. No.
                  165349
                  LIB3177-088-P1-K1-G3
Seq. ID
Method
                  BLASTX
                  g4102703
NCBI GI
BLAST score
                  662
E value
                  1.0e-69
Match length
                  134
                  99
% identity
                  (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No.

```
Seq. ID
                   LIB3177-088-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   g11244
BLAST score
                   377
E value
                   0.0e + 00
                   392
Match length
                   99
% identity
NCBI Description
                  A.thaliana chloroplast DNA for transfer RNA-Ile and
                   ribosomal protein
                   165351
Seq. No.
Seq. ID
                   LIB3177-088-P1-K1-G5
Method
                   BLASTN
NCBI GI
                   g3510343
BLAST score
                   157
                   7.0e-83
E value
Match length
                   462
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MJC20, complete sequence [Arabidopsis thaliana]
                   165352
Seq. No.
Seq. ID
                   LIB3177-088-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   g3201608 ·
BLAST score
                   307
E value
                   1.0e-172
Match length
                   385
                   99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F7F1 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165353
                  LIB3177-088-P1-K1-G7
Seq. ID
Method
                   BLASTX
                   g1145697
NCBI GI
BLAST score
                   591
E value
                   2.0e-61 ·
Match length
                   120
                   51
% identity
NCBI Description
                  (U39485) delta tonoplast integral protein [Arabidopsis
                   thaliana]
Seq. No.
                   165354
Seq. ID
                  LIB3177-088-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g1175011
BLAST score
                   566
                   2.0e-58
E value
Match length
                   106
                   100
% identity
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN
                  A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665)
                  plasma membrane intrinsic protein 1B [Arabidopsis thaliana]
```

```
Seq. ID
                  LIB3177-088-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g2062167
BLAST score
                   609
                  2.0e-63
E value
Match length
                  115
                  100
% identity
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165356
Seq. ID
                  LIB3177-088-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q121075
BLAST score
                  555
                  4.0e-57
E value
                  134
Match length
                  84
% identity
NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi 166725
                  (M82921) H-Protein precursor [Arabidopsis thaliana]
                  >gi_861215 (U27144) glycine decarboxylase complex H-protein
                  precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                 glycine decarboxylase complex H-protein [Arabidopsis
                  thaliana] >gi_445119_prf__1908425A Gly
                  decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
Seq. No..
                  165357
Seq. ID
                  LIB3177-088-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q2289011
BLAST score
                  581
                  3.0e-60
E value
Match length
                  131
% identity
NCBI Description
                  (AC002335) MYB transcription factor isolog [Arabidopsis
                  thaliana]
Seq. No.
                  165358
Seq. ID
                  LIB3177-088-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q4432856
BLAST score
                  686
E value
                  2.0e-72
Match length
                  135
% identity
                  99
NCBI Description (AC006300) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                  165359
Seq. ID
                  LIB3177-088-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2618723
BLAST score
                  463
E value
                  1.0e-46
Match length
                  96
                  92
% identity
NCBI Description
                  (U49073) IAA17 [Arabidopsis thaliana] >gi 2921756
                  (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]
```

```
gb H36782 and gb_F14074 come from this gene. [Arabidopsis
                   thaliana]
                                            . :
 Seq. No.
                   165360
 Seq. ID
                   LIB3177-088-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q4508075
BLAST score
                   168
E value
                   2.0e-12
Match length
                   47
 % identity
                   66
NCBI Description
                   (AC005882) 50259 [Arabidopsis thaliana]
Seq. No.
                   165361
                   LIB3177-088-P1-K1-H4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g166633
BLAST score
                   114
E value
                   3.0e-57
Match length
                   246
% identity
                   99
NCBI Description
                   Arabidopsis thaliana vacuolar H+ - pyrophosphatase (AVP-3)
                   mRNA, complete cds
Seq. No.
                   165362
Seq. ID
                   LIB3177-088-P1-K1-H5
Method
                   BLASTN
NCBI GI
                   q4589409
BLAST score
                   335
E value
                   0.0e + 00
Match length
                   375
% identity
                   97
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F17P19, complete sequence
Seq. No.
                   165363
Seq. ID
                   LIB3177-088-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g459009
BLAST score
                   166
                   6.0e-12
E value
Match length
                   46
% identity
                   65
NCBI Description
                   (U00037) similar to multifunctional aminoacyl-tRNA
                   synthetase, especially to the prolyl-tRNA synthetase region
                   [Caenorhabditis elegans]
Seq. No.
                   165364
Seq. ID
                  LIB3177-088-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q132110
BLAST score
                   429
E value
                  2.0e-42
Match length
                  84
% identity
                  98
```

>gi_4389514_gb_AAB70451_ (AC000104) Identical to Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs

Match length

```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   165365
                   LIB3177-089-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3786017
BLAST score
                   346
E value
                   3.0e-33
Match length
                   69
% identity
                   99
NCBI Description
                  (AC005499) putative non-green plastid inner envelope
                   membrane protein [Arabidopsis thaliana]
Seq. No.
                   165366
Seq. ID
                   LIB3177-089-P1-K1-A11
Method
                   BLASTN
NCBI GI
                   g4468103
BLAST score
                   110
E value
                   3.0e-55
Match length
                  197
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
                  (ESSA project)
Seq. No.
                  165367
Seq. ID
                  LIB3177-089-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4455284
BLAST score
                  367
E value
                  2.0e-35
Match length
                  82
% identity
                  84
NCBI Description
                  (AL035527) beta-glucosidase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  165368
Seq. ID
                  LIB3177-089-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  q207553
BLAST score
                  34
E value
                  1.0e-09
Match length
                  50
% identity
                  92
NCBI Description Rat transcription factor UBF2 mRNA
Seq. No.
                  165369
Seq. ID
                  LIB3177-089-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  492
E value
                  6.0e-50
```

NCBI Description

```
% identity
                   100
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540 (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP-AB 180) [Arabidopsis thaliana]
Seq. No.
                  165370
Seq. ID
                  LIB3177-089-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q1168258
BLAST score
                  478
E value
                  3.0e-48
Match length
                  114
% identity
                  85
NCBI Description
                  ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR
                   (TRANSAMINASE A) >gi_693692 (U15034) aspartate
                  aminotransferase [Arabidopsis thaliana]
Seq. No.
                  165371
Seq. ID
                  LIB3177-089-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q2119846
BLAST score
                  549
E value
                  1.0e-56
Match length
                  107
                  97
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165372
                  LIB3177-089-P1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                  102
E value
                  2.0e-50
Match length
                  170
                  97
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  165373
Seq. ID
                  LIB3177-089-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g4467094
BLAST score
                  151
                  1.0e-79
E value
Match length
                  232
% identity
                  100
```

Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10

(ESSA project)

```
Seq. No.
                   165374
 Seq.-ID
                   LIB3177-089-P1-K1-A8
 Method-
                   BLASTN
 NCBI GI
                   g4467094
 BLAST score
                   39
 E value
                   1.0e-12
 Match length
                   135
 % identity
                   82
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
                   (ESSA project)
 Seq. No.
                   165375
 Seq. ID
                   LIB3177-089-P1-K1-B1
 Method
                   BLASTN
 NCBI GI
                   g4741959
 BLAST score
                   122
 E value
                   3.0e-62
 Match length
                   168
 % identity
                   93
                   Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
 NCBI Description
Seq. No.
                   165376
 Seq. ID
                   LIB3177-089-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g1172873
BLAST score
                   313
E value
                   4.0e-34
Match length
                   114
 % identity
                   70
NCBI Description
                   CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
                   drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                   precursor - Arabidopsis thaliana >gi_435619 dbj BAA02374
                   (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                   165377
Seq. ID
                   LIB3177-089-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g3273743
BLAST score
                   597
E value
                   3.0e-62
Match length
                   116
% identity
                   98
NCBI Description
                   (AF057357) lipid transfer protein 2 precursor [Arabidopsis
                   thaliana] >gi 3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
Seq. No.
                   165378
Seq. ID
                   LIB3177-089-P1-K1-B12
Method
                   BLASTN
NCBI GI
                   g2358139
BLAST score
                   248
E value
                   1.0e-137
Match length
                   342
```

99

% identity

```
NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
                   sequence [Arabidopsis thaliana]
Seq. No.
                   165379
Seq. ID
                   LIB3177-089-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g1621463
BLAST score
                   49
E value
                   3.0e-51
                   134
Match length
                   75
% identity
NCBI Description
                  (U73104) laccase [Liriodendron tulipifera]
Seq. No.
                   165380
Seq. ID
                   LIB3177-089-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   g3985932
BLAST score
                   73
E value
                   8.0e-33
Match length
                   326
% identity
                   83
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K22J17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165381
Seq. ID
                  LIB3177-089-P1-K1-B4
Method ·
                  BLASTX
NCBI GI
                  g2252863
BLAST score
                  305
E value
                   5.0e-28
Match length
                  96
% identity
                  31
NCBI Description
                  (AF013294) similar to nucleolin protein [Arabidopsis
                  thaliana]
Seq. No.
                  165382
                  LIB3177-089-P1-K1-B5
Seq. ID
Method
                  BLASTX
                                NCBI GI
                  g2252863
BLAST score
                  285
E value
                  2.0e-25
Match length
                  99
                  53
% identity
NCBI Description
                  (AF013294) similar to nucleolin protein [Arabidopsis
                  thaliana]
Seq. No.
                  165383
Seq. ID
                  LIB3177-089-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2760833
BLAST score
                  427
E value
                  5.0e-50
Match length
                  105
% identity
NCBI Description
                  (AC003105) unknown protein [Arabidopsis thaliana]
Seq. No.
                  165384
```

```
Seq. ID
                    LIB3177-089-P1-K1-B9
 Method
                    BLASTX
 NCBI GI
                    g3286693
 BLAST score
                    645
 E value
                    9.0e-68
 Match length
                   130
 % identity
                    99
 NCBI Description
                    (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                    (OEC) in photosystem II [Arabidopsis thaliana]
 Seq. No.
                   165385
 Seq. ID
                   LIB3177-089-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   g3608126
BLAST score
                   308
E value
                   1.0e-173
Match length
                   370
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T32F12 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165386
Seq. ID
                   LIB3177-089-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g1710424
BLAST score
                   528
E value
                   5.0e-54
Match length
                   123
% identity
                   88
NCBI Description
                   50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
                   >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis
                   thaliana >gi 11\overline{49}573 emb CAA89887 (Z49787) chloroplast
                   ribosomal large subunit protein L21 [Arabidopsis thaliana]
Seq. No.
                   165387
Seq. ID
                   LIB3177-089-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3894197
BLAST score
                   685
E value
                   2.0e-72
Match length
                   136
% identity
NCBI Description
                   (AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   165388
Seq. ID
                  LIB3177-089-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   q4589428
BLAST score
                   446
E value
                   0.0e + 00
Match length
                   488
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFH8, complete sequence
Seq. No.
                  165389
Seq. ID
```

LIB3177-089-P1-K1-C4

BLAST score

```
Method
                    BLASTX
 NCBI GI
                    g3080395
 BLAST score
                    254
 E value
                    7.0e-22
Match length
                    103
 % identity
                    61
NCBI Description (AL022603) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    165390
 Seq. ID
                    LIB3177-089-P1-K1-C6
Method
                    BLASTX
NCBI GI
                    g1208408
BLAST score
                    344
E value
                    6.0e-33
Match length
                    74
% identity
                    91
NCBI Description
                    (D14824) nitrite reductase [Arabidopsis thaliana]
                    >gi_2289780_dbj_BAA21672_ (AB006032) nitrite reductase
[Arabidopsis thaliana] >gi_4335728_gb_AAD17406_ (AC006248)
                    nitrate reductase [Arabidopsis thaliana]
Seq. No.
                    165391
Seq. ID
                    LIB3177-089-P1-K1-C7
Method
                    BLASTX
NCBI GI
                    g535780
BLAST score
                    703
E value
                    2.0e-74
Match length
                    135
% identity
                    100
NCBI Description (D26609) transmembrane protein [Arabidopsis thaliana]
Seq. No.
                   165392
Seq. ID
                   LIB3177-089-P1-K1-C8
Method
                   BLASTN
NCBI GI
                    g4454004
BLAST score
                    362
E value
                    0.0e+00
Match length
                    374
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
                    (ESSAII project)
Seq. No.
                   165393
Seq. ID
                   LIB3177-089-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g4105798
BLAST score
                   342
E value
                   3.0e-32
Match length
                   94
% identity
                   59
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.
                   165394
Seq. ID
                   LIB3177-089-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g115767
```

NCBI GI

BLAST score

```
E value
                  7.0e-74
Match length
                  143
% identity
                  94
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165395
Seq. ID
                  LIB3177-089-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1922937
BLAST score
                  477
E value
                  4.0e-48
Match length
                  93
                  100
% identity
NCBI Description
                  (AC000106) Similar to Glycine SRC2 (gb AB000130). ESTs
                  gb H76869, gb T21700, gb ATTS5089 come from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  165396
Seq. ID
                  LIB3177-089-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g131398
                  586
BLAST score
E value
                  9.0e-61
Match length
                  135
% identity
                  88
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi 3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb X55970. ESTs gb Z17693, gb N37616,
                  gb_T41858, gb T88021, gb R37531, gb T04679, gb N37520,
                  gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  165397
Seq. ID
                  LIB3177-089-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  g3763944
BLAST score
                  120
E value
                  7.0e-61
Match length
                  372
                  98
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                  (ESSAII project)
Seq. No.
                  165398
Seq. ID
                  LIB3177-089-P1-K1-D4
Method
                  BLASTX
```

g2062161

```
E value
                    2.0e-11
 Match length
                    140
 % identity
                    15
 NCBI Description
                    (AC001645) jasmonate inducible protein isolog [Arabidopsis
                    thaliana)
 Seq. No.
                    165399
 Seq. ID
                    LIB3177-089-P1-K1-D6
 Method
                    BLASTX
 NCBI GI
                    g133938
 BLAST score
                    563
 E value
                    5.0e-58
 Match length
                    147
 % identity
                    75
 NCBI Description
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN-S3 >gi_70866_pir__R3SP3
                    ribosomal protein S3 - spinach chloroplast >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3
                    [Spinacia oleracea]
Seq. No.
                    165400
                    LIB3177-089-P1-K1-D7
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4741952
BLAST score
                    563
E value
                    4.0e-58
Match length
                    108
% identity
                    73
NCBI Description
                    (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                    165401
Seq. ID
                    LIB3177-089-P1-K1-D8
Method
                    BLASTN
NCBI GI
                    g3548797
BLAST score
                    116
E value
                    2.0e-58
Match length
                   348
% identity
                   95
NCBI Description Arabidopsis thaliana chromosome II BAC T18E12 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165402
Seq. ID
                   LIB3177-089-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g4490737
BLAST score
                   577
E value
                   9.0e-60
Match length
                   126
% identity
                   90
NCBI Description
                   (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   165403
Seq. ID
                   LIB3177-089-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   q3869280
BLAST score
                   610
E value
                   2.0e-63
Match length
```

% identity

```
% identity
                   74
NCBI Description
                   (AF064786) beta-galactosidase precursor [Carica papaya]
Seq. No.
                   165404
Seq. ID
                   LIB3177-089-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g3236240
BLAST score
                   62
E value
                   9.0e-46
Match length
                   117
                   77
% identity
                  (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                   165405
Seq. No.
Seq. ID
                   LIB3177-089-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   629
E value
                   7.0e-66
Match length
                   114
                   100
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                   165406
Seq. No.
                  LIB3177-089-P1-K1-E3
Seq. ID
Method
                   BLASTN
NCBI GI
                  g3152602
BLAST score
                   256
E value
                  1.0e-142
Match length
                   328
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F27L4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165407
Seq. ID
                  LIB3177-089-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  95
                  1.0e-55
E value
Match length
                  114
                  95
% identity
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi_984052_emb CAA61592 (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  165408
Seq. ID
                  LIB3177-089-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g421836
BLAST score
                  503
E value
                  3.0e-51
Match length
                  102
```

Match length

```
NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >gi 553040
                   (M96855) GF14 [Arabidopsis thaliana]
Seq. No.
                   165409
Seq. ID
                   LIB3177-089-P1-K1-E7
                   BLASTX
Method
NCBI GI
                   g461903
BLAST score
                   226
                   4.0e-19
E value
                   50
Match length
% identity
                   92
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 405129
                   (L14844) cyclophilin [Arabidopsis thaliana]
                   >gi_4490326_emb_CAB38608.1_ (AL035656) peptidylprolyl
isomerase ROC1 [Arabidopsis thaliana]
                   165410
Seq. No.
Seq. ID
                   LIB3177-089-P1-K1-E8
                   BLASTN
Method
NCBI GI
                   q1707006
BLAST score
                   304
E value
                   1.0e-170
                   357
Match length
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC T1B8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165411
Seq. ID
                   LIB3177-089-P1-K1-E9
Method
                   BLASTN
NCBI GI
                   g4589434
BLAST score
                   148
                   1.0e-77
E value
                   263
Match length
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MNJ7, complete sequence
Seq. No.
                   165412
Seq. ID
                   LIB3177-089-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   g166695.
BLAST score
                   107
E value
                   2.0e-53
                   138
Match length
                   93
% identity
NCBI Description
                  Arabidopsis thaliana recombination and DNA-damage
                   resistance protein (DRT112) mRNA, complete cds
Seq. No.
                   165413
                   LIB3177-089-P1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4204285
BLAST score
                   342 -
                   3.0e-32
E value
```

```
% identity
                    (AC003027) lcl_prt_seq No definition line found
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    165414
Seq. ID
                    LIB3177-089-P1-K1-F2
 Method
                    BLASTN
 NCBI GI
                    q3193282
 BLAST score
                    77
 E value
                    1.0e-35
Match length
                    132
 % identity
                    90
NCBI Description Arabidopsis thaliana BAC T14P8
Seq. No.
                    165415
Seq. ID
                   LIB3177-089-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g135860
BLAST score
                    629
E value
                   3.0e-67
Match length
                   147
% identity
                    67
NCBI Description
                   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                    (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic
                   protein gamma - Arabidopsis thaliana
                   >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                   protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                   >gi_445129_prf__1908432B tonoplast intrinsic protein gamma
                   [Arabidopsis thaliana]
Seq. No.
                   165416
                   LIB3177-089-P1-K1-F4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2688838
BLAST score
                   94
                   2.0e-45
E value
Match length
                   198
% identity
                   87
NCBI Description Thlaspi goesingense ATP phosphoribosyltransferase (THG1)
                   mRNA, complete cds
Seq. No.
                   165417
Seq. ID
                   LIB3177-089-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g2119846
BLAST score
                   745
E value
                   2.0e-79
Match length
                   148
% identity
                   95
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b \overline{b} binding protein [Arabidopsis
                   thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
```

```
Seq. No.
                   165418
 Seq. ID
                   LIB3177-089-P1-K1-F6
 Method
                   BLASTN
 NCBI GI
                    g1946354
 BLAST score
                    319
E value
                    1.0e-179
Match length
                    379
 % identity
                   96
                   Arabidopsis thaliana chromosome II BAC T06B20 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   165419
Seq. ID
                   LIB3177-089-P1-K1-F7
Method
                   BLASTN
NCBI GI
                   g2618599
BLAST score
                   66
E value
                   1.0e-28
Match length
                   185
% identity
                   84
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBD2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165420
Seq. ID
                   LIB3177-089-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g1769905
BLAST score
                   272
E value
                   4.0e-24
Match length
                   102
% identity
                   57
NCBI Description
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                   165421
Seq. ID
                   LIB3177-089-P1-K1-F9
Method
                   BLASTN
NCBI GI
                   g2656030
BLAST score
                   33
E value
                   6.0e-09
Match length
                   168
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUL8
Seq. No.
                   165422
Seq. ID
                   LIB3177-089-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   569
E value
                   7.0e-59
Match length
                   105
% identity
                   100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
```

Al precursor - Arabidopsis thaliana

Match length

```
Seq. No.
                   165423
 Seq. ID.
                   LIB3177-089-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g730645
BLAST score
                   675
E value
                   3.0e-71
Match length
                   144
 % identity
                   92
NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal
                   protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_
                   (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                   >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15
                   [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
                   Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                   gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   165424
Seq. ID
                  LIB3177-089-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  g3386593
BLAST score
                  230
E value
                  1.0e-126
Match length.
                   463
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165425
                  LIB3177-089-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  a295792
BLAST score
                  205
E value
                  1.0e-34
Match length
                  99
% identity
                  83
NCBI Description
                  (X13611) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  165426
Seq. ID
                  LIB3177-089-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g4741962
BLAST score
                  384
E value
                  1.0e-37
Match length
                  80
% identity
                  66
NCBI Description
                  (AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.
                  165427
Seq. ID
                  LIB3177-089-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q3298544
BLAST score
                  142
E value
                  3.0e-09
```

```
% identity
                   100
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                   165428
Seq. ID
                   LIB3177-089-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   g4580745
BLAST score
                   107
E value
                   1.0e-53
Match length
                   122
% identity
                   98
                  Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
NCBI Description
                   complete sequence
Seq. No.
                   165429
Seq. ID
                   LIB3177-089-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   g3702735
BLAST score
                   291
E value
                   1.0e-163
Match length
                   295
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165430
Seq. ID
                  LIB3177-089-P1-K1-G8
Method
                   BLASTN
NCBI GI
                  g3702735
BLAST score
                   127
E value
                   3.0e-65
Match length
                  150
% identity
                   96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165431
Seq. ID
                  LIB3177-089-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q282865
BLAST score
                  538
E value
                  3.0e-55
Match length
                  111
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  165432
                  LIB3177-089-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132863
BLAST score
                  597
E value
                  4.0e-62
```

Method

BLASTX

```
Match length
                   113
% identity
                   97
NCBI Description
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L2
                   >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2
                   [Sinapis alba]
                                                           . .
Seq. No.
                   165433
Seq. ID
                   LIB3177-089-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q3122038
BLAST score
                   268
                   2.0e-23
E value
Match length
                  113
% identity
                   50
                  DIHYDROPYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (COLLAPSIN
NCBI Description
                  RESPONSE MEDIATOR PROTEIN 4) (CRMP-4) >qi 1399542 (U52104)
                  rCRMP-4 [Rattus norvegicus]
Seq. No.
                  165434
Seq. ID
                  LIB3177-089-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1769905
BLAST score
                  532
E value
                  2.0e-54
Match length
                  142
% identity
                  73
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                  [Arabidopsis thaliana]
Seq. No.
                  165435
Seq. ID
                  LIB3177-089-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4220457
BLAST score
                  646
E value
                  9.0e-68
Match length
                  156
% identity
                  31
NCBI Description
                  (AC006216) Similar to gi_3413714 T19L18.21 putative
                  myrosinase-binding protein from Arabidopsis thaliana BAC
                  gb_AC004747. EST gb_N96478 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  165436
Seq. ID
                  LIB3177-089-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4249379
BLAST score
                  517
E value
                  7.0e-53
Match length
                  105
% identity
                  (AC005966) Strong similarity to gb_X82030 chloroplast RNA
NCBI Description
                  binding protein (RNP1) from Phaseolus vulgaris.
                  [Arabidopsis thaliana]
Seq. No.
                  165437
Seq. ID
                  LIB3177-089-P1-K1-H3
```

€. .

Seq. ID Method

```
NCBI GI
                   g115385
BLAST score
                   66
E value
                   3.0e-67
Match length
                   137
% identity
                   95
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
                   165438
Seq. No.
Seq. ID
                   LIB3177-089-P1-K1-H4
                   BLASTX
Method
NCBI GI
                   g4583542
BLAST score
                   428
E value
                   4.0e-42
Match length
                   154
                   62
% identity
NCBI Description
                   (Y16847) 16 kDa polypeptide of oxygen-evolving complex
                   [Arabidopsis thaliana]
                   165439
Seq. No.
Seq. ID
                   LIB3177-089-P1-K1-H6
Method
                   BLASTN
NCBI GI
                   g4185120
BLAST score
                   82
E value
                   2.0e-38
Match length
                   130
                   72
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F5F19 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   165440
                  LIB3177-089-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q421826
BLAST score
                   421
                   2.0e-41
E value
                  121
Match length
                  71
% identity
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana)
                  165441
Seq. No.
Seq. ID
                  LIB3177-089-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  q3046851
BLAST score
                  48
                  6.0e-18
E value
Match length
                  128
% identity
                  84
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165442
```

LIB3177-090-P1-K1-A10

BLASTX

```
NCBI GI
                    q3068713
 BLAST score
                    366
 E value
                    5.0e-35
 Match length
                    72
 % identity
                    100
 NCBI Description (AF049236) unknown [Arabidopsis thaliana]
 Seq. No.
                    165443
 Seq. ID
                    LIB3177-090-P1-K1-A11
 Method
                    BLASTX
 NCBI GI
                    q115767
 BLAST score
                    731
 E value
                    9.0e-78
 Match length
                    143
 % identity
                    96
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
 Seq. No.
                   165444
Seq. ID
                   LIB3177-090-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q4193388
BLAST score
                   396
E value
                   2.0e-38
Match length
                   122
% identity
                   67
NCBI Description (AF091455) translationally controlled tumor protein [Hevea
                   brasiliensis
Seq. No.
                   165445
Seq. ID
                   LIB3177-090-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g1934726
BLAST score
                   519
E value
                   5.0e-53
Match length
                   124
% identity
NCBI Description (U95034) germin-like protein [Arabidopsis thaliana]
Seq. No.
                   165446
Seq. ID
                  LIB3177-090-P1-K1-A3
Method
                  BLASTX
NCBI GI
                   q1617268
BLAST score
                  300
E value
                  1.0e-27
Match length
                  72
% identity
NCBI Description (Z72153) acyl CoA synthetase [Brassica napus]
Seq. No.
                  165447
Seq. ID
                  LIB3177-090-P1-K1-A4
Method.
```

BLASTX

```
NCBI GI
                    g1546706
 BLAST score
                    537
 E value
                    9.0e-68
 Match length
                    148
 % identity
                    93.
 NCBI Description (X98855) peroxidase ATP8a [Arabidopsis thaliana]
 Seq. No.
                    165448
 Seq. ID
                    LIB3177-090-P1-K1-A5
 Method
                    BLASTN
 NCBI GI
                    g2618599
 BLAST score
                    42
 E value
                    3.0e-14
 Match length
                    231
 % identity
                    82
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                   MBD2, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   165449
                   LIB3177-090-P1-K1-A6
 Seq. ID
Method
                   BLASTN
NCBI GI
                   q3047074
BLAST score
                   160
E value
                   1.0e-84
Match length
                   421
% identity
                   95
NCBI Description Arabidopsis thaliana BAC F21E10
Seq. No.
                   165450
Seq. ID
                   LIB3177-090-P1-K1-A7
Method
                   BLASTN
NCBI GI
                   q4376087
BLAST score
                   257
E value
                   1.0e-142
Match length
                   289
% identity
                   98
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                   fragment No
Seq. No.
                   165451
Seq. ID
                   LIB3177-090-P1-K1-A8
Method
                   BLASTN
NCBI GI
                   g4581084
BLAST score
                   260
E value
                   1.0e-144
Match length
                   377
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
                   sequence, complete sequence
Seq. No.
                   165452
Seq. ID
                   LIB3177-090-P1-K1-B1
Method
                   BLASTN
NCBI GI
                  g3510339
BLAST score
                   457
E value
                  0.0e+00
Match length
```

```
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                   K3K7, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   165453
 Seq. ID
                   LIB3177-090-P1-K1-B10
 Method
                   BLASTX
 NCBI GI
                   q4204266
 BLAST score
                   449
 E value
                   7.0e-45
 Match length
                   114
 % identity
                   83
 NCBI Description (AC005223) 52263 [Arabidopsis thaliana]
 Seq. No.
                   165454
 Seq. ID
                   LIB3177-090-P1-K1-B11
 Method
                   BLASTX
 NCBI GI
                   g2213882
 BLAST score
                   584
 E value
                   1.0e-60
Match length
                   133
 % identity
                   83
                   (AF004165) 2-isopropylmalate synthase [Lycopersicon
NCBI Description
                   pennellii]
Seq. No.
                   165455
Seq. ID
                   LIB3177-090-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q3688799
BLAST score
                   415
E value
                   9.0e-41
Match length
                   108
% identity
                   78
NCBI Description
                   (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
                   thaliana]
Seq. No.
                   165456
Seq. ID
                   LIB3177-090-P1-K1-B2
Method
                   BLASTN
NCBI GI
                   q3510339
BLAST score
                   150
E value
                   1.0e-78
Match length
                   154
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3K7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165457
Seq. ID
                  LIB3177-090-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g402614
BLAST score
                  130
E value
                  7.0e-67
Match length
                  248
% identity
                  86
NCBI Description B.rapa chloroplast mRNA for ribosomal protein L32
```

Method

BLASTX

```
Seq. No.
                  165458
Seq. ID
                  LIB3177-090-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q113026
BLAST score
                  542 ·
E value
                  1.0e-55
Match length
                  123
% identity
                  86 .
NCBI Description
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                  >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape
                  >gi_255220_bbs_112862 isocitrate lyase, threo-D
                  S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
                  napus, seedlings, Peptide, 576 aa] >gi 167144 (L08482)
                  isocitrate lyase [Brassica napus] >gi 447142 prf 1913424A
                  isocitrate lyase [Brassica napus]
Seq. No.
                  165459
Seq. ID
                  LIB3177-090-P1-K1-B5
Method
                  BLASTX
                  g2143227
NCBI GI
BLAST score
                  222
E value
                  2.0e-18
Match length
                  68
% identity
                  74
NCBI Description
                 (Y13356) glyoxysomal isocitrate lyase [Brassica napus]
Seq. No.
                  165460
                  LIB3177-090-P1-K1-B6 .
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2246621
BLAST score
                  403
E value
                  3.0e-39
Match length
% identity
                  83
NCBI Description
                  (AF004393) salt-stress induced tonoplast intrinsic protein
                  [Arabidopsis thaliana]
Seq. No.
                  165461
Seq. ID
                  LIB3177-090-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2119848
BLAST score
                  661
E value
                  1.0e-69
Match length
                  129
% identity
                  96
                  chlorophyll a/b-binding protein type I precursor Lhb1B1 -
NCBI Description
                  Arabidopsis thaliana >gi_16366_emb_CAA45789 (X64459)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128229 (AC004077) putative
                  photosystem II type I chlorophyll a/b binding protein
                  [Arabidopsis thaliana] >gi_3337372 (AC004481) putative
                  photosystem II type I chlorophyll a/b binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  165462
Seq. ID
                  LIB3177-090-P1-K1-B9
```

BLAST score

```
NCBI GI
                    q4741948
 BLAST score
                    720
 E value
                    2.0e-76
 Match length
                    138
 % identity
                    99
 NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana]
 Seq. No.
                    165463
 Seq. ID
                    LIB3177-090-P1-K1-C1
 Method
                   BLASTX
 NCBI GI
                    g4835233
 BLAST score
                    546
 E value
                    3.0e-56
 Match length
                   113
 % identity
                   96
 NCBI Description
                    (AL049862) putative protein 1 photosystem II
                   oxygen-evolving complex [Arabidopsis thaliana]
 Seq. No.
                   165464
 Seq. ID
                   LIB3177-090-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   g3763944
 BLAST score
                   92
E value
                   2.0e-44
Match length
                   212
 % identity
                   86
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                   (ESSAII project)
Seq. No.
                   165465
Seq. ID
                   LIB3177-090-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g4262225
BLAST score
                   337
                   2.0e-31
E value
Match length
                   80
% identity
                   70
NCBI Description
                   (AC006200) putative phosphatidic acid phosphatase
                   [Arabidopsis thaliana]
Seq. No.
                   165466
Seq. ID
                   LIB3177-090-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g1709205
BLAST score
                   567
E value
                   2.0e-58
Match length
                   140
% identity
                   75
NCBI Description
                  MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMP 3) (INOSITOL
                  MONOPHOSPHATASE 3) >gi_1098971 (U39059) myo-inositol
                  monophosphatase 3 [Lycopersicon esculentum]
Seq. No.
                  165467
Seq. ID
                  LIB3177-090-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3080371
```

Seq. No.

```
E value
                    4.0e-79
 Match length
                    136
 % identity
                    100
                    (AL022580) putative pectinacetylesterase protein
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                   165468
 Seq. ID
                   LIB3177-090-P1-K1-C3
 Method
                   BLASTX
 NCBI GI
                   q543841
 BLAST score
                   560
 E value
                   1.0e-57
 Match length
                   129
 % identity
                   87
                   ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__$28875
 NCBI Description
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
 Seq. No.
                   165469
 Seq. ID
                   LIB3177-090-P1-K1-C4
Method
                  · BLASTX
 NCBI GI
                   g115385
 BLAST score
                   554
E value
                   4.0e-57
Match length
                   107
% identity
                   99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   165470
Seq. ID
                   LIB3177-090-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1363489
BLAST score
                   348
E value
                   4.0e-35
Match length
                  100
% identity
                  78
NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  165471
Seq. ID
                  LIB3177-090-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q2191138
BLAST score
                  716
E value
                  6.0e-76
Match length
                  142
% identity
                  100
                  (AF007269) A_IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No.

Seq. ID

165476

LIB3177-090-P1-K1-D10

```
LIB3177-090-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160158
BLAST score
                   474
E value
                   1.0e-47
                   90
Match length
                   99
% identity
NCBI Description
                   (AC000132) Similar to elongation factor 1-gamma
                   (gb EF1G XENLA). ESTs gb T20564,gb T45940,gb T04527 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   165473
Seq. ID
                   LIB3177-090-P1-K1-C8
Method
                   BLASTN
NCBI GI
                   q3445196
BLAST score
                   43
E value
                   4.0e-15
Match length
                   107
% identity
                   85
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20K9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165474
Seq. ID
                   LIB3177-090-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   793
E value
                   6.0e-85
Match length
                   145
% identity
                   100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   165475
Seq. ID
                   LIB3177-090-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g1755156
BLAST score
                   546
E value
                   5.0e-56
Match length
                   152
% identity
                   75
NCBI Description
                   (U75189) germin-like protein [Arabidopsis thaliana]
                   >gi 1755158 (U75190) germin-like protein [Arabidopsis
                   thaliana] >gi 1755170 (U75196) germin-like protein
                  [Arabidopsis thaliana] >gi_1755172 (U75197) germin-like protein [Arabidopsis thaliana] >gi_1755180 (U75201)
                   germin-like protein [Arabidopsis thaliana] >gi_1755190
                   (U75206) germin-like protein [Arabidopsis thaliana]
                   >gi_1934728 (U95035) germin-like protein [Arabidopsis
                  thaliana] >gi_4154285 (AF090733) germin-like protein 1
                   [Arabidopsis thaliana] >gi 4666248 dbj BAA77207.1 (D89055)
                   germin-like protein precursor [Arabidopsis thaliana]
```

```
Method
                    BLASTX
 NCBI GI
                    q115767
 BLAST score
                    53
 E value
                    9.0e-72
 Match length
                    137
 % identity
 NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
 Seq. No.
                   165477
 Seq. ID
                   LIB3177-090-P1-K1-D11
 Method
                   BLASTN
 NCBI GI
                   g2351066
 BLAST score
                   228
 E value
                   1.0e-125
 Match length
                   446
 % identity
                   96
 NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOP9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165478
Seq. ID
                   LIB3177-090-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   g3449326
BLAST score
                   415.
E value
                   0.0e+00
Match length
                   446
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K19M22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165479
Seq. ID
                  LIB3177-090-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g4757405
BLAST score
                  376
E value
                  0.0e + 00
Match length
                  488
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOJ10, complete sequence
Seq. No.
                  165480
Seq. ID
                  LIB3177-090-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g120675
BLAST score
                  547
E value
                  4.0e-56
Match length
                  141
% identity
                  66
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
```

>gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate

```
>gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                    alba].
 Seq. No.
Seq. ID
                    165481
                    LIB3177-090-P1-K1-D6
 Method
                    BLASTX
 NCBI GI
                    g3643594
 BLAST score
                    344
 E value
                    2.0e-32
 Match length
                    70
 % identity
                    97
 NCBI Description
                   (AC005395) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    165482
 Seq. ID
                    LIB3177-090-P1-K1-D7
 Method
                    BLASTX
 NCBI GI
                    g4741960
 BLAST score
                    587
 E value
                    7.0e-61
 Match length
                    130
 % identity
                    86
 NCBI Description
                   (AF134130) Lhcb6 protein [Arabidopsis thaliana]
 Seq. No.
                   165483
 Seq. ID
                   LIB3177-090-P1-K1-D9
 Method
                   BLASTX
 NCBI GI
                   g1408473
 BLAST score
                   588
 E value
                   6.0e-61
                                *
Match length
                   113
 % identity
NCBI Description
                   (U48939) actin depolymerizing factor 2 [Arabidopsis
                   thaliana]
Seq. No.
                   165484
Seq. ID
                   LIB3177-090-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g2129636
BLAST score
                   639
E value
                   6.0e-67
Match length
                   134
% identity
                   92
                   lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   165485
Seq. ID
                   LIB3177-090-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g4741948
BLAST score
                   301
E value
                  2.0e-27
Match length
                  132
% identity
                  52
NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  165486
```

dehydrogenase (EC 1.2.1.12), cytosolic - white mustard

```
Seq. ID
                   LIB3177-090-P1-K1-E11
 Method
                   BLASTX
 NCBI GI
                   g115767
 BLAST score
                   760
 E value
                   4.0e-81
 Match length
                   146
 % identity
                   99
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir_ A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
 Seq. No.
                   165487
 Seq. ID
                   LIB3177-090-P1-K1-E12
 Method
                   BLASTN
 NCBI GI
                   g2584827
 BLAST score
                   173
 E value
                   2.0e-92
 Match length
                   391
 % identity
                   96
 NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                   complete sequence [Arabidopsis thaliana]
 Seq. No.
                   165488
 Seq. ID
                   LIB3177-090-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2129636
BLAST score
                   399
E value
                   7.0e-39
Match length
                   85
% identity
                   89
NCBI Description lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase
                   [Arabidopsis thaliana]
Seq. No.
                  165489
Seq. ID
                  LIB3177-090-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2781354
BLAST score
                  493
E value
                  2.0e-64
Match length
                  131
% identity
                  92
NCBI Description (AC003113) F2401.10 [Arabidopsis thaliana]
Seq. No.
                  165490
Seq. ID
                  LIB3177-090-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2781354
BLAST score
                  402
E value
                  3.0e-39
Match length
                  85
% identity
                  91
NCBI Description (AC003113) F2401.10 [Arabidopsis thaliana]
```

Method

BLASTX

```
Seq. No.
                    165491
 Seq. ID
                    LIB3177-090-P1-K1-E5
 Method
                    BLASTX
 NCBI GI
                    q4567202
 BLAST score
                    675
 E value
                    3.0e-71
 Match length
                    136
 % identity
                    98
 NCBI Description
                    (AC007168) putative myo-inositol 1-phosphate synthase
                    [Arabidopsis thaliana]
 Seq. No.
                   165492
 Seq. ID
                   LIB3177-090-P1-K1-E6
 Method
                   BLASTX
 NCBI GI
                   g2541876
 BLAST score
                   214
 E value
                   4.0e-17
 Match length
                   98
 % identity
                   53
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
 NCBI Description
                   [Nicotiana tabacum]
 Seq. No.
                   165493
 Seq. ID
                   LIB3177-090-P1-K1-E7
 Method
                   BLASTN
 NCBI GI
                   g4510360
BLAST score
                   114
E value
                   3.0e⇒57
Match length
                   391
 % identity
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   165494
Seq. ID
                   LIB3177-090-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g4454036
BLAST score
                   538
E value
                   3.0e-55
Match length
                   108
% identity
                   94
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                   thaliana |
Seq. No.
                  165495
Seq. ID
                 · LIB3177-090-P1-K1-E9.
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  414
E value
                  1.0e-40
Match length
                  116
% identity
                  73
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  165496
Seq. ID
                  LIB3177-090-P1-K1-F10
```

```
NCBI GI
                    q4689474
 BLAST score
                    554
 E value
                    3.0e-57
 Match length
                   112
 % identity
                   99
 NCBI Description (AC007213) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   165497
 Seq. ID
                   LIB3177-090-P1-K1-F11
 Method
                   BLASTX
 NCBI GI
                   g3461819
 BLAST score
                   212
 E value
                   6.0e-17
 Match length
                   132
 % identity
                   44
 NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   165498
 Seq. ID
                   LIB3177-090-P1-K1-F12
 Method
                   BLASTX
 NCBI GI
                   g4206610
 BLAST score
                   606
 E value
                   4.0e-63
 Match length
                   126
 % identity
                   96
NCBI Description (AF066851) ATP synthase beta subunit [Trichilia emetica]
 Seq. No.
                   165499
 Seq. ID
                   LIB3177-090-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g4741960
BLAST score
                   526
E value
                   1.0e-53
Match length
                   101
 % identity
                   97
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                   165500
Seq. ID
                   LIB3177-090-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   q2062158
BLAST score
                   747
E value
                   1.0e-79
Match length
                   144
% identity
                   50
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  165501
Seq. ID
                  LIB3177-090-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3080371
BLAST score
                  670
·E value
                  1.0e-70
Match length
                  126
% identity
NCBI Description (AL022580) putative pectinacetylesterase protein
```

Match length

NCBI Description

% identity

112

99

[Arabidopsis thaliana] Seq. No. 165502 Seq. ID LIB3177-090-P1-K1-F7 Method BLASTX NCBI GI g1532135 BLAST score 251 E value 2.0e-21 Match length 62 % identity 77 NCBI Description (U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea] Seq. No. 165503 Seq. ID LIB3177-090-P1-K1-F8 Method BLASTX NCBI GI g430947 BLAST score 95 E value 3.0e-03 Match length 144 % identity 81 NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana] Seq. No. 165504 Seq. ID LIB3177-090-P1-K1-F9 Method BLASTX NCBI GI g4586255 BLAST score 280 E value 3.0e-25 Match length 70 % identity NCBI Description (AL049640) putative protein [Arabidopsis thaliana] Seq. No. 165505 Seq. ID LIB3177-090-P1-K1-G1 Method BLASTN NCBI GI g2980757 BLAST score 336 E value 0.0e+00 Match length 360 % identity 98 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project) Seq. No. 165506 Seq. ID LIB3177-090-P1-K1-G10 Method BLASTX NCBI GI g115385 BLAST score 574 E value 2.0e-59

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Match length

```
Seq. No.
                   165507
 Seq. ID
                   LIB3177-090-P1-K1-G11
 Method
                   BLASTX
 NCBI GI
                   g115767
 BLAST score
                   775
 E value
                   7.0e-83
 Match length .
                   147
 % identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
 NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
 Seq. No.
                   165508
 Seq. ID
                   LIB3177-090-P1-K1-G12
 Method
                   BLASTX
 NCBI GI
                   g4587525
BLAST score
                   294
E value
                   2.0e-26
Match length
                   146
 % identity
                   40
NCBI Description
                   (AC007060) Contains the PF_00650 CRAL/TRIO
                   phosphatidyl-inositol-transfer protein domain. ESTs
                   gb_T76582, gb_N06574 and gb_Z25700 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   165509
Seq. ID
                   LIB3177-090-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   q4454051
BLAST score
                   585
E value
                   1.0e-60
Match length
                   117
% identity
                   94
NCBI Description
                  (AL035394) putative polygalacturonase [Arabidopsis
                  thaliana]
Seq. No.
                  165510
Seq. ID
                  LIB3177-090-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g3608153
BLAST score
                  252
E value
                  2.0e-21
Match length
                  146
% identity
                  43
NCBI Description
                  (AC005314) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  165511
Seq. ID
                  LIB3177-090-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  g4585952
BLAST score
                  143
E value
                  8.0e-75
```

```
% identity
                   99
 NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F26F24,
                   complete sequence
 Seq. No.
                   165512
 Seq. ID
                   LIB3177-090-P1-K1-G5
 Method
                   BLASTX
 NCBI GI
                   g166702
 BLAST score
                   218
                   6.0e-18
 E value
Match length
                   51
 % identity
NCBI Description
                   (M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit
                   [Arabidopsis thaliana]
Seq. No.
                   165513
Seq. ID
                   LIB3177-090-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g3334128
BLAST score
                   661
E value
                   2.0e-69
Match length
                   142
                   98
% identity
NCBI Description
                   BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE
                   PRECURSOR (BCCP) >gi_1066348 (U23155) acetyl-CoA
                   carboxylase biotin-containing subunit [Arabidopsis
                   thaliana]
Seq. No.
                   165514
Seq. ID
                   LIB3177-090-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q1916613
BLAST score
                   420
E value
                   3.0e-41
Match length
                   92
% identity
                   95
NCBI Description
                  (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]
Seq. No.
                  165515
Seq. ID
                  LIB3177-090-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g4159709
BLAST score
                   408
E value
                  0.0e+00
Match length
                  488
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLN21, complete sequence
Seq. No.
                  165516
Seq. ID
                  LIB3177-090-P1-K1-G9
                  BLASTX
Method
NCBI GI
                  g421826
BLAST score
                  191
E value
                  2.0e-53
Match length
                  131
% identity
                  82
```

```
NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                   >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thalianal
 Seq. No.:
                   165517
 Seq. ID
                   LIB3177-090-P1-K1-H1
 Method
                   BLASTX
 NCBI GI
                   g2160166
 BLAST score
                   229
 E value
                   4.0e-19
Match length
                   58
 % identity
                   79
NCBI Description
                  (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                   165518
Seq. ID
                   LIB3177-090-P1-K1-H10
Method
                   BLASTN
NCBI GI
                   g4454587
BLAST score
                   100
E value
                   7.0e-49
Match length
                   288
% identity
                   84
                  Arabidopsis thaliana BAC F21A20 from chromosome V near 61
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165519
Seq. ID
                   LIB3177-090-P1-K1-H11
Method
                   BLASTN
NCBI GI
                   g4757392
BLAST score
                   199
E value
                   1.0e-108
Match length
                   207
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K14A17, complete sequence
Seq. No.
                  165520
Seq. ID
                  LIB3177-090-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g2707927
BLAST score
                  255
E value
                  1.0e-141
Match length
                  290
% identity
                  97
NCBI Description A.thaliana mRNA for outward rectifying potassium channel
                KC01
Seq. No.
                  165521
Seq. ID
                  LIB3177-090-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  713
E value
                  1.0e-75
Match length
                  131
% identity
                  100
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
```

glucohydrolase [Arabidopsis thaliana] 165522 LIB3177-090-P1-K1-H3

Method BLASTX NCBI GI g4204266 BLAST score 425 E value 5.0e-42 Match length 119 % identity 77

Seq. No.

Seq. ID

NCBI Description (AC005223) 52263 [Arabidopsis thaliana]

Seq. No. 165523

Seq. ID LIB3177-090-P1-K1-H4

Method BLASTX NCBI GI g4835233 BLAST score 730 E value 1.0e-77 Match length 150 % identity 97

NCBI Description (AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No. 165524

Seq. ID LIB3177-090-P1-K1-H7

Method BLASTX NCBI GI g1669389 BLAST score 700 E value 4.0e-74 Match length 139 % identity 100

NCBI Description (U42007) actin 8 [Arabidopsis thaliana]

Seq. No. 165525

Seq. ID LIB3177-090-P1-K1-H8

Method BLASTN NCBI GI g3176694 BLAST score 300 E value 1.0e-168 Match length 387 % identity 75

NCBI Description Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 165526

Seq. ID LIB3177-090-P1-K1-H9

Method BLASTX NCBI GI g1172995 BLAST score 243 E value 2.0e-20 Match length 100 % identity 53

NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)

ribosomal protein L22 [Rattus norvegicus]

>gi_1093952_prf__2105193A ribosomal protein L22 [Rattus

norvegicus]

```
Seq. No.
                   165527
 Seq. ID
                  LIB3177-091-P1-K1-A1
 Method
                   BLASTN
 NCBI GI
                   g2264306
 BLAST score
                   321
 E value
                   0.0e+00
 Match length
                   337
 % identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MBK5, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   165528
 Seq. ID
                   LIB3177-091-P1-K1-A10
 Method
                   BLASTX
 NCBI GI
                   g4585900
 BLAST score
                   342
 E value
                   3.0e-32
 Match length
                   101
 % identity
                   71
NCBI Description (AC007133) putative histone H2A [Arabidopsis thaliana]
Seq. No.
                  165529
Seq. ID
                  LIB3177-091-P1-K1-A11
Method ·
                  BLASTX
NCBI GI
                  g115767
BLAST score
                   623
E value
                   4.0e-65
Match length
                  120
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165530
Seq. ID
                  LIB3177-091-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3413717
BLAST score
                  437
E value
                  2.0e-43
Match length
                  106
% identity
NCBI Description
                  (AC004747) unknown protein [Arabidopsis thaliana]
                  >gi 3643590 (AC005395) unknown protein [Arabidopsis
                  thaliana)
Seq. No.
                  165531
Seq. ID
                  LIB3177-091-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3386607
BLAST score
                  300
E value
                  3.0e-27
Match length
                  114
```

```
% identity
 NCBI Description
                    (AC004665) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    165532
 Seq. ID
                    LIB3177-091-P1-K1-A3
 Method
                    BLASTX
 NCBI GI
                    g3599491
 BLAST score
                    168
 E value
                    8.0e-12
 Match length
                    42
 % identity
                    81
                   (AF085149) putative aminotransferase [Capsicum chinense]
 NCBI Description
 Seq. No.
                    165533
 Seq. ID
                    LIB3177-091-P1-K1-A4
 Method
                    BLASTN
 NCBI GI
                    g3241925
 BLAST score
                    98
 E value
                    1.0e-47
 Match length
                    223
 % identity
                    94
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOK9, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   165534
 Seq. ID
                   LIB3177-091-P1-K1-A5
 Method
                   BLASTX
· NCBI GI
                   g544425
 BLAST score
                   423
 E value
                   8.0e-42
 Match length
                   83
 % identity
                   99
 NCBI Description
                   GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
                   >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8)
                   - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                   glycine rich protein [Arabidopsis thaliana] >gi_166658
                   (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)
                   RNA-binding protein [Arabidopsis thaliana]
 Seq. No.
                   165535
 Seq. ID
                   LIB3177-091-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g4585882
BLAST score
                   524
E value
                   2.0e-53
Match length
                   101
% identity
                   100
NCBI Description
                   (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   165536
Seq. ID
                   LIB3177-091-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g4191785
BLAST score
                   351
E value
                   3.0e-33
Match length
                   90
```

```
% identity
 NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana]
  Seq. No.
                    165537
  Seq. ID
                    LIB3177-091-P1-K1-A9
 Method
                    BLASTX
 NCBI GI
                    q3914658
 BLAST score
                    625
 E value
                    3.0e-65
 Match length
                    122
  % identity
                    99
 NCBI Description
                    50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
                    >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal
                    protein [Arabidopsis thaliana]
 Seq. No.
                    165538
 Seq. ID
                    LIB3177-091-P1-K1-B1
 Method
                    BLASTX
 NCBI GI
                    g1946690
 BLAST score
                    493
 E value
                    5.0e-50
 Match length
                    94
 % identity
                    100
 NCBI Description
                    (U94495) glutathione peroxidase [Arabidopsis thaliana]
                    >gi_4582452_gb_AAD24836.1_AC007071 8 (AC007071) putative
                    glutathione peroxidase [Arabidopsis thaliana]
 Seq. No.
                    165539
 Seq. ID
                   LIB3177-091-P1-K1-B10
 Method
                   BLASTX
 NCBI GI
                   g132074
 BLAST score
                    639
 E value
                   5.0e-67
 Match length
                   116
 % identity
                   100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
 Seq. No.
                   165540
                   LIB3177-091-P1-K1-B12
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q133872
 BLAST score
                   289
 E value
                   6.0e-26
Match length
                   73
 % identity
                   82
 NCBI Description
                   30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
                   >gi_282838_pir__S26494 ribosomal protein S1, chloroplast -
                   spinach >gi_322404_pir A44121 small subunit ribosomal
                   protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >gi<sup>2</sup>170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
 Seq. No.
```

```
Seq. ID
                   LIB3177-091-P1-K1-B2
 Method
                   BLASTX
 NCBI GI
                   g115767
 BLAST score
                   509
 E value
                   6.0e-52
 Match length
                   97
 % identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
 NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
 Seq. No.
                   165542
 Seq. ID
                   LIB3177-091-P1-K1-B3
 Method
                   BLASTN
 NCBI GI
                   g1769904
                   202
 BLAST score
 E value
                   1.0e-110
 Match length
                   213
 % identity
                   99
NCBI Description A.thaliana psbP gene
Seq. No.
                   165543
Seq. ID
                   LIB3177-091-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q115767
BLAST score
                   526
E value
                   6.0e-54
Match length
                   103
% identity
                   98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir_ A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165544
Seq. ID
                  LIB3177-091-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  g22564
BLAST score
                  128
E value
                  8.0e-66
Match length
                  215
% identity
                  97
NCBI Description A.thaliana tufA gene for elongation factor Tu
Seq. No.
                  165545
Seq. ID
                  LIB3177-091-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g4539292
BLAST score
                  435
E value
```

3.0e-43

```
Match length
                    85
 % identity
                    (ALO49480) putative ribosomal protein S10 [Arabidopsis
 NCBI Description
                    thalianal
 Seq. No.
                    165546
 Seq. ID
                    LIB3177-091-P1-K1-B9
 Method
                    BLASTX
 NCBI GI
                    g2702281
 BLAST score
                    464
 E value
                    9.0e-47
 Match length
                    91
 % identity
                    59
 NCBI Description
                    (AC003033) putative protein disulfide isomerase precursor
                    [Arabidopsis thaliana]
 Seq. No.
                    165547
 Seq. ID
                    LIB3177-091-P1-K1-C1
 Method
                    BLASTX
 NCBI GI
                    g2781354
 BLAST score
                    468
 E value
                    4.0e-47
 Match length
                    92
 % identity
                    95
 NCBI Description
                  (AC003113) F2401.10 [Arabidopsis thaliana]
Seq. No.
                   165548
Seq. ID
                   LIB3177-091-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g1850546
BLAST score
                   271
E value
                   7.0e-24
Match length
                   55
% identity
NCBI Description
                   (U88045) syntaxin related protein AtVam3p [Arabidopsis
                   thaliana]
Seq. No.
                   165549
Seq. ID
                   LIB3177-091-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   785
E value
                   4.0e-84
Match length
                   147
% identity
                   99
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1.1.39}) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   165550
Seq. ID
                   LIB3177-091-P1-K1-C12
Method
                 BLASTX
NCBI GI
                   g3236259
BLAST score
                   413
E value
                   8.0e-41
Match length
                   91
```

```
% identity
 NCBI Description
                   (AC004684) putative alcohol dehydrogenase [Arabidopsis
                   thaliana]
 Seq. No.
                   165551
 Seq. ID
                   LIB3177-091-P1-K1-C2
                                                                           er er
 Method
                   BLASTX
 NCBI GI
                   g4584527
 BLAST score
                   223
 E value
                   3.0e-18
 Match length
                   105
 % identity
                   39
 NCBI Description (AL049607) putative protein [Arabidopsis thaliana]
 Seq. No.
                   165552
 Seq. ID
                   LIB3177-091-P1-K1-C3
 Method
                   BLASTX
 NCBI GI
                   g1769905
 BLAST score
                   408
 E value
                   5.0e-40
 Match length
                   118
 % identity
                   68
 NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                   165553
Seq. ID
                   LIB3177-091-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g4262156
BLAST score
                   551
E value
                   1.0e-56
Match length
                   133
% identity
                   81
NCBI Description
                  (AC005275) putative component of cytochrome B6-F complex
                   [Arabidopsis thaliana]
Seq. No.
                   165554
Seq. ID
                   LIB3177-091-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g1321731
BLAST score
                  173
E value
                  2.0e-12
Match length
                  129
% identity
                  40
NCBI Description (Z72439) major allergen Cor a 1 [Corylus avellana]
Seq. No.
                  165555
Seq. ID
                  LIB3177-091-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4741954
BLAST score
                  656
E value
                  6.0e-69
Match length
                  141
% identity
NCBI Description (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
Seq. No.
                  165556
```

```
Seq. ID
                    LIB3177-091-P1-K1-C8
 Method
                    BLASTN
 NCBI GI
                    q3763915
 BLAST score
                    151
 E value
                    2.0e-79
 Match length
                    176
 % identity
                    95
                   Arabidopsis thaliana chromosome II BAC F14B2 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    165557
 Seq. ID
                   LIB3177-091-P1-K1-D1
 Method
                   BLASTX
 NCBI GI
                   q421836
 BLAST score
                    660
 E value
                   2.0e-69
Match length
                   131
 % identity
                   99
NCBI Description
                   G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040
                   (M96855) GF14 [Arabidopsis thaliana]
Seq. No.
                   165558
Seq. ID
                   LIB3177-091-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g4204274
BLAST score
                   755
E value
                   1.0e-80
Match length
                   148
% identity
                   99
                   (AC004146) ribulose bisphosphate carboxylase, small subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   165559
Seq. ID
                   LIB3177-091-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g4455359
BLAST score
                   637
E value
                   8.0e-67
Match length
                   133
% identity
                   95
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   165560
                   LIB3177-091-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4417280
BLAST score
                   615
E value
                   4.0e-64
Match length
                   137
% identity
                   91
NCBI Description
                  (AC007019) putative ATP synthase [Arabidopsis thaliana]
Seq. No.
                  165561
Seq. ID
                  LIB3177-091-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g132102
BLAST score
```

% identity

```
E value
                   9.0e-57
 Match length
                   113
 % identity.
                   96
 NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 2B) >gi 68061_pir _RKMUB2
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B2 precursor - Arabidopsis thaliana >gi 16194 emb CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
 Seq. No.
                   165562
 Seq. ID
                   LIB3177-091-P1-K1-D4
 Method
                   BLASTX
 NCBI GI
                   g543841
 BLAST score
                   536
 E value
                   6.0e-55
 Match length
                   106
 % identity
                   98
 NCBI Description
                   ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                   165563
                   LIB3177-091-P1-K1-D6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2454181
BLAST score
                   287
                   1.0e-160
E value
Match length
                   343
% identity
                   99
NCBI Description
                  Arabidopsis thaliana pyruvate dehydrogenase E1 alpha
                   subunit mRNA, nuclear gene encoding plastid protein,
                   complete cds
Seq. No.
                   165564
Seq. ID
                   LIB3177-091-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g115385
BLAST score
                   346
E value
                  7.0e-33
Match length
                  72
% identity
                  96
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165565
                  LIB3177-091-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3785981
BLAST score
                  544
E value
                  8.0e-56
Match length
                  136
```

```
NCBI Description (AC005560) putative major latex protein [Arabidopsis
                    thaliana]
 Seq. No.
                    165566
 Seq. ID
                    LIB3177-091-P1-K1-D9
 Method
                    BLASTX
 NCBI GI
                    g4115379
 BLAST score
                    466
 E value
                    1.0e-46
 Match length
                    111
 % identity
                    79
                   (ACO05967) putative carbonyl reductase [Arabidopsis
 NCBI Description
                    thalianal
 Seq. No.
                    165567
 Seq. ID
                    LIB3177-091-P1-K1-E10
 Method
                    BLASTX
 NCBI GI
                    g132074
 BLAST score
                    786
 E value
                    3.0e-84
Match length
                    151
 % identity
                    97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                    (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                    ribulose-bisphosphate carboxy\overline{lase} (EC 4.1.1.39) small chain
                    Al precursor - Arabidopsis thaliana
Seq. No.
                    165568
Seq. ID
                   LIB3177-091-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g2129755
BLAST score
                   482
E value
                   8.0e-49
Match length
                   96
% identity
                   100
NCBI Description
                   tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis
                   thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp
                   synthase:SUBUNIT=alpha [Arabidopsis thaliana]
Seq. No.
                   165569
Seq. ID
                   LIB3177-091-P1-K1-E12
Method
                   BLASTN
NCBI GI
                   q1304412
BLAST score
                   50
E value
                   4.0e-20
Match length
                   54.
% identity
                   98
NCBI Description
                   Arabidopsis thaliana Rac-like protein (ARAC3) gene,
                   complete cds
Seq. No.
                   165570
Seq. ID
                   LIB3177-091-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q3342249
BLAST score
                   306
E value
                   8.0e-32
```

```
Match length
                    106
 % identity
                    75
 NCBI Description
                    (AF047719) GA3 [Arabidopsis thaliana] >gi_3342251
                    (AF047720) GA3 [Arabidopsis thaliana]
 Seq. No.
                    165571
 Seq. ID
                    LIB3177-091-P1-K1-E3
 Method
                    BLASTN
 NCBI GI
                    g4454004
 BLAST score
                    163
 E value
                    1.0e-86
 Match length
                    185
 % identity
                    100
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
                    (ESSAII project)
 Seq. No.
                   165572
 Seq. ID
                   LIB3177-091-P1-K1-E4
 Method
                   BLASTN
 NCBI GI
                   g2924729
 BLAST score
                   406 .
 E value
                   0.0e+00
 Match length
                   426
 % identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MNA5, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   165573
Seq. ID
                   LIB3177-091-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g1871181
BLAST score
                   175
E value
                   1.0e-12
Match length
                   110
% identity
                   48
                   (U90439) ring zinc finger protein isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   165574
Seq. ID
                  LIB3177-091-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g3096931
BLAST score
                   561
E value
                   8.0e-58
Match length
                   110
% identity
NCBI Description
                   (AL023094) putative ribosomal protein S16 [Arabidopsis
                   thaliana]
Seq. No.
                  165575
Seq. ID
                  LIB3177-091-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  625
E value
                  2.0e-65
Match length
                  118
% identity
                  100
```

NCBI GI

```
NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi_3337371 (AC004481) photosystem II type I
                   chlorophyll a7b binding protein [Arabidopsis thaliana]
 Seq. No.
                   165576
 Seq. ID
                   LIB3177-091-P1-K1-E8
 Method
                   BLASTX
 NCBI GI
                   q3522929
BLAST score
                   51
E value
                   3.0e-21
Match length
                   55
 % identity
                   98
                   (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                   dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.
                   165577
Seq. ID
                   LIB3177-091-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g3287695
BLAST score
                   415
E value
                   1.0e-40
Match length
                   111
% identity
                   67
                  (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                   gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                   thaliana]
Seq. No.
                  165578
Seq. ID
                  LIB3177-091-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3212869 6
BLAST score
                  648
E value
                  4.0e-68
Match length
                  133
% identity
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  165579
Seq. ID
                  LIB3177-091-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  q4757414
BLAST score
                  117
E value
                  2.0e-59
Match length
                  189
% identity
                  91
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
Seq. No.
                  165580
Seq. ID
                  LIB3177-091-P1-K1-F4
Method
                  BLASTX
```

g2642435

Seq. No.

```
BLAST score
                    489
                    2.0e-49
 E value
 Match length
                    98
 % identity
                    94
 NCBI Description
                   (AC002391) MYB-related protein [Arabidopsis thaliana]
 Seq. No.
                    165581
 Seq. ID
                    LIB3177-091-P1-K1-F5
Method
                    BLASTX
NCBI GI
                    q3834312
BLAST score
                    594
E value
                    1.0e-61
Match length
                    135
% identity
                    (AC005679) Strong similarity to glycoprotein EP1 gb_L16983
NCBI Description
                    Daucus carota and a member of S locus glycoprotein \overline{\mathtt{family}}
                    PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815, gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248,
                    gb_AA728536, gb_Z30816 an
Seq. No.
                    165582
Seq. ID
                    LIB3177-091-P1-K1-F6
Method
                    BLASTX
NCBI GI
                    g548653
BLAST score
                    42
E value
                    3.0e - 33
Match length
                    104
% identity
                    82
NCBI Description
                   50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)
                   >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast
                    - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046)
                   ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.
                   165583
                   LIB3177-091-P1-K1-F7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1890129
BLAST score
                   386
E value
                   0.0e+00
Match length
                   406
% identity
                   99
                   Arabidopsis thaliana valyl tRNA synthetase (valRS) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   165584
Seq. ID
                   LIB3177-091-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g132863
BLAST score
                   708
E value
                   5.0e-75
Match length
                   136
% identity
                   97
NCBI Description
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L2
                   >gi_12214_emb_CAA46568 (X65615) ribosomal protein L2
                   [Sinapis alba]
```

E value

7.0e-72

```
Seq. ID
                    LIB3177-091-P1-K1-F9
 Method
                    BLASTN
 NCBI GI
                    g405130
 BLAST score
                    361
 E value
                    0.0e + 00
 Match length
                    373
 % identity
                    99
 NCBI Description
                    Arabidopsis thaliana nuclear-encoded chloroplast stromal
                    cyclophilin (ROC4) mRNA, complete cds
 Seq. No.
                    165586
 Seq. ID
                    LIB3177-091-P1-K1-G1
 Method
                    BLASTX
 NCBI GI
                    g730645
 BLAST score
                    463
 E value
                    2.0e-46
Match length
                    109
 % identity
                    86
NCBI Description
                   40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal
                   protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679
                    (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                   >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15
                   [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza_40S ribosomal protein S15. ESTs
                    gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   165587
Seq. ID
                   LIB3177-091-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g2129577
BLAST score
                   335
E value
                   2.0e-31
Match length
                   76
% identity
                   88
NCBI Description
                   DnaJ homolog protein - Arabidopsis thaliana >gi 727357
                   (U22340) DnaJ homolog [Arabidopsis thaliana]
Seq. No.
                   165588
Seq. ID
                   LIB3177-091-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g267069
BLAST score
                   732
E value
                   6.0e-78
Match length
                   138
% identity
                   99
NCBI Description
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183_pir__JQ1594
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   165589
Seq. ID
                   LIB3177-091-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g4204274
BLAST score
                   681
```

Match length

```
Match length
                    133
 % identity
                    92
 NCBI Description
                    (AC004146) ribulose bisphosphate carboxylase, small subunit
                    [Arabidopsis thaliana]
 Seq. No.
                   165590
 Seq. ID
                   LIB3177-091-P1-K1-G3
 Method
                   BLASTX
 NCBI GI
                   g4539335
 BLAST score
                   215
 E value
                   2.0e-17
Match length
                   86
 % identity
                   53
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                   165591
Seq. ID
                   LIB3177-091-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g1213442
BLAST score
                   747
E value
                   1.0e-79
Match length
                   146
% identity
                   99
NCBI Description
                   (U48961) isopentenyl pyrophosphate isomerase [Arabidopsis
                   thaliana]
Seq. No.
                   165592
Seq. ID
                   LIB3177-091-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g2244750
BLAST score
                   510
E value
                   6.0e-52
Match length
                   113
% identity
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                  >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
Seq. No.
                   165593
Seq. ID
                  LIB3177-091-P1-K1-G6
Method
                   BLASTX
NCBI GI
                  g140285
BLAST score
                  286
E value
                  1.0e-25
Match length
                  60
% identity
                  93
NCBI Description
                  HYPOTHETICAL 19 KD PROTEIN (ORF 168)
                  >gi_2924263_emb_CAA77415_ (Z00044) Ycf3 protein [Nicotiana
                  tabacum]
Seq. No.
                  165594
Seq. ID
                  LIB3177-091-P1-K1-G7
Method
                  BLASTX
NCBÎ GI
                  g2829862
BLAST score
                  512
E value
                  4.0e-52
```

E value

5.0e-39

```
% identity
 NCBI Description
                   (AC002396) Similar to glucosyltransferases [Arabidopsis
 Seq. No.
                   165595
 Seq. ID
                   LIB3177-091-P1-K1-G8
 Method
                   BLASTX
 NCBI GI
                   g4741960
 BLAST score
                   740
 E value
                   7.0e-79
 Match length
                   136
 % identity
                   99
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
 Seq. No.
                   165596
Seq. ID
                   LIB3177-091-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g2865623
BLAST score
                   540
E value
                   2.0e-55
Match length
                   109
% identity
                   99
NCBI Description
                   (AF045286)
                   GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
Seq. No.
                   165597
Seq. ID
                   LIB3177-091-P1-K1-H11
Method
                   BLASTN
NCBI GI
                   g4510360
BLAST score
                   33
E value
                   6.0e-09
Match length
                   65
% identity
                   88
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
                  sequence, complete sequence
Seq. No.
                  165598
Seq. ID
                  LIB3177-091-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2507587
BLAST score
                  284
E value
                  2.0e-25
Match length
                  57
% identity
                  88
NCBI Description
                  METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)
                  >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis
                  thaliana >gi_55\overline{59}76 (U15108) metallothionein-like protein
                  [Arabidopsis thaliana] >gi_1580892 prf 2116236A
                  metallothionein 1 [Arabidopsis thaliana]
Seq. No.
                  165599
Seq. ID
                  LIB3177-091-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4262242
BLAST score
                  387
```

```
Match length
                   95
 % identity
 NCBI Description (AC006200) NADC homolog [Arabidopsis thaliana]
 Seq. No.
                   165600
 Seq. ID
                   LIB3177-091-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q3004560
 BLAST score
                   417
 E value
                   5.0e-41
Match length
                   112
 % identity
                   (AC003673) putative ATP binding protein [Arabidopsis
 NCBI Description
                   thalianal
Seq. No.
                   165601
Seq. ID
                   LIB3177-091-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   g3046849
BLAST score
                   147
E value
                   6.0e-77
Match length
                   408
                   95
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165602
Seq. ID
                   LIB3177-091-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g1172873
BLAST score
                   536
E value
                   5.0e-55
Match length
                   106
% identity
                   100
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                   (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  165603
Seq. ID
                  LIB3177-091-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  g499159
BLAST score
                  313
E value
                  1.0e-176
Match length
                  345
% identity
                  98
NCBI Description A.thaliana mRNA Athb-5
Seq. No.
                  165604
Seq. ID
                  LIB3177-091-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3819164
BLAST score
                  451
E value
                  5.0e-53
Match length
                  116
% identity
                  88
```

```
NCBI Description (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
                   max]
 Seq. No.
                   165605
 Seq. ID
                   LIB3177-091-P1-K1-H8
 Method
                   BLASTX
 NCBI GI
                   g2231312
 BLAST score
                   462
 E value
                   3.0e-46
Match length
                   100
 % identity
                   91
NCBI Description
                   (U75603) AtRab18 [Arabidopsis thaliana]
Seq. No.
                   165606
Seq. ID
                   LIB3177-091-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g2062158
BLAST score
                   376
E value
                   3.0e-36
Match length
                   82
% identity
                   44
NCBI Description
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   165607
                   LIB3177-092-P1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455360
BLAST score
                   138
E value
                   1.0e-08
Match length
                   89
% identity
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                  165608
Seq. ID
                  LIB3177-092-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2407314
BLAST score
                  143
E value
                  2.0e-26
Match length
                  81
% identity
                  67
                  (AF017998) chlorophyll a/b binding protein [Tetraselmis sp.
NCBI Description
                  RG-15]
Seq. No.
                  165609
Seq. ID
                  LIB3177-092-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g3297806
BLAST score
                  224
E value
                  1.0e-123
Match length
                  224
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5
                  (ESSA project)
Seq. No.
                  165610
```

```
Seq. ID
                    LIB3177-092-P1-K1-A12
 Method
                    BLASTN
 NCBI GI
                    q4455262
 BLAST score
                    351
 E value
                    0.0e+00
 Match length
                    351
 % identity
                    100
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                    (ESSAII project)
 Seq. No.
                    165611
 Seq. ID
                    LIB3177-092-P1-K1-A2
 Method
                   BLASTN
 NCBI GI
                   q1769904
 BLAST score
                   149
 E value
                   2.0e-78
 Match length
                   153
 % identity
                   99
 NCBI Description A.thaliana psbP gene
 Seq. No.
                   165612
 Seq. ID
                   LIB3177-092-P1-K1-A4
Method
                   BLASTX
 NCBI GI
                   g3892722
 BLAST score
                   44.
 E value
                   4.0e-51
Match length
                   104
 % identity
                   100
NCBI Description
                   (AL033545) putative protein [Arabidopsis thaliana]
Seq. No.
                   165613
Seq. ID
                   LIB3177-092-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q1617013
BLAST score
                   225
E value
                   1.0e-18
Match length
                   49
% identity
                   90
                  (Y07745) histone H2B like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   165614
Seq. ID
                   LIB3177-092-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g4455223
BLAST score
                   296
E value
                   1.0e-26
Match length
                   101
% identity
                   38
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                  165615
Seq. ID
                  LIB3177-092-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1169201
BLAST score
                  427
E value
```

3.0e-42

Seq. No.

```
Match length
                  129
% identity
                  70
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                  thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  165616
Seq. ID
                  LIB3177-092-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  532
E value
                  2.0e-58
Match length
                  114
% identity
                  93
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  165617
Seq. ID
                  LIB3177-092-P1-K1-B1
Method
                  BLASTX
                  g115767
NCBI GI
BLAST score.
                  643
E value
                  8.0e-70
Match length
                  140
% identity
                  96
NCBI Description, CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir_ A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165618
Seq. ID
                  LIB3177-092-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  q4589436
BLAST score
                  320
E value
                  1.0e-180
Match length
                  340
                  99
% identity
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MPA22, complete sequence
Seq. No.
                  165619
Seq. ID
                  LIB3177-092-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3915865
BLAST score
                  343
E value
                  1.0e-32
Match length
                  67
% identity
                  99
NCBI Description 40S RIBOSOMAL PROTEIN S4
```

```
Seq. ID
                    LIB3177-092-P1-K1-B12
 Method
                    BLASTX
 NCBI GI
                    g1762584
 BLAST score
                    270
 E value
                    7.0e-24
 Match length
                    76
% identity
                    67
 NCBI Description
                    (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
                    [Arabidopsis thaliana]
 Seq. No.
                    165621
 Seq. ID
                    LIB3177-092-P1-K1-B2
Method
                    BLASTX
NCBI GI
                    g4586256
BLAST score
                    56
E value
                    5.0e-47
Match length
                    153
% identity
                    69
NCBI Description
                    (AL049640) probable photosystem I chain XI precursor
                    [Arabidopsis thaliana]
Seq. No.
                    165622
Seq. ID
                    LIB3177-092-P1-K1-B4
Method
                    BLASTN
NCBI GI
                    g1483149
BLAST score
                    209
E value
                    1.0e-114
Match length
                    258
% identity
                    95
NCBI Description
                   Arabidopsis thaliana mRNA for monodehydroascorbate
                    reductase, complete cds
Seq. No.
                    165623
Seq. ID
                    LIB3177-092-P1-K1-B5
Method
                   BLASTX
NCBI GI
                    g421929
BLAST score
                    61
E value
                   5.0e-43
Match length
                   114
% identity
                   13
NCBI Description
                   ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156)
                   ubiquitin [Lycopersicon esculentum]
Seq. No.
                   165624
Seq. ID
                   LIB3177-092-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g114122
BLAST score
                   373
E value
                   6.0e-36
Match length
                   87
% identity
                   84
NCBI Description ADP-RIBOSYLATION FACTOR 2 >gi_423228_pir__A45422
                   ADP-ribosylation factor 2 - bovine >gi_2137127 pir JC4946
                   ADP-ribosylation factor type 2 - mouse >gi_162682 (J03794)
                   ADP-ribosylation factor protein [Bos taurus] >gi_163668
                   (M88292) ADP-ribosylation factor 2 [Bos taurus] >gi 304249 (M88287) ADP-ribosylation factor 2 [Bos taurus] >gi 438864
```

```
>gi_740260 prf_2004472B phospholipase D-activating factor
                  [Bos taurus]
Seq. No.
                  165625
Seq. ID
                  LIB3177-092-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  g2337888
BLAST score
                  228
                  1.0e-125
E value
                  420
Match length
                  98
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F14J16,
                  complete sequence [Arabidopsis thaliana]
                  165626
Seq. No.
                  LIB3177-092-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4544393
                  88
BLAST score
E value
                  3.0e - 34
                  102
Match length
% identity
                  (AC007047) putative ribosomal protein S25 [Arabidopsis
NCBI Description
                  thaliana]
                  165627
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  437
                  3.0e-43
E value
                  137
Match length
                  64
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
                  165628
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  g3641835
BLAST score
                  124
E value
                  3.0e-63
Match length
                  164
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
                  (ESSAII project)
                  165629
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-C10
                  BLASTN
Method
NCBI GI
                  g975645
BLAST score
                  37
E value
                  2.0e-11
                  37
Match length
                  100
% identity
NCBI Description A.thaliana cor47 gene
```

(L12381) ADP-ribosylation factor 2 [Rattus norvegicus] >gi_1565209_dbj_BAA13491_ (D87899) ARF2 [Mus musculus]

Match length

```
Seq. No.
                   165630
Seq. ID
                   LIB3177-092-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g4678924
BLAST score
                   50
                   2.0e-70
E value
Match length
                   139
% identity
                   96
NCBI Description
                  (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3177-092-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q3377835
BLAST score
                   314
                   5.0e-29
E value
Match length
                   108
% identity
                   60
NCBI Description
                   (AF075598) contains similarity to Arabidopsis thaliana
                   downy mildew resistance protein RPP5 (GB:U97106)
                   [Arabidopsis thaliana]
                   165632
Seq. No.
Seq. ID
                   LIB3177-092-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   q2119846
BLAST score
                   654
E value
                   9.0e-69
                   125
Match length
% identity
                   98
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi_3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   165633
Seq. ID
                  LIB3177-092-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  g4757405
BLAST score
                  85
E value
                  6.0e-40
Match length
                  423
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOJ10, complete sequence
Seq. No.
                  165634
Seq. ID
                  LIB3177-092-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q2129637
BLAST score
                  384
E value
                  5.0e-37
```



```
% identity
NCBI Description
                  low temperature-induced protein cor47 - Arabidopsis
                  thaliana >gi_975646_emb_CAA62449_ (X90959) dehydrin
                   [Arabidopsis thaliana]
Seq. No.
                  165635
Seq. ID
                  LIB3177-092-P1-K1-C6
Method
                  BLASTX
                  g4741950
NCBI GI
BLAST score
                  608
E value
                  2.0e-63
                  126
Match length
                  92
% identity
NCBI Description
                  (AF134125) Lhcb2 protein [Arabidopsis thaliana]
                  165636
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q1143511
BLAST score
                  812
E value
                  3.0e-87
                  149
Match length
                  98
% identity
                  (Z47076) Ser/Thr protein phosphatase homologous to PPX
NCBI Description
                  [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein
                  phosphatase [Malus domestica]
Seq. No.
                  165637
Seq. ID
                  LIB3177-092-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g4583542
BLAST score
                  297
E value
                  7.0e-27
Match length
                  136
% identity
                  53
NCBI Description
                  (Y16847) 16 kDa polypeptide of oxygen-evolving complex
                  [Arabidopsis thaliana]
Seq. No.
                  165638
Seq. ID
                  LIB3177-092-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  598
E value
                  3.0e-62
Match length
                  116
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
```

II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I

chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 165639

Seq. ID LIB3177-092-P1-K1-D12

Method BLASTN

```
NCBI GI
                  g4159701
BLAST score
                  373
E value
                  0.0e+00
Match length
                  420
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K22G18, complete sequence
                  165640
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-D3
                  BLASTX
Method
NCBI GI
                  q3367515
                  727
BLAST score
                  3.0e-77
E value
                  147
Match length
% identity
                  98
                  (AC004392) Similar to
NCBI Description
                  glucose-6-phosphate/phosphate-translocator (GPT)
                  gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
Seq. No.
                  165641
                  LIB3177-092-P1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4454036
                  369
BLAST score
                  1.0e-75
E value
Match length
                  137
                  90
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165642
Seq. ID
                  LIB3177-092-P1-K1-D5
                  BLASTX
Method
NCBI GI
                  g1351272
BLAST score
                  435
E value
                  4.0e-43
                  86
Match length
                  98
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550
NCBI Description
                  (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                  thaliana] >gi 742408 prf 2009415A triose phosphate
                  isomerase [Arabidopsis thaliana]
Seq. No.
                  165643
                  LIB3177-092-P1-K1-D6
Seq. ID
                  BLASTX
Method
                  g1168609
NCBI GI
BLAST score
                  531
E value
                  2.0e-54
                  120
Match length
                  88
% identity
                  AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir__$35071
NCBI Description
                  auxin-resistance protein AXR1 - Arabidopsis thaliana
                  >gi 304104 (L13922) ubiquitin-activating enzyme E1
                  [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to
```

Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana]

NCBI GI

```
[Arabidopsis thaliana]
                  165644
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  q166645
BLAST score
                  102
E value
                  4.0e-50
                  152
Match length
                  94
% identity
NCBI Description
                  Arabidopsis thaliana light-harvesting chlorophyll
                  a/b-binding protein (Cab4) mRNA, complete cds
                  165645
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q126766
BLAST score
                  654
E value
                  1.0e-68
                  142
Match length
                  89
% identity
                  MALATE SYNTHASE, GLYOXYSOMAL >gi 68216 pir SYRPMA malate
NCBI Description
                  synthase (EC 4.1.3.2), glyoxysomal - rape >gi 167150
                  (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]
Seq. No.
                  165646
Seq. ID
                  LIB3177-092-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  465
E value
                  8.0e-47
Match length
                  97
                  69
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  165647
Seq. ID
                  LIB3177-092-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q1169476
BLAST score
                  624
E value
                  3.0e-65
Match length
                  123
                  98
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
                  165648
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-E10
Method
                  BLASTX
```

>gi 448755 prf 1917337A ubiquitin-activating enzyme E1

g2244750

```
BLAST score
                   643
E value
                   2.0e-67
Match length
                   124
% identity
                   99
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
Seq. No.
                   165649
Seq. ID
                   LIB3177-092-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   607
E value
                   3.0e-63
Match length
                   114
% identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) (Arabidopsis
                   thaliana]
Seq. No.
                   165650
Seq. ID
                   LIB3177-092-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q231586
BLAST score
                   617
E value
                   2.0e-64
Match length
                   132
% identity
                   92
                   ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_82027_pir__S20504 H+-transporting ATP synthase (EC
3.6.1.34) beta chain, mitochondrial - Para rubber tree
                   >gi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase
                   beta-subunit [Hevea brasiliensis]
Seq. No.
                   165651
Seq. ID
                   LIB3177-092-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   q3128142
BLAST score
                   300
E value
                   1.0e-168
                   316
Match length
% identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MQN23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165652
Seq. ID
                   LIB3177-092-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g480450
BLAST score
                   62
E value
                   1.0e-51
Match length
                   108
% identity
                   89
                   ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                   thaliana >gi_402552_emb_CAA49506 (X69880) ketol-acid
```

reductoisomerase [Arabidopsis thaliana]

Seq. No.

```
Seq. No.
                   165653
Seq. ID
                   LIB3177-092-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g1145699
BLAST score
                   605
E value
                   6.0e-63
Match length
                   126
% identity
                   97
                   (U39486) delta tonoplast integral protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   165654
Seq. ID
                   LIB3177-092-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g166834
BLAST score
                   56
                   9.0e-59
E value
Match length
                   128
% identity
                   93
NCBI Description
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
                   activase [Arabidopsis thaliana] >gi_2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
Seq. No.
                   165655
Seq. ID
                   LIB3177-092-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   g2244991
BLAST score
                   100
                   2.0e-49
E value
Match length
                   128
% identity
                   94
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                  165656
Seq. ID
                  LIB3177-092-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4574208
BLAST score
                   446
E value
                  1.0e-44
Match length
                  92
% identity
                  99
NCBI Description (AF093108) histone H3 [Tortula ruralis]
Seq. No.
                  165657
Seq. ID
                  LIB3177-092-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q4455253
BLAST score
                  569
E value
                  7.0e-59
Match length
                  122
% identity
                  89
NCBI Description
                  (AL035523) superoxide dismutase (EC 1.15.1.1)
                  (Fe) (fragment) [Arabidopsis thaliana]
```

```
Seq. ID
                   LIB3177-092-P1-K1-F10
Method
                . BLASTX
NCBI GI
                   g4469408
BLAST score
                   459
E value
                   8.0e-46
Match length
                   133
% identity
                   71
                   (AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis
NCBI Description
                   thaliana] >gi 4469410 gb AAD21249 (AF116528) MADS box
                   protein FLOWERING LOCUS F [Arabidopsis thaliana]
Seq. No.
                   165659
Seq. ID
                   LIB3177-092-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g4741952
BLAST score
                   703
                   2.0e-74
E value
                   136
Match length
                   70
% identity
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                   165660
Seq. ID
                   LIB3177-092-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   581
                   3.0e-60
E value
                   112
Match length
                   96
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   165661
                   LIB3177-092-P1-K1-F2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g166695
BLAST score
                   34
E value
                   1.0e-09
Match length
                   226
% identity
                  Arabidopsis thaliana recombination and DNA-damage
NCBI Description
                   resistance protein (DRT112) mRNA, complete cds
Seq. No.
                   165662
Seq. ID
                  LIB3177-092-P1-K1-F3
Method
                   BLASTX
NCBI GI
                  g3036805
BLAST score
                   657
E value
                   4.0e-69
Match length
                  127
% identity
                  98
NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]
```

```
Seq. No.
                  165663
Seq. ID
                  LIB3177-092-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3420008
BLAST score
                  240
                4.0e-20
E value
                  123
Match length
% identity
                  38
NCBI Description (AF000307) steroid sulfotransferase 3 [Brassica napus]
Seq. No.
                  165664
                  LIB3177-092-P1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3157944
BLAST score
                  548
E value
                  3.0e-56
Match length
                  109
% identity
                  95
                  (AC002131) Very strong similarity to aminomethyltransferase
NCBI Description
                  precursor gb U79769 from Mesembryanthemum crystallinum.
                  ESTs gb T43167, gb T21076, gb H36999, gb T22773,
                  gb N38038, gb T13742, gb Z26545, gb T20753 and gb W43123
                  come from this ge
                  165665
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-F8
Method
                  BLASTX
                  g115783
NCBI GI
BLAST score
                  568
                  1.0e-58
E value
Match length
                  112
% identity
                  95
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  165666
Seq. ID
                  LIB3177-092-P1-K1-F9
Method
                  BLASTX
                  g2970034
NCBI GI
BLAST score
                  202
                  2.0e-16,
E value
                  50
Match length
                  70
% identity
NCBI Description (D88536) delta 9 desaturase [Arabidopsis thaliana]
                 165667
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-G10
                  BLASTN
Method
                  q2244950
NCBI GI
                  325
BLAST score
                  0.0e+00
E value
Match length
                  341
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
```

fragment No

```
165668
Seq. No.
Seq. ID
                  LIB3177-092-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g3123188
BLAST score
                   685
E value
                   2.0e-72
                   140
Match length
% identity
                   95
NCBI Description
                  CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis
                   thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis
                   thaliana]
Seq. No.
                   165669
Seq. ID
                  LIB3177-092-P1-K1-G12
Method
                  BLASTX
NCBI GI
                   g116343
BLAST score
                   321
E value
                  1.0e-29
Match length
                  138
% identity
                  43
NCBI Description BASIC ENDOCHITINASE PRECURSOR
Seq. No.
                  165670
Seq. ID
                  LIB3177-092-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  g11244
BLAST score
                  38
E value
                  6.0e-13
Match length
                  54
                  93
% identity
                  A.thaliana chloroplast DNA for transfer RNA-Ile and
NCBI Description
                  ribosomal protein
Seq. No.
                  165671
Seq. ID
                  LIB3177-092-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q625977
BLAST score
                  531
E value
                  2.0e-54
Match length
                  108
% identity
                  96
                  p40 protein homolog - Arabidopsis thaliana >gi 402904
NCBI Description
                  (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  165672
Seq. ID
                  LIB3177-092-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  500
E value
                  7.0e-51
Match length
                  97
% identity
                  99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
```

thaliana] Seq. No. 165673 Seq. ID LIB3177-092-P1-K1-G5 Method BLASTX NCBI GI g4741952 BLAST score 430 1.0e-42 E value Match length 98 % identity 83 (AF134126) Lhcb3 protein [Arabidopsis thaliana] NCBI Description 165674 Seq. No. Seq. ID LIB3177-092-P1-K1-G6 BLASTX Method NCBI GI g2583125 77 BLAST score 1.1e-01 E value 54 Match length % identity 65 NCBI Description (AC002387) putative transketolase precursor [Arabidopsis thaliana] 165675 Seq. No. Seq. ID LIB3177-092-P1-K1-G7 Method BLASTX NCBI GI g2244750 543 BLAST score 9.0e-56 E value 113 Match length % identity 96 NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana] 165676 Seq. No. Seq. ID LIB3177-092-P1-K1-G8 BLASTX Method NCBI GI g3080415 BLAST score 514 E value 2.0e-52 Match length 111 82 % identity (AL022604) cysteine proteinase-like protein [Arabidopsis NCBI Description thaliana] 165677 Seq. No. LIB3177-092-P1-K1-G9 Seq. ID BLASTX Method q1172873 NCBI GI 459 BLAST score 5.0e-46 E value Match length 117 % identity 74 CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719 NCBI Description

drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374

(D13043) thiol protease [Arabidopsis thaliana] Seq. No. 165678 Seq. ID LIB3177-092-P1-K1-H1 Method BLASTX NCBI GI g687844 BLAST score 292 E value 2.0e-26 Match length 119 % identity 50 (U21320) contains TPR domain-like repeats [Caenorhabditis NCBI Description elegans] Seq. No. 165679 Seq. ID LIB3177-092-P1-K1-H10 Method BLASTX NCBI GI g3913733 BLAST score 734 E value 4.0e-78 Match length 141 % identity 97 NCBI Description HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME (GLYOXALASE II) (GLX II) >gi_1924921_emb_CAA69644 (Y08357) hydroxyacylglutathione hydrolase [Arabidopsis thaliana] Seq. No. 165680 LIB3177-092-P1-K1-H11 Seq. ID Method BLASTX NCBI GI g132110

```
BLAST score
                  594
E value
                  9.0e-62
Match length
                  112
% identity
                  97
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  165681
                  LIB3177-092-P1-K1-H2
Seq. ID
                  BLASTX
                  q3688173
```

Method NCBI GI BLAST score 384 E value 6.0e-46 Match length 133 % identity

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 165682 Seq. ID LIB3177-092-P1-K1-H3 Method BLASTX NCBI GI q3550519 BLAST score 493 E value 7.0e-50 Match length

Match length

```
% identity
                   80
NCBI Description
                  (AJ007630) oxygenase [Nicotiana tabacum]
Seq. No.
                   165683
Seq. ID
                   LIB3177-092-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   g4678315
BLAST score
                   150
E value
                   9.0e-79
Match length
                   173
% identity
                   97
                  Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15
NCBI Description
                   (ESSA project)
Seq. No.
                  165684
Seq. ID
                  LIB3177-092-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                   666
E value
                  2.0e-71
Match length
                  138
                   98
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165685
Seq. ID
                  LIB3177-092-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3319347
BLAST score
                  305
E value
                  3.0e-28
Match length
                  72
% identity
                  82
NCBI Description (AF077407) No definition line found [Arabidopsis thaliana]
Seq. No.
                  165686
Seq. ID
                  LIB3177-092-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q4006934
BLAST score
                  411
E value
                  2.0e-40
Match length
                  100
% identity
                  76
NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                  165687
Seq. ID
                  LIB3177-092-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g3985952
BLAST score
                  340
E value
                  0.0e + 00
```

```
98
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MRC8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165688
                   LIB3177-092-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2199574
BLAST score
                   394
E value
                   1.0e-38
Match length
                   76
% identity
                   99
NCBI Description
                  (AF004293) aquaporin [Brassica rapa]
                   165689
Seq. No.
Seq. ID
                   LIB3177-093-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g3738088
BLAST score
                   363
E value
                   0.0e+00
Match length
                   425
% identity
                   96
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T30L20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165690 '
Seq. ID
                  LIB3177-093-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2129583
BLAST score
                   329
E value
                  1.0e-30
Match length
                  84
% identity
                  82
NCBI Description
                  ferritin - Arabidopsis thaliana >gi_1246401_emb_CAA63932
                   (X94248) ferritin [Arabidopsis thalīana]
Seq. No.
                  165691
Seq. ID
                  LIB3177-093-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g3341671
BLAST score
                  273
E value
                  1.0e-152
Match length
                  431
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F16B22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165692
Seq. ID
                  LIB3177-093-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q3695023
BLAST score
                  242
E value
                  2.0e-20
Match length
                  96
% identity
                  51
NCBI Description (AF055850) unknown [Arabidopsis thaliana]
```

```
Seq. No.
                    165693
 Seq. ID
                    LIB3177-093-P1-K1-A2
 Method
                    BLASTX
 NCBI GI
                    g1710780
 BLAST score
                    501
 E value
                    9.0e-51
 Match length
                    131
                                                                 e .
 % identity
                    74
                    40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917 emb CAA65433
 NCBI Description
                     (X96613) cytoplasmic ribosomal protein S7 [Podospora
                    anserina]
 Seq. No.
                    165694
 Seq. ID
                    LIB3177-093-P1-K1-A3
 Method
                    BLASTN
 NCBI GI
                    g4584351
 BLAST score
                    302
 E value
                    1.0e-169
                    357
 Match length
 % identity
                    96
 NCBI Description
                    Arabidopsis thaliana chromosome II BAC T12H3 genomic
                    sequence, complete sequence
                    165695
 Seq. No.
                                                           ٠,٠
· Seq. ID
                    LIB3177-093-P1-K1-A4
 Method
                    BLASTN
 NCBI GI
                    g2351073
 BLAST score
                    175
                    1.0e-93
 E value
                    400
 Match length
 % identity
                    98
 NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MYJ24, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    165696
 Seq. ID
                    LIB3177-093-P1-K1-A5
 Method
                    BLASTN
 NCBI GI
                    g3004543
 BLAST score
                    55
 E value
                    5.0e-22
 Match length
                    280
 % identity
                    86
 NCBI Description
                    Arabidopsis thaliana chromosome II BAC F19F24 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
                    165697
 Seq. No.
 Seq. ID
                    LIB3177-093-P1-K1-A6
 Method
                    BLASTX
 NCBI GI
                    g232031
 BLAST score
                    336
                    2.0e-31
 E value
                    116
 Match length
                    54
 % identity
                    ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224
translation elongation factor eEF-1 beta' chain - rice
 NCBI Description
                    >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                    [Oryza sativa]
```

BLAST score

```
Seq. No.
                  165698
Seq. ID
                  LIB3177-093-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g4538963
BLAST score
                  66
E value
                  1.0e-57
                  111
Match length
% identity
                  75
                  (AL049488) chlorophyll a/b-binding protein-like
NCBI Description
                  [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                  (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                  165699
Seq. ID
                  LIB3177-093-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g131770
BLAST score
                  271
                  6.0e-24
E value
Match length
                  94
% identity
                  56
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
                  (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                  [Dictyostelium discoideum]
Seq. No.
                  165700
Seq. ID
                  LIB3177-093-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g166879
BLAST score
                  197
                  1.0e-107
E value
Match length
                  232
% identity
                . 97
NCBI Description A.thaliana gene sequence, exon
Seq. No.
                  165701
                  LIB3177-093-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  716
E value
                  5.0e-76
Match length
                  134
                  99
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  165702
                  LIB3177-093-P1-K1-B11 `
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4335745
```

```
E value
                    1.0e-39
 Match length
                    142
 % identity
                    55
 NCBI Description
                   (AC006284) putative hydrolase (contains an
                   esterase/lipase/thioesterase active site serine domain
                  " (prosite: PS50187) [Arabidopsis thaliana]
 Seq. No.
                   165703
 Seq. ID
                   LIB3177-093-P1-K1-B12
 Method
                   BLASTX
 NCBI GI
                   g4512655
 BLAST score
                   401
 E value
                   4.0e-39
 Match length
                   74
 % identity
                   99
 NCBI Description
                   (AC007048) putative protein phosphatase 2C [Arabidopsis
                   thaliana]
 Seq. No.
                   165704
 Seq. ID
                   LIB3177-093-P1-K1-B2
 Method
                   BLASTX
NCBI GI
                   g1351271
BLAST score
                   666
E value
                   4.0e-70
Match length
                   144
% identity
NCBI Description
                   TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
                   >gi_1084309_pir__S52032 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - spinach >gi_806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
Seq. No.
                   165705
Seq. ID
                   LIB3177-093-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g4454036
BLAST score
                   807
E value
                   1.0e-86
Match length
                   148
% identity
                   100
NCBI Description
                  (AL035394) putative major latex protein [Arabidopsis
                  thaliana]
Seq. No.
                  165706
Seq. ID
                  LIB3177-093-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g115385
BLAST score
                  615
E value
                  4.0e-64
Match length
                  123
% identity
                  98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165707
Seq. ID
                  LIB3177-093-P1-K1-B5
```

```
Method
                    BLASTN
NCBI GI
                    g2645198
BLAST score
                    45
E value
                    5.0e-16
Match length
                    162
 % identity
                    83
NCBI Description
                   Arabidopsis thaliana chromosome I BAC T26J12 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    165708
Seq. ID
                   LIB3177-093-P1-K1-B6
Method
                   BLASTX
NCBI GI
                    g115767
BLAST score
                    734
E value
                    4.0e-78
Match length
                   142
                   97
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi 16368_emb CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   165709
Seq. ID
                   LIB3177-093-P1-K1-B7
Method
                   BLASTN
NCBI GI
                   g4115352
BLAST score
                   77
E value
                   3.0e - 35
Match length
                   168
                   93
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T15J14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165710
Seq. ID
                   LIB3177-093-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   q1082054
BLAST score
                   150
E value
                   1.0e-09
Match length
                   136
% identity
                   30
NCBI Description
                   (Z49859) copper transporter protein [Arabidopsis thaliana]
Seq. No.
                   165711
Seq. ID
                   LIB3177-093-P1-K1-B9
Method
                   BLASTN
NCBI GI
                   g2673901
BLAST score
                   251
E value
                   1.0e-139
Match length
                   449
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T24P15 genomic
```

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  165712
Seq. ID
                  LIB3177-093-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  745
E value
                  2.0e-79
Match length
                  143
% identity
                  99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165713
Seq. ID
                  LIB3177-093-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  g4757392
BLAST score
                  83
                  9.0e-39
E value
Match length
                  219
% identity
                  85
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14A17, complete sequence
Seq. No.
                  165714
Seq. ID
                  LIB3177-093-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g3241923
BLAST score
                  361
E value
                  0.0e+00
                  361
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165715
Seq. ID
                  LIB3177-093-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3600058
BLAST score
                  526
E value
                  1.0e-53
Match length
                  110
% identity
                  (AF080120) similar to vacuolar ATPases [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165716
Seq. ID
                  LIB3177-093-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1171642
BLAST score
                  188
E value
                  5.0e-14
                  73
Match length
% identity
                  49
```

Seq. No.

```
NCBI Description PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
                   >gi 481206 pir S38326 protein kinase - Arabidopsis
                   thaliana >gi_166809 (L07248) protein kinase [Arabidopsis
                   thaliana]
                   165717
 Seq. No.
 Seq. ID
                   LIB3177-093-P1-K1-C5
 Method
                   BLASTX
 NCBI GI
                   g132102
 BLAST score
                   724
 E value
                   6.0e-77
 Match length
                   137
 % identity
                   98
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
 NCBI Description
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                   ribulose-bisphosphate carboxylase (EC 4.\overline{1.1.39}) small chain
                   B2 precursor - Arabidopsis thaliana >gi_16194 emb CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
 Seq. No.
                   165718
 Seq. ID
                   LIB3177-093-P1-K1-C6
 Method
                   BLASTN
 NCBI GI
                   g4757392
· BLAST score
                   68
 E value
                   3.0e - 30
 Match length
                   116
 % identity
                   90
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                   K14A17, complete sequence
 Seq. No.
                   165719
 Seq. ID
                   LIB3177-093-P1-K1-C8
 Method
                  BLASTX
                   g99696
 NCBI GI
 BLAST score
                   801
 E value
                   5.0e-86
 Match length
                   144
                   99
 % identity
 NCBI Description
                   glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                   chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                   >gi_240070 bbs 69728 (S69727) light-regulated glutamine
                   synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                   aa] [Arabidopsis thaliana] >gi 228453 prf 1804333A Gln
                   synthetase [Arabidopsis thaliana]
                   165720
 Seq. No.
 Seq. ID
                   LIB3177-093-P1-K1-C9
 Method
                   BLASTX
NCBI GI
                   q2244863
BLAST score
                   174
                   2.0e-12
E value
Match length
                   132
 % identity
                   38
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. ID
                     LIB3177-093-P1-K1-D11
 Method
                     BLASTX
 NCBI GI
                     g4115925
 BLAST score
                     690
 E value
                     5.0e-73
 Match length
                     135
 % identity
                     60
 NCBI Description
                     (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                    >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
                     [Arabidopsis thaliana]
 Seq. No.
                    165722
Seq. ID
                    LIB3177-093-P1-K1-D12
 Method
                    BLASTX
 NCBI GI
                    q4006898
 BLAST score
                    304
 E value
                    8.0e-28
 Match length
                    58
 % identity
NCBI Description
                    (Z99708) splicing factor-like protein [Arabidopsis
                    thaliana]
                                                                                į.
Seq. No.
                    165723
Seq. ID
                    LIB3177-093-P1-K1-D2
Method
                    BLASTX
«NCBI GI
                    q2829871
BLAST score
                    792
E value
                    7.0e-85
Match length
                    150
% identity
                    99
NCBI Description
                   (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    165724
Seq. ID
                    LIB3177-093-P1-K1-D3
Method
                    BLASTX
NCBI GI
                    g132102
BLAST score
                    639
E value
                    5.0e-67
Match length
                    128
% identity
                    95
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1.1.39}) small chain
                   B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana]
Seq. No.
                    165725
Seq. ID
                   LIB3177-093-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g2956690
BLAST score
                   443
E value
                   1.0e-48
Match length
                   135
% identity
NCBI Description
                   (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928
```

```
(AF079800) PsbY precursor [Arabidopsis thaliana]
 Seq. No.
                   165726
 Seq. ID
                   LIB3177-093-P1-K1-D6
 Method
                   BLASTX
 NCBI GI
                   g132090
 BLAST score
                   208
 E value ·
                   7.0e-17
 Match length
                   50
 % identity
                   84
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
 Seq. No.
                   165727
 Seq. ID
                   LIB3177-093-P1-K1-D7
 Method
                   BLASTX
 NCBI GI
                   g4678259
 BLAST score
                   555
 E value
                   4.0e-57
Match length
                   144
 % identity
                   78
NCBI Description (AL049657) putative protein [Arabidopsis thaliana]
Seq. No.
                   165728
Seq. ID
                   LIB3177-093-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g2062164
BLAST score
                   403
E value
                   1.0e-39
Match length
                   76
% identity
                   99
NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                  .165729
Seq. ID
                  LIB3177-093-P1-K1-E1
Method
                  BLASTX
NCBI GI
                   q4581146
BLAST score
                  734
E value
                   4.0e-78
Match length
                  152
% identity
                  93
                 (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                  cytoplasmic [Arabidopsis thaliana]
Seq. No.
                  165730
Seq. ID
                  LIB3177-093-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  g3236234
BLAST score
                  148
E value
                  1.0e-77
Match length
                  279
% identity
                  98
```

E value

1.0e-64

```
NCBI Description Arabidopsis thaliana chromosome II BAC F13M22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165731
Seq. ID
                   LIB3177-093-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g3377797
BLAST score
                   336
E value
                   2.0e-31
Match length
                   67
                   99
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
Seq. No.
                   165732
Seq. ID
                  LIB3177-093-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g166834
BLAST score
                   662
E value
                   9.0e-70
Match length
                  128
% identity
                  98
NCBI Description
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
                  activase [Arabidopsis thaliana] >gi_2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
Seq. No.
                  165733
Seq. ID
                  LIB3177-093-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  q4309719
BLAST score
                  294
                  1.0e-164
E value
Match length
                  400
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T30D6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165734
Seq. ID
                  LIB3177-093-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q4678332
BLAST score
                  150
E value
                  1.0e-09
Match length
                  85
% identity
                  (AL049658) putative peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165735
Seq. ID
                  LIB3177-093-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  618
```

Method

NCBI GI

BLASTX

g3288821

```
119
Match length
% identity.
                  98
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165736
Seq. ID
                  LIB3177-093-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g401169
BLAST score
                  262
E value
                  5.0e-23
                  53
Match length
% identity
                  94
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
Seq. No.
                  165737
                  LIB3177-093-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4218123
BLAST score
                  441
E value
                  1.0e-43
Match length
                  143
% identity
                  65
                  (AL035353) photosystem I subunit PSI-E-like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  165738
Seq. ID
                  LIB3177-093-P1-K1-E9
Method
                 BLASTX
NCBI GI
                  g1709825
BLAST score
                  663
E value
                  9.0e-70
Match length
                  134
                  100
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  165739
Seq. ID
                  LIB3177-093-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  q2088638
BLAST score
                  232
E value
                  1.0e-127
Match length
                  465
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165740
Seq. ID
                  LIB3177-093-P1-K1-F10
```

BLAST score

```
BLAST score
                   505
E value
                   2.0e-51
Match length
                   113
% identity
                   86
NCBI Description
                   (AF063901) alanine:glyoxylate aminotransferase;
                   transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                   alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                   165741
Seq. ID
                   LIB3177-093-P1-K1-F11
Method
                   BLASTN
NCBI GI
                   g2264317
BLAST score
                   55
E value
                   5.0e-22
Match length
                   196
% identity
                   87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165742
Seq. ID
                   LIB3177-093-P1-K1-F12
Method
                   BLASTN
NCBI GI
                   g3297806
BLAST score
                   39
E value
                   1.0e-12
Match length
                   288
                   87
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5
                   (ESSA project)
Seq. No.
                   165743
                  LIB3177-093-P1-K1-F3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4454022
BLAST score
                   210
E value
                   1.0e-115
Match length
                   230
% identity
                   98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
                   (ESSAII project)
Seq. No.
                  165744
Seq. ID
                  LIB3177-093-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4678935
BLAST score
                   637
E value
                   2.0e-69
Match length
                  152
% identity
NCBI Description (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
                  165745
Seq. ID
                  LIB3177-093-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q2245144
```

Method

BLASTX

```
E value
                  1.0e-44
Match length
                  138
% identity
                  64
                  (Y10846) O-acetylserine(thiol) lyase [Brassica juncea]
NCBI Description
Seq. No.
                  165746
Seq. ID
                  LIB3177-093-P1-K1-F7
                  BLASTX
Method
NCBI GI
                  q2415406
                  150
BLAST score
                  1.0e-09
E value
                  84
Match length
                  37
% identity
                  (AF015775) YodT [Bacillus subtilis]
NCBI Description
                  >gi 2634366 emb CAB13865 (Z99114) similar to
                  adenosylmethionine-8-amino-7-oxononanoate aminotransferase
                  [Bacillus subtilis]
                  165747
Seq. No.
Seq. ID
                  LIB3177-093-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  184
                  4.0e-99
E value
                  313
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  165748
Seq. No.
Seq. ID
                  LIB3177-093-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g548604
BLAST score
                  483
                  6.0e-49
E value
                  102
Match length
% identity
                  86
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi 1076728 pir S51813 photosystem-I PSI-F chain precursor
                  - barley >gi_469560 (U08135) photosystem-I PSI-F subunit
                  precursor [Hordeum vulgare]
                  165749
Seq. No.
Seq. ID
                  LIB3177-093-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4539316
BLAST score
                  633
E value
                  4.0e-69
                  144
Match length
                  98
% identity
                  (AL035679) putative fructose-bisphosphate aldolase
NCBI Description
                  [Arabidopsis thaliana]
                  165750
Seq. No.
Seq. ID
                  LIB3177-093-P1-K1-G10
```

```
NCBI GI
                   q4454036
BLAST score
                   492
E value
                   5.0e-50
Match length
                  91
                   99
% identity
                   (AL035394) putative major latex protein [Arabidopsis
NCBI Description
Seq. No.
                   165751
Seq. ID
                  LIB3177-093-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  q3108025
BLAST score
                  309
E value
                  1.0e-174
Match length
                  317
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T13D8, complete
                  sequence [Arabidopsis thaliana]
Seq. No.
                  165752
Seq. ID
                  LIB3177-093-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g135860
                  576
BLAST score
E value
                  1.0e-59
Match length
                  116
                  100
% identity.
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi 99761 pir S22202 tonoplast intrinsic
                  protein gamma - Arabidopsīs thaliana
                  >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi 166732
                  (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >gi 445129 prf 1908432B tonoplast intrinsic protein gamma
                  [Arabidopsis thaliana]
Seq. No.
                  165753
Seq. ID
                  LIB3177-093-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  504
E value
                  4.0e-51
Match length
                  118
% identity
                  83
NCBI Description
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  165754
Seq. ID
                  LIB3177-093-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q66618
BLAST score
                  622
E value
                  6.0e-65
Match length
                  141
% identity
                  87
NCBI Description
                  3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
```

precursor - Arabidopsis thaliana

% identity .

```
Seq. No.
                      165755
  Seq. ID
                      LIB3177-093-P1-K1-G4
 Method
                      BLASTX
  NCBI GI
                      g1169599
  BLAST score
                      574
                      2.0e-59
  E value
 Match length
                      125
  % identity
                      86
                     OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
  NCBI Description
                      >gi_541883_pir__JQ2336 omega-3 fatty acid desaturase (EC
1.14.99.-) CFD - Arabidopsis thaliana >gi_408481 (L22961)
                      omega-3 fatty acid desaturase [Arabidopsis thaliana]
                      >gi_468434_dbj_BAA05040_ (D26019) plastid fatty acid
desaturase [Arabidopsis thaliana] >gi_541653_dbj_BAA03106_
                      (D14007) omega-3-desaturase [Arabidopsis thaliana]
                      165756
 Seq. No.
 Seq. ID
                      LIB3177-093-P1-K1-G5
 Method
                      BLASTN
 NCBI GI
                      g2673901
 BLAST score
                      255
 E value
                      1.0e-141
                      423

    Match length

                      99
  % identity
 NCBI Description
                     Arabidopsis thaliana chromosome II BAC T24P15 genomic
                      sequence, complete sequence [Arabidopsis thaliana]
                      165757
 Seq. No.
 Seq. ID
                     LIB3177-093-P1-K1-G6
 Method
                     BLASTN
 NCBI GI
                      g4741184
 BLAST score
                      321
 E value
                      0.0e+00
                      347
 Match length
                     100
 % identity
 NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7
                      (ESSA project)
 Seq. No.
                     165758
 Seq. ID
                     LIB3177-093-P1-K1-G7
 Method
                     BLASTX
 NCBI GI
                     g4210334
 BLAST score
                     150
 E value
                     1.0e-09
 Match length
                     29
 % identity
                     97
 NCBI Description
                     (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
                      [Arabidopsis thaliana]
 Seq. No.
                     165759
 Seq. ID
                     LIB3177-093-P1-K1-G9
 Method
                     BLASTN
 NCBI GI
                     g4468801
 BLAST score
                     290
 E value
                     1.0e-162
 Match length
                     294
                     100
```

Match length

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
                    (ESSA project)
Seq. No.
                    165760
Seq. ID
                    LIB3177-093-P1-K1-H10
Method
                    BLASTX
NCBI GI
                    g2129729
BLAST score
                    633
E value
                    3.0e-66
Match length
                    124
% identity
                    98
NCBI Description senescence-associated protein sen1 - Arabidopsis thaliana
                    >gi_1046270 (U26945) senescence-associated protein
                    [Arabidopsis thaliana] >gi_3367595_emb_CAA20047_ (AL031135) senescence-associated protein sen1 [Arabidopsis thaliana]
                    >gi_3805843_emb_CAA21463_ (AL031986) senescence-associated protein sen1 [Arabidopsis thaliana]
Seq. No.
                    165761
Seq. ID
                    LIB3177-093-P1-K1-H11
Method
                    BLASTX
NCBI GI
                    g1931655
BLAST score
                    181
E value
                    1.0e-13
Match length
                    36
% identity
NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana]
Seq. No.
                   165762
                   LIB3177-093-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539405
BLAST score
                   287
E value
                   2.0e-26
Match length
                   73
% identity
NCBI Description
                   (AL049524) putative ribosomal protein L9, cytosolic
                   [Arabidopsis thaliana]
Seq. No.
                   165763
Seq. ID
                   LIB3177-093-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q2257743
BLAST score
                   232
E value
                   1.0e-19
Match length
                   58
% identity
                   84
                   (U62020) lysine-sensitive aspartate kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   165764
Seq. ID
                   LIB3177-093-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g1703108
BLAST score
                   414
E value
                   1.0e-71
```

Seq. No.

Seq. ID

Method

NCBI GI

165769

BLASTX

q126766

LIB3177-093-P1-K1-H8

```
97
 % identity
                    ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
NCBI Description
                     thaliana] >g\overline{i} 1943863 (U27811) actin7 (Arabidopsis
                thaliana]
Seq. No.
                    165765
Seq. ID
                    LIB3177-093-P1-K1-H4
Method
                    BLASTN
NCBI GI
                    g2275194
BLAST score
                    254
E value
                    1.0e-141
Match length
                    262
% identity
                    100
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T08I13 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    165766
Seq. ID
                    LIB3177-093-P1-K1-H5
Method
                    BLASTX
NCBI GI
                    g4587525
BLAST score
                    210
E value
                    5.0e-17
Match length
                    90
% identity
                    48
NCBI Description
                    (AC007060) Contains the PF_00650 CRAL/TRIO
                    phosphatidyl-inositol-transfer protein domain. ESTs
                    gb_T76582, gb_N06574 and gb_Z25700 come from this gene.
                    [Arabidopsis thaliana]
Seq. No.
                    165767
                    LIB3177-093-P1-K1-H6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3738261
BLAST score
                    284
E value
                    2.0e-25
Match length
                    97
% identity
                    68
NCBI Description
                    (AB018412) chloroplast phosphoglycerate kinase [Populus
                    nigra]
Seq. No.
                    165768
Seq. ID
                    LIB3177-093-P1-K1-H7
Method
                    BLASTX
NCBĮ GI
                    g2257743
BLAST score
                    241
E value
                    1.0e-20
Match length
                    58
% identity
NCBI Description
                   (U62020) lysine-sensitive aspartate kinase [Arabidopsis
                   thaliana]
```

22283

٠..

NCBI GI

```
49
BLAST score
                   2.0e-71
E value
Match length
                   139
% identity
                   97
                  MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate
NCBI Description
                   synthase (EC 4.1.3.2), glyoxysomal - rape >gi 167150
                   (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]
Seq. No.
                   165770
Seq. ID
                   LIB3177-093-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q3023216
                   505
BLAST score
E value
                   3.0e-51
Match length
                   105
% identity
                   98
                  14-3-3-LIKE PROTEIN GF14 MU >gi 1531629 (U60444) GF14 mu
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   165771
Seq. ID
                  LIB3177-094-P1-K1-A1
Method
                  BLASTX
NCBI GI
                   g3025205
BLAST score
                   157
E value 🦠
                  1.0e-10
Match length
                  103
                   33
% identity
                  HYPOTHETICAL 65.1 KD PROTEIN SLR1919
NCBI Description
                  >gi 1652223_dbj_BAA17147_ (D90903) ABC1-like [Synechocystis
                   sp.]
Seq. No.
                  165772
Seq. ID
                  LIB3177-094-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q126985
BLAST score
                  643
E value
                  2.0e-67
Match length
                  126
% identity
                  98
NCBI Description
                  MERI-5 PROTEIN >gi 166778 (M63166) meri-5 [Arabidopsis
                  thaliana]
                  165773
Seq. No.
                  LIB3177-094-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062158
BLAST score
                  592
E value '
                  2.0e-61
Match length
                  122
% identity
                  47
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
                  165774
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-A12
Method
                  BLASTX
```

22284

g1370188

```
BLAST score
                  404
E value
                  1.0e-39
Match length
                  96
                  84
% identity
NCBI Description
                  (Z73943) RAB7D [Lotus japonicus]
                  165775
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q2497733
BLAST score
                  570
                  7.0e-59
E value
                  118
Match length
                  95
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >gi 1177796 (M80567) non-specific lipid transfer protein
                  [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  165776
Seq. ID
                  LIB3177-094-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  g3600062
                  122
BLAST score
E value
                  2.0e-62
Match length
                  215
% identity
                  68
NCBI Description Arabidopsis thaliana BAC T25C13
Seq. No.
                  165777
Seq. ID
                  LIB3177-094-P1-K1-A4
Method
                  BLASTX
                  g4827050
NCBI GI
BLAST score
                  357
                  6.0e-34
E value
Match length
                  121
                  55
% identity
NCBI Description
                  ubiquitin specific protease 14 (tRNA-quanine
                  transglycosylase) >gi 1729927 sp P54578 TGT HUMAN QUEUINE
                  TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE)
                  (GUANINE INSERTION ENZYME) >gi 940182 (U30888) tRNA-Guanine
                  Transglycosylase [Homo sapiens]
```

Seq. No. 165778

Seq. ID LIB3177-094-P1-K1-A5

Method BLASTX
NCBI GI g4586256
BLAST score 365
E value 4.0e-35
Match length 83
% identity 88

NCBI Description (AL049640) probable photosystem I chain XI precursor

[Arabidopsis thaliana]

Seq. No. 165779

Seq. ID LIB3177-094-P1-K1-A6

Method BLASTX

```
NCBI GI
                    g4538963
BLAST score
                    141
                    5.0e-09
E value
                    30
Match length
                    97
% identity
NCBI Description
                    (AL049488) chlorophyll a/b-binding protein-like
                     [Arabidopsis thaliana] >gi_4741958 gb_AAD28776.1_AF134129 1
                    (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                    165780
Seq. ID
                  LIB3177-094-P1-K1-A7
Method
                 · BLASTX
NCBI GI
                    q1076366
BLAST score
                    678
E value
                    1.0e-71
Match length
                    130
                    98
% identity
NCBI Description
                    peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis
                    thaliana >gi 460968 (U07276) peptidyl-prolyl cis-trans
                    isomerase [Arabidopsis thaliana] >gi 992643 (U32186)
                    cyclophilin [Arabidopsis thaliana]
                    >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase
                    [Arabidopsis thaliana]
Seq. No.
                    165781
Seq. ID
                    LIB3177-094-P1-K1-A8
Method
                    BLASTX
NCBI GI
                    g1076440
BLAST score
                    375
E value
                    4.0e-36
Match length
                    84
% identity
                    86
                   acyl-CoA binding protein - rape >gi_1076441_pir__S49102
acyl-CoA binding protein - rape >gi_509265_emb_CAA54390_
(X77134) acyl-CoA binding protein [Brassica napus]
NCBI Description
Seq. No.
                    165782
                    LIB3177-094-P1-K1-A9
Seq. ID
Method
                    BLASTN
NCBI GI
                    g3413696
BLAST score
                    386
E value
                    0.0e+00
Match length
                    425
% identity
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T19L18 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    165783
Seq. ID
                    LIB3177-094-P1-K1-B1
Method
                    BLASTX
NCBI GI
                    g4584110
BLAST score
                    306
E value
                    5.0e-28
Match length
                    119
% identity
                    50
NCBI Description (AJ133639) SAH7 protein [Arabidopsis thaliana]
```

NCBI Description

```
Seq. No.
                     165784
  Seq. ID
                     LIB3177-094-P1-K1-B10
  Method
                     BLASTX
  NCBI GI
                     g3023848
  BLAST score
                     462
  E value
                    2.0e-46
  Match length
                    111
  % identity
                    85
  NCBI Description
                    GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                    PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                    >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis
                    thaliana]
  Seq. No.
                    165785
  Seq. ID
                    LIB3177-094-P1-K1-B11
 Method
                    BLASTX
 NCBI GI
                    g115385
 BLAST score
                    464
 E value
                    1.0e-46
 Match length
                    90
 % identity
                    100
 NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                    chlorophyll a/b binding protein [Arabidopsis thaliana]
 Seq. No.
                   .165786
 Seq. ID
                   LIB3177-094-P1-K1-B12
 Method
                   BLASTX
 NCBI GI
                   g973313
 BLAST score
                   538
 E value
                   4.0e-55
 Match length
                   111
 % identity
                   93
 NCBI Description
                   (U30250) myo-inositol 1-phosphate synthase isozyme-2
                   [Arabidopsis thaliana]
Seq. No.
                   165787
Seq. ID
                   LIB3177-094-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   q4753655
BLAST score
                   407
E value
                   8.0e-40
Match length
                   115
% identity
                   65
NCBI Description
                   (AL049751) pectate lyase like protein [Arabidopsis
                   thaliana]
Seq. No.
                   165788
Seq. ID
                   LIB3177-094-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   g2264316
BLAST score
                   46
E value
                  8.0e-17
Match length
                  304
% identity
```

MRO11, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

```
165789
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-B6
                  BLASTX
Method
NCBI GI
                   g2651314
BLAST score
                   379
E value
                   1.0e-36
                   109
Match length
% identity
                   70
                   (ACO02336) putative ribosomal protein S26 [Arabidopsis
NCBI Description
                   thaliana]
                   165790
Seq. No.
                   LIB3177-094-P1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2052379
BLAST score
                   632
                   3.0e-66
E value
                   120
Match length
% identity
                   98
NCBI Description
                   (U66343) calreticulin [Arabidopsis thaliana]
Seq. No.
                   165791
                  LIB3177-094-P1-K1-B8.
Seq. ID
Method
                   BLASTN
                  g2618602
NCBI GI
BLAST score
                   359
                   0.0e+00
E value
                   445
Match length
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165792
Seq. ID
                   LIB3177-094-P1-K1-B9
Method
                  BLASTN
NCBI GI
                   g4584351
BLAST score
                   303
                   1.0e-170
E value
                   342
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC T12H3 genomic
NCBI Description
                   sequence, complete sequence
                  165793
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-C10
Method
                  BLASTX
NCBI GI
                   g2393775
BLAST score
                   286
                  1.0e-25
E value
                   58
Match length
                   81
% identity
                  (U82230) prolamin box binding factor [Zea mays]
NCBI Description
                  165794
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-C11
Method
                  BLASTX
```

```
NCBI GI
                  q3122724
BLAST score
                   351
E value
                  3.0e-33
                  69
Match length
                  100
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
                  protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                  165795
Seq. ID
                  LIB3177-094-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  q4587641
BLAST score
                  352
E value
                  0.0e + 00
Match length
                  422
% identity
                  96
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                  165796
Seq. ID
                  LIB3177-094-P1-K1-C2
                  BLASTX
Method
NCBI GI
                  q4263525
                  590
BLAST score
E value
                  3.0e-61
Match length
                  138
% identity
                  84
NCBI Description
                  (AC004044) putative photosystem I reaction center subunit
                  II precursor [Arabidopsis thaliana]
Seq. No.
                  165797
Seq. ID
                  LIB3177-094-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3786014
BLAST score
                  435
E value
                  4.0e-43
Match length
                  130
% identity
                  81
NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  165798
Seq. ID
                  LIB3177-094-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3885511
BLAST score
                  431
E value
                  1.0e-42
Match length
                  109
% identity
                  80
NCBI Description
                  (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
Seq. No.
                  165799
Seq. ID
                  LIB3177-094-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g4455348
BLAST score
                  358
```

0.0e+00

E value

```
457
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8
NCBI Description
                   (ESSAII project)
                  165800
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-C7
                  BLASTX
Method
NCBI GI
                  g119975
BLAST score
                   516
E value
                   1.0e-52
                   119
Match length
                  89
% identity
                  FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin
NCBI Description
                   [2Fe-2S] precursor - Arabidopsīs thaliana
                  >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
                   [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
                  165801
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-C8
                  BLASTN
Method
NCBI GI
                  g3241927
BLAST score
                  165
E value
                  6.0e-88
Match length
                  215
% identity
                  94
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165802
                  LIB3177-094-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132102
BLAST score
                  454
E value
                  2.0e-45
Match length
                  92
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir RKMUB2
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1.1.39}) small chain
                  B2 precursor - Arabidopsis thaliana >gi_16194_emb CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  165803
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3929651
BLAST score
                  583
E value
                  2.0e-60
                  116
Match length
                  100
% identity
                  (AJ131206) microbody NAD-dependent malate dehydrogenase
NCBI Description
                  [Arabidopsis thaliana]
```

165804

Seq. No.

```
LIB3177-094-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3985952
BLAST score
                  458
                  0.0e+00
E value
                  470
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MRC8, complete sequence [Arabidopsis thaliana]
                  165805
Seq. No.
                  LIB3177-094-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g4097567
NCBI GI
BLAST score
                  164
                  8.0e-12
E value
                  34
Match length
                  97
% identity
NCBI Description
                 (U64921) ATGP4 [Arabidopsis thaliana]
                  165806
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-D2
Method
                  BLASTX
NCBÎ GI
                  g2055273
BLAST score
                  582
                  2.0e-60
E value
                  131
Match length
                  86
% identity
NCBI Description
                  (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
Seq. No.
                  165807
Seq. ID
                  LIB3177-094-P1-K1-D3
Method
                  BLASTX
                  g115767
NCBI GI
BLAST score
                  693
E value
                  2.0e-73
Match length
                  131
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165808
                  LIB3177-094-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1490554
BLAST score
                  738
E value
                  2.0e-78
Match length
                  157
                  92
% identity
                  (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
```

thaliana]

E value

1.0e-10

```
Seq. No.
                  165809
Seq. ID
                  LIB3177-094-P1-K1-D5 ...
                  BLASTX .
Method
NCBI GI
                  g115767
BLAST score
                  758
.E value
                  7.0e-81
                  144
Match length
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >qi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  165810
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-D7
Method
                  BLASTX
                  g4531437
NCBI GI
BLAST score
                  591
                  2.0e-61
E value
                  121
Match length
% identity
NCBI Description
                   (AC006224) putative isopropylmalate dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                  165811
Seq. ID
                  LIB3177-094-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2911085
BLAST score
                  181
                  9.0e-20
E value
Match length
                  122
                  56
% identity
NCBI Description
                  (AL021960) photosystem II oxygen-evolving complex protein
                  3-like [Arabidopsis thaliana] >gi 3402748 emb CAA20194.1
                   (AL031187) photosystem II oxygen-evolving complex protein 3
                  - like [Arabidopsis thaliana]
Seq. No.
                  165812
Seq. ID
                  LIB3177-094-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g3367567
BLAST score
                  262
E value
                  1.0e-145
Match length
                  292
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20
NCBI Description
                  (ESSAII project)
Seq. No.
                  165813
Seq. ID
                  LIB3177-094-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3776578
BLAST score
                  157
```

BLAST score

```
Match length
                   66
                   50
% identity
                   (AC005388) ESTs gb F13915 and gb F13916 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
Seq. No.
                  165814
Seq. ID
                  LIB3177-094-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q1169201
BLAST score
                  391
                  4.0e-38
E value
                  108
Match length
                  77
% identity
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                  thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  165815
Seq. ID
                  LIB3177-094-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  q4581103
BLAST score
                  29
                  8.0e-07
E value
Match length
                  173
                  90
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T24I21 genomic
                  sequence, complete sequence
Seq. No.
                  165816
Seq. ID
                  LIB3177-094-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g1709687
BLAST score
                  495
                  3.0e-50
E value
                  104
Match length
                  91
% identity
                  PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O)
NCBI Description
                  REDUCTASE) >gi 2129643 pir S71275 methionine sulfoxide
                  reductase - Arabidopsis thaliana >gi 1279212 emb CAA65991
                  (X97326) methionine sulfoxide reductase [Arabidopsis
                  thaliana]
Seq. No.
                  165817
Seq. ID
                  LIB3177-094-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2947062
BLAST score
                  152
E value
                  7.0e-10
Match length
                  141
                  32
% identity
                  (AC002521) unknown protein [Arabidopsis thaliana]
NCBI Description
                  165818
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g132074
```

Seq. ID

```
1.0e-68
E value
                   123
Match length
                   99
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
                   165819
Seq. No.
Seq. ID
                   LIB3177-094-P1-K1-E6
Method
                   BLASTX
                   q4490732
NCBI GI
BLAST score
                   201
                   5.0e-16
E value
                   43
Match length
% identity
                   93
                   (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                   protein [Arabidopsis thaliana]
                   165820
Seq. No.
Seq. ID
                   LIB3177-094-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   q4757404
BLAST score
                   259
E value
                   1:0e-144
                   266
Match length
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MLJ15, complete sequence
Seq. No.
                   165821
Seq. ID
                   LIB3177-094-P1-K1-E8
                   BLASTX
Method
NCBI GI
                   g4454051
                   500
BLAST score
                   9.0e-51
E value
Match length
                   99
% identity
                   98
                   (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   165822
Seq. ID
                   LIB3177-094-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g125576
BLAST score
                   640
E value
                   4.0e-67
                   136
Match length
% identity
                   92
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana
                   >gi 16441 emb CAA41155 (X58149) Ribulose-5-phosphate
                   kinase [Arabidopsis thaliana]
Seq. No.
                   165823
```

LIB3177-094-P1-K1-F10

```
Method
                    BLASTX
NCBI GI
                    g4567207
BLAST score
                    773
E value
                    1.0e-82
Match length
                    148
                    98
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
Seq. No.
                    165824
Seq. ID
                    LIB3177-094-P1-K1-F11
Method
                    BLASTX
NCBI GI
                    g132102
BLAST score
                    61
E value
                    9.0e-35
Match length
                    78
                    96
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir_RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    B2 precursor - Arabidopsis thaliana >gi_16194 emb CAA32701
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana]
                   165825
Seq. No.
Seq. ID
                   LIB3177-094-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g132090
BLAST score
                    707
E value
                    5.0e-75
Match length
                   135
% identity
                    97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana]
Seq. No.
                   165826
Seq. ID
                   LIB3177-094-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2583134
BLAST score
                   445
E value
                   3.0e-44
Match length
                   83
% identity
NCBI Description
                   (AC002387) putative proline-rich protein [Arabidopsis
                   thaliana]
Seq. No.
                   165827
Seq. ID
                   LIB3177-094-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g2494175
BLAST score
                   819
E value
                   5.0e-88
Match length
                   160
% identity
                   98
```

```
NCBI Description GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi 1184960 (U46665)
                   glutamate decarboxylase 2 [Arabidopsis thaliana]
                   >gi 1236619 (U49937) glutamate decarboxylase [Arabidopsis
                   thaliana]
                   165828
 Seq. No.
                   LIB3177-094-P1-K1-F5
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2252825
 BLAST score
                   627
 E value
                   2.0e-65
                   119
 Match length
                   100
 % identity
                   (AF013293) Similar to transmembrane protein; coded for by
 NCBI Description
                   A. thaliana cDNA H37637; coded for by A. thaliana cDNA
                   T41850; coded for by A. thaliana cDNA T13717; coded for by
                   A. thaliana cDNA T04371; coded for by A. thaliana cDNA
                   T43789; coded
                   165829
 Seq. No.
 Seq. ID
                   LIB3177-094-P1-K1-F6
                   BLASTX
 Method
 NCBI GI
                   g115767
                   <del>7</del>71
.BLAST score
 E value
                   2.0e-82
 Match length
                   146
                   100
 % identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
 NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
 Seq. No.
                   165830
 Seq. ID
                   LIB3177-094-P1-K1-F7
                   BLASTX
 Method
 NCBI GI
                   q1657617
 BLAST score
                   585
 E value
                   1.0e-60
 Match length
                   117
 % identity
 NCBI Description
                   (U72503) G2p [Arabidopsis thaliana] >gi 3068707 (AF049236)
                   putative nuclear DNA-binding protein G2p [Arabidopsis
                   thaliana]
 Seq. No.
                   165831
                   LIB3177-094-P1-K1-F9
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3885511
 BLAST score
                   390
 E value
                   7.0e-38
 Match length
                   99
 % identity
                   80
 NCBI Description
                   (AF084200) similar to PSI-K subunit of photosystem I from
```

barley [Medicago sativa]

2....

```
Seq. No.
                   165832
 Seq. ID
                   LIB3177-094-P1-K1-G1
 Method
                   BLASTX
 NCBI GI
                   g2501555
 BLAST score
                   528
 E value
                   5.0e-54
 Match length
                   122
 % identity
                   78
NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148)
                   possible apospory-associated protein [Pennisetum ciliare]
 Seq. No.
                   165833
 Seq. ID
                   LIB3177-094-P1-K1-G10
 Method
                   BLASTX
 NCBI GI
                   q132110
 BLAST score
                   561
 E value
                   6.0e-58
 Match length
                   105
                   99
 % identity
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
 Seq. No.
                   165834
 Seq. ID
                   LIB3177-094-P1-K1-G11
 Method
                   BLASTX
 NCBI GI
                   g4587989
 BLAST score
                   651
 E value
                   1.0e-68
 Match length
                   114
 % identity
                   98
 NCBI Description
                   (AF085279) hypothetical Cys-3-His zinc finger protein
                   [Arabidopsis thaliana]
 Seq. No.
                   165835
 Seq. ID
                   LIB3177-094-P1-K1-G12
 Method
                   BLASTN
 NCBI GI
                   g4589437
 BLAST score
                   457
 E value
                   0:0e+00
 Match length
                   480
 % identity
                   99
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MPN9, complete sequence
 Seq. No.
                   165836
 Seq. ID
                   LIB3177-094-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g4164473
BLAST score
                   191
E value
                   1.0e-14
Match length
                   55
 % identity
                   69
```

```
(AF061157) negatively light-regulated protein [Vernicia
NCBI Description
                  fordii]
                  165837
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-G3
Method
                  BLASTX
                  g4056494
NCBI GI
                  421
BLAST score
E value
                  1.0e-41
Match length
                  98
% identity
                  84
                  (AC005896) putative protein translocase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165838
Seq. ID
                  LIB3177-094-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  g4678219
BLAST score
                  183
E value
                  8.0e-99
Match length
                  190
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F9C22 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  165839
Seq. ID
                  LIB3177-094-P1-K1-G5
                  BLASTX
Method
NCBI GI
                  g3885331
BLAST score
                  367
E value
                  2.0e-35
                  98
Match length
% identity
                  68
                  (AC005623) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                  thaliana]
                  165840
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-G6
                  BLASTX
Method
NCBI GI
                  g2688824
BLAST score
                  254
                  6.0e-24
E value
Match length
                  88
% identity
                  72
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                  armeniaca]
                  165841
Seq. No.
Seq. ID
                  LIB3177-094-P1-K1-G7
                  BLASTX
Method
NCBI GI
                  g2244990
BLAST score
                  312
                  6.0e-29
E value
Match length
                  116
                  69
% identity
                  (Z97340) similarity to LIM homeobox protein -
NCBI Description
```

Caenorhabditis [Arabidopsis thaliana]

```
Seq. No.
                   165842
Seq. ID
                  LIB3177-094-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g4741952
BLAST score
                   607
E value
                   3.0e-63
Match length
                   113
% identity
                   74
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                   165843
Seq. ID
                   LIB3177-094-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g2795803
BLAST score
                   378
E value
                   1.0e-36
Match length
                   106
                   68
% identity
NCBI Description
                   (AC003674) putative beta-1,3-endoglucanase [Arabidopsis
                   thaliana] >gi 3355491 (AC004218) putative
                  beta-1,3-endoglucanase [Arabidopsis thaliana]
Seq. No.
                   165844
Seq. ID
                  LIB3177-094-P1-K1-H1
Method
                  BLASTN
NCBI GI
                   g4557061
BLAST score
                   98
E value
                   8.0e-48
                  252
Match length
% identity
                   97
                  Arabidopsis thaliana chromosome II BAC F23M2 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  165845
Seq. ID
                  LIB3177-094-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1709825
BLAST score
                  527
E value
                  6.0e-54
Match length
                  115
% identity
                  95
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                  (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  165846
Seq. ID
                  LIB3177-094-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g1362078
BLAST score
                  391
E value
                  6.0e-38
Match length
                  97
% identity
                  ·73
                  endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
NCBI Description
                  - common nasturtium >gi_311835_emb_CAA48324_ (X68254)
```

cellulase [Tropaeolum majus]

```
Seq. No.
                   165847
Seq. ID
                   LIB3177-094-P1-K1+H2
Method
                   BLASTN
NCBI GI
                   g4662640
BLAST score
                   353
E value
                   0.0e + 00
Match length
                   374
% identity
                   98
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F15K19 genomic
                   sequence, complete sequence
Seq. No.
                   165848
Seq. ID
                   LIB3177-094-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g3335366
BLAST score
                   306
E value
                   6.0e-28
Match length
                   115
                   47
% identity
NCBI Description
                   (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                   165849
Seq. ID
                   LIB3177-094-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q1076366
BLAST score
                   738
E value
                   1.0e-78
Match length
                   137
                   99
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis
                   thaliana >gi 460968 (U07276) peptidyl-prolyl cis-trans
                   isomerase [Arabidopsis thaliana] >gi 992643 (U32186)
                   cyclophilin [Arabidopsis thaliana]
                  >gi 1091580 prf 2021266A peptidyl-Pro cis-trans isomerase
                   [Arabidopsis thaliana]
Seq. No.
                  165850
Seq. ID
                  LIB3177-094-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g4210334
BLAST score
                  286
E value
                  1.0e-25
Match length
                  59
% identity
                  93
                   (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  165851
Seq. ID
                  LIB3177-094-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g4678353
BLAST score
                  678
                  2.0e-71
E value
Match length
                  128
% identity
                  98
                  (AL049659) cysteine endopeptidase precursor-like protein
NCBI Description
```

[Arabidopsis thaliana]

```
Seq. No.
                  165852
Seq. ID
                  LIB3177-094-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4049350
                                                    ...
BLAST score
                  601
E value
                  1.0e-62
Match length
                  115
% identity
                  99
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                  165853
Seq. ID
                  LIB3177-094-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g4581084
BLAST score
                  257
E value
                  1.0e-142
Match length
                  332
% identity
                  98
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  165854
Seq. ID
                  LIB3177-095-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  504
E value
                  2.0e-51
                  98
Match length
% identity
                  98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  165855
Seq. ID
                  LIB3177-095-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g4558521
                  146
BLAST score
E value
                  1.0e-76
                  250
Match length
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T10024,
                  complete sequence
Seq. No.
                  165856
Seq. ID
                  LIB3177-095-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2160168
BLAST score
                  471
                  2.0e-47
E value
Match length
                  99
% identity
                  88
```

```
NCBI Description
                  (AC000132) Strong similarity to R. communis
                  phosphoglycerate mutase (gb X70652). ESTs
                  gb_T41853,gb_T76648 come from this gene. [Arabidopsis
                  thaliana]
                  165857
Seq. No.
                  LIB3177-095-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2980771
BLAST score
                  481
                  1.0e-48
E value
                  93
Match length
% identity
                  91
                  (AL022198) chloroplast omega-6 fatty acid desaturase (fad6)
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  165858
Seq. ID
                  LIB3177-095-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4490303
                  450
BLAST score
                  4.0e-45
E value
                  98
Match length
                  91
% identity
NCBI Description
                  (AL035678) putative protein [Arabidopsis thaliana]
                  165859
Seq. No.
                  LIB3177-095-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4185120
                  139
BLAST score
                  1.0e-72
E value
Match length
                  166
% identity
                  49
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F5F19 sequence,
                  complete sequence [Arabidopsis thaliana]
                  165860
Seq. No.
                  LIB3177-095-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4454022
BLAST score
                  39
                  1.0e-12
E value
                  99
Match length
% identity
                  91
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
                  (ESSAII project)
Seq. No.
                  165861
                  LIB3177-095-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1769907
BLAST score
                  464
                  2.0e-46
E value
                  89
Match length
% identity
                  97
NCBI Description (X92975) xyloglucan endo-transglycosylase [Arabidopsis
```

Match length

NCBI Description

% identity

332

thaliana] 165862 Seq. No. LIB3177-095-P1-K1-B10 Seq. ID Method BLASTX NCBI GI q115385 153 BLAST score 1.0e-10 E value Match length 35 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana] 165863 Seq. No. LIB3177-095-P1-K1-B6 Seq. ID Method BLASTN NCBI GI q1107482 BLAST score 211 1.0e-115 E value Match length 242 97 % identity NCBI Description A.thaliana mRNA for 30S ribosomal protein S13 165864 Seq. No. LIB3177-095-P1-K1-C1 Seq. ID BLASTX Method g2062158 NCBI GI BLAST score 610 E value 1.0e-63 Match length 132 47 % identity (ACO01645) jasmonate inducible protein isolog [Arabidopsis NCBI Description thaliana] Seq. No. 165865 LIB3177-095-P1-K1-C10 Seq. ID Method BLASTN g3510340 NCBI GI BLAST score 301 1.0e-169 E value Match length 354 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MDN11, complete sequence [Arabidopsis thaliana] Seq. No. 165866 LIB3177-095-P1-K1-C11 Seq. ID BLASTN Method NCBI GI g4220627 BLAST score 90 E value 7.0e-43

K20J1, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

```
165867
Seq. No.
Seq. ID
                  LIB3177-095-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2494174
BLAST score
                  53
E value
                  9.0e-75
Match length
                  146
% identity
                  99
                  GLUTAMATE DECARBOXYLASE 1 (GAD 1) >qi 497979 (U10034)
NCBI Description
                  glutamate decarboxylase [Arabidopsis Thaliana]
Seq. No.
                  165868
Seq. ID
                  LIB3177-095-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                  462
                  3.0e-46
E value
                  125
Match length
                  70
% identity
NCBI Description
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
                  - spinach >gi_1066153_dbj_BAA07177 (D37963) cysteine
                  synthase [Spinacia oleracea]
                  165869
Seq. No.
                  LIB3177-095-P1-K1-C3
Seq. ID
                                               ٠.
                  BLASTX
Method
                  g3819710
NCBI GI
BLAST score
                  473
E value
                  1.0e-47
                  87
Match length
% identity
                  99
                  (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
NCBI Description
                  thaliana]
                  165870
Seq. No.
Seq. ID
                  LIB3177-095-P1-K1-C4
                  BLASTN
Method
NCBI GI
                  g3510340
BLAST score
                  184
                  3.0e-99
E value
Match length
                  233
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDN11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165871
Seq. ID
                  LIB3177-095-P1-K1-C5
                  BLASTN
Method
NCBI GI
                  g2244991
BLAST score
                  66
E value
                  4.0e-29
                  132
Match length
% identity
                  96
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
```

165872

Seq. No.

NCBI GI

```
LIB3177-095-P1-K1-C9
Seq. ID
               BLASTN
Method
NCBI GI
                  g1167960
BLAST score
                  38
                  7.0e-12
E value
                  455
Match length
                  22
% identity
NCBI Description Arabidopsis thaliana extensin (atExt1) gene, complete cds
Seq. No.
                  165873
Seq. ID
                  LIB3177-095-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q1353163
BLAST score
                  202
E value
                  5.0e-16
                  67
Match length
                  57
% identity
                  HYPOTHETICAL 19.6 KD PROTEIN C23G10.2 IN CHROMOSOME III
NCBI Description
                  PRECURSOR >gi 1055071 (U39851) C23G10.2 gene product
                  [Caenorhabditis elegans]
Seq. No.
                  165874
                  LIB3177-095-P1-K1-D10
Seq. ID
                  BLASTX
Method
                  q445612
NCBI GI
BLAST score
                  387
                  1.0e-37
E value
                  86
Match length
                  88
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                  165875
                  LIB3177-095-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832611
BLAST score
                  275
E value
                  1.0e-153
                  308
Match length
                  98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
NCBI Description
                  (ESSAII project)
Seq. No.
                  165876
Seq. ID
                  LIB3177-095-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g4432863
BLAST score
                  567
                  1.0e-58
E value
                  116
Match length
                  99
% identity
                  (AC006300) putative phosphate/phosphoenolpyruvate
NCBI Description
                  translocator protein [Arabidopsis thaliana]
                  165877
Seq. No.
                  LIB3177-095-P1-K1-D3
Seq. ID
                  BLASTX
Method
```

4 ÷.

q4210334

Seq. ID

```
BLAST score
                   179
E value
                   1.0e-13
Match length
                   63
% identity
                   67
NCBI Description
                   (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
                   [Arabidopsis thaliana]
                   165878
Seq. No.
Seq. ID
                   LIB3177-095-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q1170203
BLAST score
                   432
E value
                   6.0e-43
Match length
                   109
% identity
                   81
NCBI Description
                  GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi 454359
                   (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]
Seq. No.
                   165879
Seq. ID
                   LIB3177-095-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   q4587641
BLAST score
                   284
E value
                  1.0e-159
                   300
Match length
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                   165880
Seq. ID
                  LIB3177-095-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   377
E value ·
                   1.0e-36
Match length
                  79
% identity
                   95
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi 68060 pir RKMUB3
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                  B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  165881
Seq. No.
Seq. ID
                  LIB3177-095-P1-K1-D8
Method
                  BLASTN
                  g4587641
NCBI GI
                  386
BLAST score
                  0.0e+00
E value
Match length
                  402
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                  165882
```

LIB3177-095-P1-K1-D9

```
Method
                  BLASTN
NCBI GI
                  q1737217
BLAST score
                  195
E value
                  1.0e-105
Match length
                  270
% identity
                   93
NCBI Description
                  Arabidopsis thaliana vacuolar sorting receptor homolog
                  mRNA, complete cds
                  165883
Seq. No.
Seq. ID
                  LIB3177-095-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2501188
BLAST score
                   560
E value
                  1.0e-57
Match length
                  135
% identity
                  85
NCBI Description
                  THIAZOLE BIOSYNTHETIC ENZYME >gi 2129750 pir S71191 TH14
                  protein homolog - Arabidopsis thaliana > gi 1113783 (U17589)
                  Thil protein [Arabidopsis thaliana]
Seq. No.
                  165884
                  LIB3177-095-P1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2499811 *
BLAST score
                   566
E value
                   2.0e-58
Match length
                  109
% identity
                   98
                  PROFILIN 2 >gi 1353766 (U43323) profilin 2 [Arabidopsis
NCBI Description
                  thaliana] >gi 1353772 (U43326) profilin 2 [Arabidopsis
                   thaliana]
Seq. No.
                  165885
                  LIB3177-095-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2119848
BLAST score
                   646
E value
                   9.0e-68
Match length
                   121
% identity
                   99
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B1 -
                  Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459)
                  photosystem II type I ch\overline{lorophyll} \overline{a} /b bind\overline{ing} protein
                  [Arabidopsis thaliana] >gi_3128229 (AC004077) putative
                  photosystem II type I chlorophyll a/b binding protein
                   [Arabidopsis thaliana] >gi_3337372 (AC004481) putative
                  photosystem II type I chlorophyll a/b binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  165886
Seq. ID
                  LIB3177-095-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g3420043
BLAST score
                  237
E value
                  1.0e-131
Match length
                  279
```

Match length

```
% identity
                   Arabidopsis thaliana chromosome II BAC F23F1 genomic
 NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   165887
 Seq. ID
                   LIB3177-095-P1-K1-E3
 Method
                   BLASTX
                   g1709446
 NCBI GI
 BLAST score
                   468
 E value
                   4.0e-47
Match length
                   115
. % identity
                   90
                   PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
NCBI Description
                   PRECURSOR (PDHE1-A) >gi_2117533_pir__JC4358 pyruvate
                   dehydrogenase (lipoamide) (EC 1.2.4.1) complex El alpha
                   chain - Arabidopsis thaliana mitochondrion >gi 710400
                    (U21214) pyruvate dehydrogenase E1 alpha subunit
                   [Arabidopsis thaliana]
 Seq. No.
                   165888
                   LIB3177-095-P1-K1-E4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4741944
 BLAST score
                   273
                   1:0e-24
 E value
 Match length
                   60
                   90
 % identity
                   (AF134122) Lhcb2 protein [Arabidopsis thaliana]
 NCBI Description
                   165889
 Seq. No.
                   LIB3177-095-P1-K1-E5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q4582787
 BLAST score
                   494
 E value
                   4.0e-50
 Match length
                   124
 % identity
                   75
                   (AJ012281) adenosine kinase [Zea mays]
 NCBI Description
 Seq. No.
                   165890
 Seq. ID
                   LIB3177-095-P1-K1-E7
 Method
                   BLASTN
                   q2760168
 NCBI GI
 BLAST score
                   59
                   9.0e-25
 E value
 Match length
                   162
 % identity
                   75
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MEE6, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   165891
                   LIB3177-095-P1-K1-E8
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g4159706
 BLAST score
                   228
 E value
                   1.0e-125
```

% identity

```
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MGL6, complete sequence
Seq. No.
                   165892
Seq. ID
                   LIB3177-095-P1-K1-E9
Method
                   BLASTN
NCBI GI
                   q457403
BLAST score
                   54
E value
                   4.0e-22
Match length
                   88
% identity
NCBI Description
                   Arabidopsis thaliana mRNA for MAP kinase, complete cds
Seq. No.
Seq. ID
                   165893
                   LIB3177-095-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   g3738275
BLAST score
                   271
                   1.0e-151
E value
                   435
Match length
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F17A22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165894
Seq. ID
                   LIB3177-095-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g119975
BLAST score
                   638
E value
                   7.0e-67
Match length
                   145
% identity
                   90
NCBI Description
                   FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin
                   [2Fe-2S] precursor - Arabidopsis thaliana
                   >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
Seq. No.
                   165895
Seq. ID
                   LIB3177-095-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g4755189
BLAST score
                   417
E value
                   6.0e-41
Match length
                   147
% identity
                   57
                   (AC007018) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   165896
                   LIB3177-095-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   607
E value
                   3.0e-63
Match length
                   115
```

Match length

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana)
Seq. No.
                  165897
Seq. ID
                  LIB3177-095-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  g1209241
BLAST score
                  114
E value
                  2.0e-57
Match length
                  230
% identity
                  87
NCBI Description Arabidopsis thaliana metallothionein mRNA sequence
Seq. No.
                  165898
Seq. ID
                  LIB3177-095-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  646
E value
                  8.0e-68
Match length
                  127
% identity
                  98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  165899
Seq. No.
                  LIB3177-095-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172977
BLAST score
                  56
E value
                  9.0e-41
Match length
                  105
% identity
                  85
NCBI Description
                  60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  165900
Seq. ID
                  LIB3177-095-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g4314354
BLAST score
                  76
E value
                  2.0e-35
Match length
                  79
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9I22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165901
Seq. ID
                  LIB3177-095-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  701
E value
                  3.0e-74
```

BLAST score

```
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  165902
Seq. ID
                  LIB3177-095-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q3953473
BLAST score
                  625
E value
                  2.0e-65
Match length
                  126
                  100
% identity
NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]
Seq. No.
                  165903
Seq. ID
                  LIB3177-095-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q4741960
BLAST score
                  540
E value
                  2.0e-55
Match length
                  102
% identity
                  62
NCBI Description
                 (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  165904
Seq. ID
                  LIB3177-095-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  785
E value
                  4.0e-84
Match length
                  147
% identity
                  99
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                  165905
Seq. No.
Seq. ID
                  LIB3177-095-P1-K1-G4
                  BLASTX
Method
NCBI GI
                  q115783
BLAST score
                  654
E value
                  9.0e-69
Match length
                  126
% identity
                  98
                 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >qi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  165906
Seq. No.
Seq. ID
                 LIB3177-095-P1-K1-G5
                 BLASTX
Method
                  g4049341
NCBI GI
```

E value

1.0e-76

```
E value
                    3.0e-10
 Match length
                    58
 % identity
                    48
                   (AL034567) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   165907
                   LIB3177-095-P1-K1-G6
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                    g4455290
 BLAST score
                    57
                    2.0e-23
 E value
 Match length
                    94
 % identity
                    66
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5
 NCBI Description
                    (ESSAII project)
                   165908
 Seq. No.
                    LIB3177-095-P1-K1-G7
 Seq. ID
 Method
                    BLASTX
                    g3869251
 NCBI GI
                    297
 BLAST score
                   5.0e-27
 E value
 Match length
                    95
 % identity
                    64
                   (U39287) ferredoxin-dependent glutamate synthase precursor
 NCBI Description
                    [Arabidopsis thaliana]
                    165909
 Seq. No.
                    LIB3177-095-P1-K1-G8
 Seq. ID
 Method
                   BLASTX
                   g120675
· NCBI GI
 BLAST score
                    43
                    7.0e-49
 E value
 Match length
                    125
                    89
 % identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 NCBI Description
                   >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                    dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                   >gi 21143 emb_CAA27844_ (X04,301) GAPDH (aa 1-338) [Sinapis
                    alba]
                    165910
 Seq. No.
                    LIB3177-095-P1-K1-G9
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2462840
 BLAST score
                    605
 E value
                    5.0e-63
 Match length
                    114
 % identity
                    99
 NCBI Description
                   (AF000657) cytochrome C [Arabidopsis thaliana]
                    165911
 Seq. No.
 Seq. ID
                   LIB3177-095-P1-K1-H12
 Method
                    BLASTX
 NCBI GI
                   g4567207
 BLAST score
                    721
```

BLAST score

```
135
Match length
% identity
                  99
                 (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  165912
Seq. No.
                  LIB3177-095-P1-K1-H2
Seq. ID
Method
                  BLASTN
                  g3249094
NCBI GI
                  228
BLAST score
                  1.0e-125
E value
                  315
Match length
% identity
                  99
                  Arabidopsis thaliana chromosome 1 BAC T12M4 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  165913
                  LIB3177-095-P1-K1-H4
Seq. ID
Method
                  BLASTX
                  g114654
NCBI GI
BLAST score
                  46
                  1.0e-16
E value
                  55
Match length
% identity
                  95
NCBI Description
                  ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
                  >gi 67898 pir LWNTA H+-transporting ATP synthase (EC
                  3.6.1.34) lipid-binding protein - common tobacco
                  chloroplast >gi 11812 emb_CAA77343_ (Z00044) ATPase III
                  subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase
                  subunit III [Nicotiana tabacum] > gi 224347_prf__1102209A
                  ATPase III, H translocating [Nicotiana sp.]
                  >gi 225272 prf 1211235G ATPase III [Nicotiana tabacum]
Seq. No.
                  165914
                  LIB3177-095-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4755189
BLAST score
                  381
                  1.0e-36
E value
Match length
                  138
% identity
                  57
NCBI Description (AC007018) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  165915
Seq. ID
                  LIB3177-095-P1-K1-H6
                  BLASTX
Method
                  g1350965
NCBI GI
BLAST score
                  551
E value
                  1.0e-56
Match length
                  108
% identity
                  97
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12)
Seq. No.
                  165916
                  LIB3177-095-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  g99696
NCBI GI
```

```
4.0e-21
E value
                  77
Match length
% identity
                  66
                  glutamate--ammonia ligase (EC 6.3.1.2) precursor,
NCBI Description
                  chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                  >gi_240070_bbs_69728 (S69727) light-regulated glutamine
                  synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                  aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln
                  synthetase [Arabidopsis thaliana]
                  165917
Seq. No.
                  LIB3177-095-P1-K1-H9
Seq. ID
Method
                  BLASTX
                  g282865
NCBI GI
                  354
BLAST score
                  2.0e-38
E value
                  93
Match length
                  87
% identity
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >gi 16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
                  165918
Seq. No.
                  LIB3177-096-P1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2529665
BLAST score
                  421
                  1.0e-41
E value
                  110
Match length
                  79
% identity
                  (AC002535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                  thaliana]
                  165919
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-A10
Method
                  BLASTX
                  a2764941
NCBI GI
                  478
BLAST score
                  3.0e-48
E value
Match length
% identity
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  165920
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-A12
                  BLASTN
Method
                  q4587641
NCBI GI
                  212
BLAST score
                   1.0e-115
E value
Match length
                  372
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic
```

NCBI GI

sequence, complete sequence

```
165921
Seq. No.
Seq. ID
                  LIB3177-096=P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3212869
BLAST score
                  551
                  7.0e-57
E value
                  108
Match length
% identity
                  98
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  165922
                  LIB3177-096-P1-K1-A4
Seq. ID
Method
                  BLASTX
                  g2129600
NCBI GI
                  57
BLAST score
E value
                  1.0e-68
                  139
Match length
                  99
% identity
                  glutathione synthase (EC 6.3.2.3) 2 - Arabidopsis thaliana
NCBI Description
                  (fragment) >gi_1107503_emb_CAA90515_ (Z50153) glutathione
                  synthetase [Arabidopsis thaliana] >gi_1585560_prf__2201360A
                  glutathione synthetase [Arabidopsis thaliana].
Seq. No.
                  165923
                  LIB3177-096-P1-K1-A5
Seq. ID.
Method
                  BLASTX
                  g2119846
NCBI GI
BLAST score
                  565
E value
                  2.0e-58
Match length
                  107
                  99
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165924
Seq. ID
                  LIB3177-096-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2708740
BLAST score
                  153
                  6.0e-10
E value
Match length
                  140
% identity
NCBI Description
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
                  >gi_4406824_gb_AAD20132_ (AC006201) hypothetical protein
                  [Arabidopsis thaliana]
Seq. No.
                  165925
Seq. ID
                  LIB3177-096-P1-K1-A7
Method
                  BLASTN
```

g4263762

```
BLAST score
                   51
E value
                   4.0e-20
                   75
Match length
% identity
                   92
                  Arabidopsis thaliana chromosome II BAC F17L24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165926
Seq. ID
                  LIB3177-096-P1-K1-A8
                  BLASTX
Method
NCBI · GI
                  q1170159
BLAST score
                   308
                   3.0e-28
E value
                   62
Match length
                  100
% identity
NCBI Description
                  HISTONE H2B
                  165927
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  q2351071
BLAST score
                   353
                                                           ÷...
                   0.0e + 00
E value
                   387
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MVA3, complete sequence [Arabidopsis thaliana]
                  165928
Seq. No.
                  LIB3177-096-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4262250
                   473
BLAST score
                  1.0e-47
E value
                   94
Match length
                  100
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                  165929
Seq. No.
                  LIB3177-096-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062161
                   700
BLAST score
                   4.0e-74
E value
                   132
Match length
% identity
                   51
                   (ACO01645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  165930
Seq. No.
                  LIB3177-096-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263525
BLAST score
                   622
E value
                  5.0e-65
                  143
Match length
% identity
                  86
```

```
(AC004044) putative photosystem I reaction center subunit
NCBI Description
                   II precursor [Arabidopsis thaliana]
Seq. No.
                  165931
Seq. ID
                  LIB3177-096-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q3128228
BLAST score
                  620
E value
                  9.0e-65
Match length
                  125
% identity
                  92
NCBI Description
                   (AC004077) putative ribosomal protein L18A [Arabidopsis-
                  thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
Seq. No.
                  165932
Seq. ID
                  LIB3177-096-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q4324967
BLAST score
                  768
E value
                  4.0e-82
Match length
                  151
% identity
                  99
NCBI Description (AF114796) ADP-ribosylation factor [Glycine max]
Seq. No.
                  165933
Seq. ID
                  LIB3177-096-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g115385
BLAST score
                  695
E value
                  2.0e-73
Match length
                  135
% identity
                  99
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  165934
Seq. ID
                  LIB3177-096-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3786324
BLAST score
                  436
E value
                  4.0e-43
                  147
Match length
                  54
% identity
NCBI Description
                  (AB015139) chlorophyll a oxygenase [Chlamydomonas
                  reinhardtii]
                  165935
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g4097549
BLAST score
                  319
                  2.0e-29
E value
Match length
                  116
% identity
                  62
                 (U64907) ATFP4 [Arabidopsis thaliana]
NCBI Description
```

```
165936
Seq. No.
                  LIB3177-096-P1-K1-B7
Seq. ID
Method
                  BLASTX
                  g3746062
NCBI GI
BLAST score
                  322
E value
                  5.0e-30
                  90
Match length
                  71
% identity
                  (AC005311) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  165937
Seq. ID
                  LIB3177-096-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  155
                  2.0e-10
E value
                  85
Match length
% identity
                  45
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                  165938
Seq. No.
                  LIB3177-096-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3420050
BLAST score
                  608
                  2.0e-63
E value
                  119-
Match length
                  92
% identity
                  (AC004680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  165939
Seq. No.
                  LIB3177-096-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  700
E value
                  4.0e-74
                  128
Match length
                  100
% identity
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                  thaliana >gi 984052 emb_CAA61592_ (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  165940
                  LIB3177-096-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4704730
BLAST score
                  263
                  7.0e-23
E value
Match length
                  125
% identity
                  41
                  (AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]
NCBI Description
                  165941
Seq. No.
                  LIB3177-096-P1-K1-C2
Seq. ID
Method
                  BLASTX
```

g2407802

NCBI GI

NCBI GI

```
BLAST score
                   426
E value
                   5.0e-42
Match length
                   87
                   100
% identity
NCBI Description
                  (Y12576) histone H2B [Arabidopsis thaliana]
                   165942
Seq No.
                   LIB3177-096-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q119975
BLAST score
                   353
E value
                   8.0e-34
Match length
                   75
                   95
% identity
                   FERREDOXIN PRECURSOR >gi_99692_pir_S09979 ferredoxin
NCBI Description
                   [2Fe=2S] precursor - Arabidopsis thaliana
                   >gi_16437_emb_CAA35754 (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
                   165943
Seq. No.
                   LIB3177-096-P1-K1-C5
Seq. ID
Method
                   BLASTX ·
                 __g4572669
NCBI GI
BLAST score
                   514
E value
                   3.0e-52
Match length
                   142
% identity
                   67
NCBI Description
                  (AC006954) putative glucosyltransferase [Arabidopsis
                   thaliana]
                   165944
Seq. No.
Seq. ID
                   LIB3177-096-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   g4757399
BLAST score
                   440
E value
                   0.0e+00 .
Match length
                   452
% identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MEE13, complete sequence
Seq. No.
                   165945
Seq. ID
                   LIB3177-096-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   g4589440
BLAST score
                   241
                   1.0e-133
E value
Match length
                   368
% identity
                   91
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MSD21, complete sequence
Seq. No.
                   165946
Seq. ID
                   LIB3177-096-P1-K1-C8
Method
                   BLASTN
```

g4589440

BLAST score

```
394
BLAST score
E value
                  0.0e+00
Match length
                  442
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSD21, complete sequence
Seq. No.
                  165947
Seq. ID
                  LIB3177-096-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q4587513
BLAST score
                  212
E value
                  7.0e-17
Match length
                  114
                  42
% identity
                  (AC007060) Contains eukaryotic protein kinase domain
NCBI Description
                  PF 00069. [Arabidopsis thaliana]
Seq. No.
                  165948
Seq. ID
                  LIB3177-096-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q3892048
BLAST score
                  717
E value
                  4.0e-76
Match length
                  142 -
                  100
% identity
NCBI Description
                  (AC002330) putative tryptophan synthase alpha 1-like
                  protein [Arabidopsis thaliana]
Seq. No.
                  165949
Seq. ID
                  LIB3177-096-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2160183
BLAST score
                  500
E value
                  1.0e-50
Match length
                  130
% identity
                  78
NCBI Description
                  (AC000132) Identical to A. thaliana U2 SnRNP-specific A'
                  protein (gb X69137). ESTs gb ATTS0705, gb ATTS0339 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  165950
Seq. ID
                  LIB3177-096-P1-K1-D11
Method
                  BLASTX
                  g4678354
NCBI GI
BLAST score
                  756
E value
                  1.0e-80
Match length
                  146
% identity
                  99
                  (AL049659) cysteine endopeptidase-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165951
Seq. ID
                  LIB3177-096-P1-K1-D12
Method
                  BLASTX
                  g3193289
NCBI GI
```

```
E value
                   9.0e-68
Match length
                  150
% identity
                  87
NCBI Description
                  (AF069298) similar to several small proteins (~100 aa) that
                  are induced by heat, auxin, ethylene and wounding such as
                  Phaseolus aureus indole-3-acetic acid induced protein ARG
                   (SW:32292) [Arabidopsis thaliana]
Seq. No.
                  165952
Seq. ID
                  LIB3177-096-P1-K1-D2
                  BLASTX
Method
NCBI GI
                  g1145697
BLAST score
                  490
E value
                  2.0e-64
Match length
                  133
% identity
NCBI Description
                  (U39485) delta tonoplast integral protein [Arabidopsis
                  thaliana]
Seq. No.
                  165953
Seq. ID
                  LIB3177-096-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  g2852453
BLAST score
                  260
E value
                  1.0e-144
Match length
                  281
                  98
% identity
NCBI Description
                  Arabidopsis thaliana gene for cystathionine gamma-synthase,
                  complete cds
Seq. No.
                  165954
Seq. ID
                  LIB3177-096-P1-K1-D4
                  BLASTX
Method
NCBI GI
                  g4006934
BLAST score
                  636
E value
                  1.0e-66
                  120
Match length
                  99
% identity
NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                  165955
Seq. ID
                  LIB3177-096-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4587515
BLAST score
                  614
E value
                  5.0e-64
Match length
                  151
% identity
NCBI Description
                  (AC007060) EST gb Z37678 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  165956
Seq. ID
                  LIB3177-096-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  g3869069
BLAST score
                  214
```

1.0e-117

E value

```
Match length
                  413
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165957
Seq. ID
                  LIB3177-096-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g4263774
BLAST score
                  233
E value
                  1.0e-128
Match length
                  312
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T20F21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165958
                  LIB3177-096-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3805755
BLAST score
                  215
E value
                  1.0e-117
Match length
                  259
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC T25N22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  165959
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-E12
Method
                  BLASTX
                  q1883006
NCBI GI
BLAST score
                  409
E value
                  5.0e-40
Match length
                  129
% identity
                  23
                  (Y11483) jasmonate inducible protein [Brassica napus]
NCBI Description
Seq. No.
                  165960
                  LIB3177-096-P1-K1-E2
Seq. ID
Method
                  BLASTN
                  g3046849
NCBI GI
BLAST score
                  183
                  2.0e-98
E value
                  456
Match length
                  50
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18L3, complete sequence [Arabidopsis thaliana]
                  165961
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-E4
                  BLASTX
Method
NCBI GI
                  g4585995
BLAST score
                  229
                  4.0e-19
E value
Match length
                  60
                  78
% identity
                  (AC005287) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

```
Seq. No.
Seq. ID
                    165962
                    LIB3177-096-P1-K1-E5
Method
                    BLASTX
NCBI GI
                    q4538963
BLAST score
                    67 .
E value
                    5.0e-63
Match length
                    143
                    69
% identity
NCBI Description
                    (AL049488) chlorophyll a/b-binding protein-like
                    [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                    (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                    165963 -
Seq. No.
Seq. ID
                    LIB3177-096-P1-K1-E6
Method
                    BLASTN
NCBI GI
                    q3608126
BLAST score
                    230
E value
                    1.0e-126
Match length
                    412
                    100
% identity
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T32F12 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    165964
Seq. ID
                    LIB3177-096-P1-K1-E7
Method
                    BLASTX
NCBI GI
                    g232033
BLAST score
                    184
E value
                    1.0e-13
Match length
                    58
% identity
                    ELONGATION FACTOR 1 BETA' >gi_479830_pir__$35501 translation elongation factor eEF-1 beta' chain - wheat
NCBI Description
                    >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta'
                    [Triticum aestivum]
Seq. No.
                    165965
                    LIB3177-096-P1-K1-E8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g232033
BLAST score
                    194
E value
                    8.0e-15
Match length
                    58
% identity
                    66
                    ELONGATION FACTOR 1 BETA' >gi_479830_pir__$35501 translation elongation factor eEF-1 beta' chain - wheat
NCBI Description
                    >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta'
                    [Triticum aestivum]
Seq. No.
                    165966
Seq. ID
                    LIB3177-096-P1-K1-E9
Method
                    BLASTX
NCBI GI
                    g4835233
BLAST score
                    413
                    1.0e-40
E value
Match length
                    92
```

```
% identity
                  89
NCBI Description
                   (AL049862) putative protein 1 photosystem II
                  oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                  165967
Seq. ID
                  LIB3177-096-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g4115918
BLAST score
                  254
E value
                  5.0e-22
Match length
                  58
% identity
                  84
                  (AF118222) similar to nascent polypeptide associated
NCBI Description
                  complex alpha chain [Arabidopsis thaliana]
                  165968
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  g3293583
BLAST score
                  32
                  3.0e-08
E value
Match length
                  171
% identity
                  87
NCBI Description Arabidopsis thaliana BAC T27D20
Seq. No.
                  165969
Seq. ID
                  LIB3177-096-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  q2708736 a
BLAST score
                  416
                  0.0e+00
E value
                  439
Match length
% identity
                  99
                  Arabidopsis thaliana BAC T13L16 from chromosome II, near 33
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165970
Seq. ID
                  LIB3177-096-P1-K1-F3
Method
                  BLASTX
                  q4454037
NCBI GI
BLAST score
                  701
E value
                  3.0e-74
Match length
                  128
% identity
                  100
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  165971
Seq. ID
                  LIB3177-096-P1-K1-F5
Method
                  BLASTX
                  g294845
NCBI GI
BLAST score
                  299
                  3.0e-27
E value
                  131
Match length
% identity
                  44
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                  H65-7052]
```

```
Seq. No.
                    165972
Seq. ID
                    LIB3177-096-P1-K1-F6
Method
                    BLASTX
NCBI GI
                    g1175011
BLAST score
                    507
E value
                    1.0e-51
Match length
                    98
                    99
% identity
NCBI Description
                    PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN
                   A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665)
                    plasma membrane intrinsic protein IB [Arabidopsis thaliana]
                    165973
Seq. No.
Seq. ID
                    LIB3177-096-P1-K1-F7
Method
                    BLASTX
NCBI GI
                    g119143
BLAST score
                    208
E value
                    8.0e-17
Match length
                    នន
% identity
                    53
NCBI Description
                    ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                    >gi 81606 pir S06724 translation elongation factor eEF-1
                    alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                    (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                    >gi_1369927_emb CAA34454 (X16431) elongation factor
                    1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                    >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                    >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                    >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
                    165974
Seq. No.
Seq. ID
                    LIB3177-096-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   q99688
BLAST score
                    428
E value
                    3.0e-42
                    141
Match length
                    65
% identity
NCBI Description
                   translation elongation factor eEF-1 alpha chain (gene A4) -
                   Arabidopsis thaliana >gi_295789_emb_CAA34456 (X16432)
                    elongation factor 1-alpha [Arabidopsis thaliana]
Seq. No.
                    165975
                   LIB3177-096-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                    g1592681
BLAST score
                    486
                   5.0e-49
E value
Match length
                   97
                   98
% identity
NCBI Description
                   (X91917) LEA D113 homologue type2 [Arabidopsis thaliana]
                   >gi 3668076 (AC004667) LEA D113 type2 protein [Arabidopsis
```

thalianal

Seq. ID

```
165976
Seq. No.
Seq. ID
                   LIB3177-096-P1-K1-G1
Method
                   BLASTN
NCBI GI
                   g246255
BLAST score
                   65
E value
                   5.0e-28
Match length
                   158
% identity
                   90
NCBI Description
                   Bcg4-4=acyl carrier protein [Brassica rapa, Genomic, 3898
                   nt]
Seq. No.
                   165977
Seq. ID
                   LIB3177-096-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g4835233
BLAST score
                   727
                   3.0e-77
E value
                   142
Match length
                   99
% identity
NCBI Description
                   (AL049862) putative protein 1 photosystem II
                   oxygen-evolving complex [Arabidopsis thaliana]
                   165978
Seq. No.
Seq. ID
                   LIB3177-096-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   g4371278
BLAST score
                   325
E value
                   0.0e + 00
Match length
                   442
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T2N18 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   165979
                   LIB3177-096-P1-K1-G12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4586098
BLAST score
                   254
                   1.0e-141
E value
Match length
                   383
                   98
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
                   (ESSA project)
Seq. No.
                   165980
Seq. ID
                   LIB3177-096-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   q4322346
BLAST score
                   183
E value
                  2.0e-13
Match length
                   67
% identity
NCBI Description
                   (AF081825) sodium-dependent high-affinity dicarboxylate
                  transporter [Rattus norvegicus]
Seq. No.
                  165981
```

LIB3177-096-P1-K1-G3

```
Method
                    BLASTN
NCBI GI
                    q4757405
BLAST score
                    147
E value
                     6.0e-77
Match length
                     398
% identity
                    99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                    MOJ10, complete sequence
Seq. No.
                    165982
Seq. ID
                    LIB3177-096-P1-K1-G4
Method
                    BLASTX
NCBI GI
                    q4835235
BLAST score
                    241
E value
                    3.0e-20
Match length
                    102
% identity
                    43
NCBI Description (ALO49862) putative protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                    LIB3177-096-P1-K1-G5
Method
                    BLASTN
NCBI GI
                    g2244747
BLAST score
                    431
E value
                    0.0e + 00
Match length
                    443
% identity
                    99
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                    fragment No
Seq. No.
                    165984
Seq. ID
                    LIB3177-096-P1-K1-G6
Method
                    BLASTX
NCBI GI
                    q266839
BLAST score
                    142
                    2.0e-10
E value
Match length
                    62
% identity
                    63
NCBI Description: PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                    COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi_478764 pir_S29240 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha
                    chain - Arabidopsis thaliana >gi_16445_emb_CAA47298 (X66825) proteosome alpha subunit [Arabidopsis thaliana]
                    >gi_3421080 (AF043522) 20S proteasome subunit PAD1
[Arabidopsis thaliana] >gi_742351_prf__2009376B
                    proteasome:SUBUNIT=alpha [Arabidopsis thaliana]
Seq. No.
                    165985
Seq. ID
                    LIB3177-096-P1-K1-G7
Method
                    BLASTX
NCBI GI
                    q99696
BLAST score
                    517
                    9.0e-53
E value
Match length
                    108
% identity
                    95
NCBI Description
                   glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                    chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
```

Seq. No.

Seq. ID

Method

```
synthetase [Arabidopsis thaliana]
Seq. No.
                 165986
Seq. ID
                   LIB3177-096-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g99696
BLAST score
                   643
E value
                   2.0e-67
Match length
                   131
% identity
                   96
NCBI Description
                   glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                   chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                   >gi_240070_bbs_69728 (S69727) light-regulated glutamine
                   synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                   aa] [Arabidopsis thaliana] >gi_228453 prf 1804333A Gln
                   synthetase [Arabidopsis thaliana]
Seq. No.
                   165987
Seq. ID
                   LIB3177-096-P1-K1-G9
Method
                 . BLASTN
NCBI GI
                   g2264310
                   208
BLAST score
                  1.0e-113
E value
Match length
                   440
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MKP11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  165988
                  LIB3177-096-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2911044
BLAST score
                   602
E value
                  1.0e-62
Match length
                  114
% identity
                  99
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  165989
Seq. ID
                  LIB3177-096-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g232033
BLAST score
                  152
E value
                  7.0e-10
Match length
                  38
% identity
                  74
NCBI Description
                  ELONGATION FACTOR 1 BETA' >gi_479830_pir__$35501
                  translation elongation factor eEF-1 beta chain - wheat
```

>gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453 prf 1804333A Gln

22328 4

[Triticum aestīvum]

LIB3177-096-P1-K1-H12

165990

BLASTX

>gi_218341_dbj_BAA02436 (D13147) elongation factor 1 beta'

- dr:

```
NCBI GI
                  g2213600
BLAST score
                  335
E value
                  3.0e-31
Match length
                  101
                  40
% identity
                  (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  165991
                  LIB3177-096-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1176658
BLAST score
                  244
E value
                  1.0e-20
                  76
Match length
% identity
                  63
                  HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
NCBI Description
                  >gi 726363 (U23168) No definition line found
                  [Caenorhabditis elegans]
Seq. No.
                  165992
Seq. ID
                  LIB3177-096-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q4741952
BLAST score
                  686
E value
                  2.0e-72
Match length
                  134
% identity
                  67
NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]
                  165993
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  629
                  8.0e-66
E value
                  120
Match length
% identity
                  98
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana)
                  165994
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  g4757400
BLAST score
                  48
                  4.0e-18
E value
                  83
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MFJ20, complete sequence
                  165995
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g4827253
```

```
BLAST score
                  154
                   3.0e-10
E value
Match length
                  35
% identity
                  83
NCBI Description (AB027002) plastidic aldolase [Nicotiana paniculata]
                  165996
Seq. No.
Seq. ID
                  LIB3177-096-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q1781348
BLAST score
                  154
E value
                  3.0e-10
Match length
                  35
% identity
NCBI Description
                  (Y10380) homologous to plastidic aldolases [Solanum
                  tuberosum]
Seq. No.
Seq. ID
                  165997
                  LIB3177-096-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  666
E value
                  4.0e-70
Match length
                  122
% identity
                  <del>:9</del>9
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  165998
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q1169201
BLAST score
                  239
E value
                  1.0e-27
Match length
                  98
                  65
% identity
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                  thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  165999
Seq. ID
                  LIB3177-097-P1-K1-A10
Method
                  BLASTX
NCBI GI ·
                  q1169476
BLAST score
                  645
                  1.0e-67
E value
                  123
Match length
                  100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
```

166000

Seq. No.

```
LIB3177-097-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2501188
BLAST score
                   692
                   4.0e-73
E value.
Match length
                   155
                   -90
% identity
                   THIAZOLE BIOSYNTHETIC ENZYME >gi 2129750 pir S71191 TH14
NCBI Description
                   protein homolog - Arabidopsis thaliana >gi 1113783 (U17589)
                   Thil protein [Arabidopsis thaliana]
                   166001
Seq. No.
                   LIB3177-097-P1-K1-A12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2191126
BLAST score
                   77
                   3.0e-35
E value
                   173
Match length
                   86
% identity
                  Arabidopsis thaliana BAC IG002N01
NCBI Description
Seq. No.
                   166002
                   LIB3177-097-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3273743
BLAST score
                   610
E value
                   2.0e-63
                   118
Match length
                   99
% identity
                   (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                   thaliana] >gi 3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
Seq. No.
                   166003
Seq. ID
                   LIB3177-097-P1-K1-A3
                   BLASTX
Method
NCBI GI
                   q4689386
BLAST score
                   406
                   7.0e-40
E value
                   88
Match length
                   86
% identity
NCBI Description
                   (AF139468) photosystem I reaction center subunit III [Vigna
                   radiata]
Seq. No.
                   166004
                   LIB3177-097-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120667
BLAST score
                   537
                   6.0e-55
E value
Match length
                   137
                   78
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                   thaliana >gi 166706 (M64116) cystolic
                   glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
```

Match length

461

```
Seq. No.
                  166005
Seq. ID
                  LIB3177-097-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q3413700
BLAST score
                  620
E value
                  9.0e-65
Match length
                  145
% identity
                  87
NCBI Description
                  (AC004747) putative YME1 protein [Arabidopsis thaliana]
Seq. No.
                  166006
                  LIB3177-097-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  668
E value
                  2.0e-70
Match length
                  124
% identity
                  98
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  166007
                  LIB3177-097-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885511
BLAST score
                  473
E value
                  2.0e-47
Match length
                  115
% identity
                  (AF084200) similar to PSI-K subunit of photosystem I from
NCBI Description
                  barley [Medicago sativa]
                  166008
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  g3510336
BLAST score
                  314
                  1.0e-176
E value
Match length
                  457
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18J17, complete sequence [Arabidopsis thaliana]
                  166009
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g3883125
BLAST score
                  406
E value
                  0.0e+00
```

thaliana] >qi 166710 (M64119) qlyceraldehyde-3-phosphate

dehydrogenase [Arabidopsis thaliana]

Match length

```
97
% identity
NCBI Description
                  Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA,
                  complete cds
                  166010
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1709534
BLAST score
                  573
E value
                  3.0e-59
Match length
                  135
% identity
                  DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A)
NCBI Description
                  [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                  GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                  (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                  (GLUTAMYL-GAMMA-SEMIALDE... >gi_2129572_pir_
                  delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis
                  thaliana >gi 829100_emb_CAA60740_ (X87330)
                  pyrroline-5-carboxylate synthetase [Arabidopsis thaliana]
                  >gi 870866 emb CAA60446 (X86777) pyrroline-5-carboxylate
                  synthetase A [Arabidopsis thaliana]
                  >gi_1041248_emb_CAA61593_ (X89414) pyrroline-5-carboxylate
                  synthase [Arabidopsis thaliana] >gi 2642162 (AC003000)
                  delta-1-pyrroline 5-carboxylase synthetase, P5C1
                  [Arabidopsis thaliana]
Seq. No.
                  166011
Seq. ID
                  LIB3177-097-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q4455198
BLAST score
                  737
                  2.0e-78
E value
Match length
                  143
% identity
                  100
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  166012
                  LIB3177-097-P1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3288821
BLAST score
                  630
E value
                  7.0e-66
Match length
                  139
% identity
                  88
NCBI Description
                  (AF063901) alanine:glyoxylate aminotransferase;
                  transaminase [Arabidopsis thaliana]
                  >gi 4733989 gb AAD28669.1 AC007209 5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                  166013
Seq. ID
                  LIB3177-097-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  g2245377
BLAST score
                  477
                  0.0e + 00
E value
```

Method

BLASTN

```
% identity
                   100
NCBI Description
                  Arabidopsis thaliana auxin response factor 1 (ARF1) mRNA,
                  complete cds
Seq. No.
                  166014
Seq. ID
                  LIB3177-097-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g4510360
BLAST score
                  33
                  7.0e-09
E value
Match length
                  65
% identity
                  88
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
                  sequence, complete sequence
Seq. No.
                  166015
Seq. ID
                  LIB3177-097-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2827559
BLAST score
                  265
E value
                  5.0e-23
Match length
                  67
% identity
                  79
NCBI Description
                  (AL021635) predicted protein [Arabidopsis thaliana]
                  >gi_3292808_emb_CAA19798_ (AL031018) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                  166016
Seq. ID
                  LIB3177-097-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q2695703
BLAST score
                  634
E value
                  2.0e-66
Match length
                  149
% identity
                  81
                  (Y10555) CONSTANS [Arabidopsis thaliana]
NCBI Description
                  >gi 2695705 emb CAA71588 (Y10556) CONSTANS [Arabidopsis
                  thaliana]
                  166017
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  662
E value
                  1.0e-69
                  127
Match length
                  98
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  166018
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-B9
```

Seq. ID

```
NCBI GI
                  q3985932
BLAST score
                  134
                  3.0e-69
E value
Match length
                  354
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                 K22J17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166019
Seq. ID
                  LIB3177-097-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  q259446
                  147
BLAST score
                  5.0e-77
E value
Match length
                  168
% identity
                  100
NCBI Description
                  glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana,
                  C24, mRNA, 680 nt]
                  166020
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q113024
BLAST score
                  712
                  2.0e-75
E value
                  136
Match length
% identity
                  99
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                  >gi 553043 (M83534) isocitrate lyase [Arabidopsis thaliana]
Seq. No.
                  166021
Seq. ID
                  LIB3177-097-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1171993
BLAST score
                  654
E value
                  8.0e-69
Match length
                  128
% identity
                  PHENYLALANINE AMMONIA-LYASE 2 >gi 1076370 pir S52991
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis
                  thaliana >gi_497421 (L33678) phenylalanine ammonia lyase
                  [Arabidopsis thaliana]
Seq. No.
                  166022
Seq. ID
                  LIB3177-097-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q2342687
BLAST score
                  800
                  8.0e-86
E value
                  154
Match length
                  98
% identity
                  (AC000106) Similar to Beta integral membrane protein .
NCBI Description
                  (gb_U43629). EST gb_W43122 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  166023
```

LIB3177-097-P1-K1-C6

```
BLASTX
Method
NCBI GI
                  g4507433
BLAST score
                  240
E value
                  4.0e-20
                  129
Match length
                  42
% identity
NCBI Description
                  testis enhanced gene transcript
                  >gi 1729891 sp P55061 TEGT HUMAN TEGT PROTEIN (TESTIS
                  ENHANCED GENE TRANSCRIPT) >gi 2136254 pir I38334 TEGT
                  (testis enhanced gene transcript) - human
                  >gi 458545 emb CAA53472 (X75861) TEGT [Homo sapiens]
                  166024
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4567208
BLAST score
                  192
                  2.0e-14
E value
                  81
Match length
                  56
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
               . 166025
Seq. No.
                  LIB3177-097-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245110
                  274
BLAST score
                  3.0e-24
E value
                  54
Match length
                  100
% identity
NCBI Description
                 (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  166026
Seq. ID
                  LIB3177-097-P1-K1-C9
                  BLASTX
Method
NCBI GI
                  g2119846
                  408
BLAST score
                  5.0e-40
E value
                  80
Match length
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  166027
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-D1
                  BLASTN
Method
NCBI GI
                  g3492855
                  355
BLAST score
                  0.0e+00
E value
                  395
Match length
                  97
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F20N2,
```

complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  166028
Seq. ID
                  LIB3177-097-P1-K1-D10
Method
                  BLASTX
                  g3046703
NCBI GI
BLAST score
                  201
                  5.0e-18
E value
Match length
                  56
% identity
                  86
                  (AL021749) protein kinase ADK1-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  166029
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-D11
                  BLASTN
Method
NCBI GI
                  g3228389
BLAST score
                  259
E value
                  1.0e-143
Match length
                  447
% identity
                  98
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  166030
Seq. No.
                  LIB3177-097-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2829899
BLAST score
                  449
E value
                  1.0e-44
Match length
                  145
% identity
                  58
NCBI Description
                  (AC002311) similar to ripening-induced protein,
                  gp AJ001449 2465015 and major#latex protein,
                  gp X91961 1107495 [Arabidopsis thaliana]
Seq. No.
                  166031
Seq. ID
                  LIB3177-097-P1-K1-D2
                  BLASTN
Method
NCBI GI
                  g4309683
BLAST score
                  460
                  0.0e+00
E value
Match length
                  480
% identity
                  Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                                                                    , t
                  166032
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-D3
Method
                  BLASTX
                  g3893081
NCBI GI
BLAST score
                  652
E value
                  2.0e-68
Match length
                  157
                  77
% identity
NCBI Description (AJ012747) MLH1 protein [Arabidopsis thaliana]
```

```
Seq. No.
                   166033
Seq. ID
                   LIB3177-097-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g119143
BLAST score
                   711
                   2.0e-75
E value
                   140
Match length
                  ÷ 98
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                 (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi 1369927 emb CAA34454 (X16431) elongation factor
                   1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455
                   (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                   >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                   >gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
                   166034
Seq. No.
                   LIB3177-097-P1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3522954
BLAST score
                   572
                   4.0e-59
E value
                   137
Match length
                   82
% identity
                  (AC004411) IAA20 [Arabidopsis thaliana]
NCBI Description
                   166035
Seq. No.
Seq. ID
                   LIB3177-097-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q119975
                   505
BLAST score
                   2.0e-51
E value
Match length
                   118
                   88
% identity
                   FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin
NCBI Description
                   [2Fe-2S] precursor - Arabidopsis thaliana
                   >gi 16437 emb CAA35754 (X51370) ferredoxin precursor
                   [Arabidopsis thaliana] >gi 166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
Seq. No.
                   166036
Seq. ID
                   LIB3177-097-P1-K1-D8
                   BLASTX
Method
NCBI GI
                   g2119846
BLAST score
                   615
E value
                   3.0e-64
                   118
Match length
                   98
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
```

thaliana] >gi 3337371 (AC004481) photosystem II type I

Method

BLASTX

chlorophyll a/b binding protein [Arabidopsis thaliana]

```
Seq. No.
                      166037
 Seq. ID
                      LIB3177-097-P1-K1-D9
Method
                      BLASTX
NCBI GI
                      g4467137
BLAST score
                      332
E value
                      4.0e-32
Match length
                      149
 % identity
                      45
NCBI Description
                     (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                      166038
Seq. ID
                      LIB3177-097-P1-K1-E1
Method
                      BLASTX
NCBI GI
                      g115470
BLAST score
                      380
E value
                      1.0e-36
Match length
                      143
% identity
                      57
NCBI Description
                      CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                      DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase
                      (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                      [Arabidopsis thaliana]
Seq. No.
                      166039
                      LIB3177-097-P1-K1-E10
Seq. ID
Method
                      BLASTX
NCBI GI
                      g1076708
BLAST score
                      587
E value
                      7.0e-61
Match length
                     120
% identity
NCBI Description
                     seed tetraubiquitin - common sunflower
                     >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
>gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
>gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin
[Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
                     Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
                     putative polyubiquitin [Arabidopsis thaliana]
                     >gi 1096513_prf 2111434A tetraubiquitin [Helianthus
                     annuus]
Seq. No.
                     166040
Seq. ID
                     LIB3177-097-P1-K1-E11
Method
                     BLASTX
NCBI GI
                     g3915826
BLAST score
                     650
E value
                     3.0e-68
Match length
                     152
% identity
                     82
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                     166041
Seq. ID
                     LIB3177-097-P1-K1-E12
```

BLAST score

```
NCBI GI
                    g1145699
 BLAST score
                    546
 E value
                    4.0e-56
 Match length
                   111
 % identity
                   99
 NCBI Description
                   (U39486) delta tonoplast integral protein [Arabidopsis
                   thaliana]
 Seq. No.
                   166042
 Seq. ID
                   LIB3177-097-P1-K1-E2
 Method
                   BLASTX
 NCBI GI
                   q4263525
 BLAST score
                   574
 E value
                   2.0e-59
 Match length
                   135
 % identity
 NCBI Description
                   (AC004044) putative photosystem I reaction center subunit
                   II precursor [Arabidopsis thaliana]
Seq. No.
                   166043
Seq. ID
                   LIB3177-097-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g4160280
BLAST score
                   313
E value
                   9-0e-29
Match length
                   95
% identity
                   61
NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]
Seq. No.
                   166044
                   LIB3177-097-P1-K1-E4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4263774
BLAST score
                   189
E value
                   1.0e-102
Match length
                   475
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20F21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166045
Seq. ID
                   LIB3177-097-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q100525
BLAST score
                   624
                  3.0e-65
E value
Match length
                  135
% identity
                  25
NCBI Description
                  ubiquitin precursor UbB2 - common sunflower (fragment)
                  >gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein
                  [Helianthus annuus]
Seq. No.
                  166046
Seq. ID
                  LIB3177-097-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g1363489
```

E value

3.0e-77

```
E value
                    6.0e-66
 Match length
                    115
 % identity
                    100
                    thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
 NCBI Description
                    thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                    glucohydrolase [Arabidopsis thaliana]
 Seq. No.
                    166047
 Seq. ID
                    LIB3177-097-P1-K1-E9
 Method
                    BLASTX
 NCBI GI
                    q166834
 BLAST score
                    445
 E value
                    3.0e-44
 Match length
                    103
 % identity
                    87
                    (M86720) ribulose bisphosphate carboxylase/oxygenase
 NCBI Description
                    activase [Arabidopsis thaliana] >gi_2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
 Seq. No.
                   166048
 Seq. ID
                   LIB3177-097-P1-K1-F1
 Method
                   BLASTX
NCBI GI
                   g2191138
 BLAST score
                   421
E value
                  ~2.0e-41
Match length
                   92
% identity
                   93
NCBI Description
                   (AF007269) A_IG002N01.18 gene product [Arabidopsis
                   thaliana]
Seq. No.
                   166049
Seq. ID
                   LIB3177-097-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q1762584
BLAST score
                   744
E value
                   3.0e-79
Match length
                   144
% identity
                   74
NCBI Description
                   (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
                   [Arabidopsis thaliana]
Seq. No.
                   166050
Seq. ID
                   LIB3177-097-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g2244759
BLAST score
                   588
E value
                   5.0e-61
Match length
                   125
% identity
NCBI Description
                  (297335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.
                  166051
Seq. ID
                  LIB3177-097-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g4587564
BLAST score
                  727
```

NCBI GI

BLAST score

```
Match length
                     152
 % identity
                     91
 NCBI Description
                     (AC006550) Strong similarity to gb\_X14017 photosystem I
                     reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,
                     gb_N65521, gb_T42498, gb_T41918, gb_N38024
 Seq. No.
                     166052
 Seq. ID
                    LIB3177-097-P1-K1-F2
 Method
                    BLASTX
 NCBI GI
                    g2529663
 BLAST score
                    618
 E value
                    1.0e-64
 Match length
                    125
 % identity
                    98
 NCBI Description
                    (AC002535) putative lysophospholipase [Arabidopsis
                    thaliana] >gi_3738277 (AC005309) putative lysophospholipase
                     [Arabidopsis thaliana]
 Seq. No.
                    166053
 Seq. ID
                    LIB3177-097-P1-K1-F3
 Method
                    BLASTX
 NCBI GI
                    g2529663
 BLAST score
                    482
 E value
                    8.0e-55
Match length
                    135
 % identity
                    84
NCBI Description
                    (AC002535) putative lysophospholipase [Arabidopsis
                    thaliana] >gi_3738277 (AC005309) putative lysophospholipase
                    [Arabidopsis Thaliana]
Seq. No.
                    166054
Seq. ID
                    LIB3177-097-P1-K1-F4
Method
                    BLASTX
NCBI GI
                    g3182982
BLAST score
                    68
E value
                    5.6e+00
Match length
                    105
% identity
                    87
NCBI Description
                   CELL ELONGATION PROTEIN DIMINUTO (CELL ELONGATION PROTEIN
                   DWARF1) >gi_602302 (L38520) diminuto [Arabidopsis thaliana]
Seq. No.
                   166055
Seq. ID
                   LIB3177-097-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g3980383
BLAST score
                   440
E value
                   1.0e-43
Match length
                   83
% identity
                   100
NCBI Description
                   (AC004561) unknown protein [Arabidopsis thaliana]
Seq. No.
                   166056
Seq. ID
                   LIB3177-097-P1-K1-F7
Method
                   BLASTN
```

g2062153

```
1.0e-10
E value
                  36
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  166057
Seq. No.
                  LIB3177-097-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  q3738291
NCBI GI
BLAST score
                  470
                  4.0e-47
E value
                  117
Match length
% identity
                  83
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  166058
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-F9
                  BLASTX
Method
NCBI GI
                  q132102
BLAST score
                  692
E value
                  3.0e-73
                  134
Match_length
                  97
% identity.
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir RKMUB2
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B2 precursor - Arabidopsis thaliana >gi 16194 emb CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  166059
Seq. ID
                  LIB3177-097-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g113617
BLAST score
                  644
E value
                  2.0e-67
                  128
Match length
                  99
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                  >gi_68199_pir__ADMU fructose-bisphosphate aldolase (EC
                  4.1.2.13) - Arabidopsis thaliana >gi 16284 emb CAA37226
                   (X53058) fructose 1,6-diphosphate aldolase [Arabidopsis
                  thaliana]
                  166060
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-G10
                  BLASTX
Method
NCBI GI
                  g4567268
BLAST score
                  456
                  1.0e-45
E value
                  102
Match length
                  96
% identity
NCBI Description
                  (AC006841) putative fructose biphosphate aldolase
                  [Arabidopsis thaliana]
```

166061

Seq. No.

E value

6.0e-14

```
Seq. ID
                   LIB3177-097-P1-K1-G11
 Method
                   BLASTX
 NCBI GI
                    g1145699
 BLAST score
                    511
 E value
                    3.0e-52
 Match length
                   104
 % identity
                   98
 NCBI Description
                    (U39486) delta tonoplast integral protein [Arabidopsis
                   thaliana]
 Seq. No.
                   166062
 Seq. ID
                   LIB3177-097-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g2119846
BLAST score
                   260
E value
                   4.0e-23
Match length
                   51
                   100
 % identity
NCBI Description
                   chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi_3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   166063
                   LIB3177-097-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g114591
BLAST score
                   643
E value
                   2.0e-67
Match length
                   132
% identity
                   98
NCBI Description
                   ATP SYNTHASE EPSILON CHAIN >gi_81663_pir_ S01903
                   H+-transporting ATP synthase (\overline{EC} \ 3.6.1.34) epsilon chain -
                   Arabidopsis thaliana chloroplast >gi_11334_emb_CAA31381_
                   (X12889) Cf1 ATPase epsilon subunit (AA 1 - 13\overline{2})
                   [Arabidopsis thaliana]
Seq. No.
                   166064
Seq. ID
                   LIB3177-097-P1-K1-G3
Method
                   BLASTN
NCBI GI
                   g2739359
BLAST score
                   171
E value
                   2.0e-91
Match length
                   178
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T9J22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166065
Seq. ID
                   LIB3177-097-P1-K1-G5
. Method
                   BLASTX
NCBI GI
                   g3122724
BLAST score
                   184
```

% identity

_ : .

```
50
Match length
                   76
% identity
                   60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
NCBI Description
                   protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                   166066
Seq. ID
                   LIB3177-097-P1-K1-G6
                   BLASTX
Method
NCBI GI
                   g3913379
BLAST score
                   479
E value
                   2.0e-48
Match length
                   98
% identity
                   91
                  CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)
NCBI Description
                   >gi 1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis
                   thaliana]
                   166067
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-G8
                  BLASTX
Method
NCBI GI
                   g4572671
BLAST score
                   206
                   3.0e-16
E value
Match length
                   104
                   41
% identity
                   (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  166068
Seq. ID
                  LIB3177-097-P1-K1-G9
Method
                  BLASTX
                  g2853090
NCBI GI
BLAST score
                   344
                  1.0e-32
E value
                  70
Match length
                  100
% identity
NCBI Description
                   (AL021768) small GTP-binding protein-like [Arabidopsis
                  thaliana]
                  166069
Seq. No.
                  LIB3177-097-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4490737
BLAST score
                  525
E value
                  1.0e-53
                  118
Match length
                  88
% identity
NCBI Description
                  (AL035708) putative protein [Arabidopsis thaliana]
                  166070
Seq. No.
Seq. ID
                  LIB3177-097-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  g2335089
BLAST score
                  235
                  1.0e-129
E value
Match length
                  302
                  99
```

.

```
NCBI Description Arabidopsis thaliana chromosome II BAC T11A7 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166071
Seq. ID
                  LIB3177-097-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                   435
E value
                  2.0e-43
Match length
                  83
% identity
                  98
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  166072
Seq. ID
                  LIB3177-097-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  g3046856
BLAST score
                  405
E value
                  0.0e + 00
Match length
                  441
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXI22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166073
Seq. ID
                  LIB3177-097-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  a2119848
BLAST score
                  668
E value
                  2.0e-70
Match length
                  126
% identity.
                  98
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B1 -
                  Arabidopsis thaliana >gi_16366_emb_CAA45789 (X64459)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128229 (AC004077) putative
                  photosystem II type I chlorophyll a/b binding protein
                  [Arabidopsis thaliana] >gi 3337372 (AC004481) putative
                  photosystem II type I chlorophyll a/b binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  166074
Seq. ID
                  LIB3177-097-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g4455336
BLAST score
                  721
E value
                  1.0e-76
Match length
                  142
% identity
                  96
NCBI Description
                  (AL035525) pectinesterase-like protein [Arabidopsis
```

thaliana]

```
166075
Seq. No.
Seq. ID
                   LIB3177-097-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g1363489
BLAST score
                   563
E value
                   3.0e-58
                   104
Match length
                   98
% identity
NCBI Description
                   thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                   thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
                   166076
Seq. No.
Seq. ID
                   LIB3177-097-P1-K1-H7
                   BLASTX
Method
NCBI GI
                   g3560243
BLAST score
                   236
E value
                   2.0e-23
Match length
                   144
                   47
% identity
                  (AL031532) putative hydrolase [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                   166077
Seq. ID
                   LIB3177-097-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g4249379
BLAST score
                   733
                   5.0e-78
E value
Match length
                   146
% identity
                   69
NCBI Description
                   (AC005966) Strong similarity to gb_X82030 chloroplast RNA
                  binding protein (RNP1) from Phaseolus vulgaris.
                   [Arabidopsis thaliana]
                   166078
Seq. No.
                  LIB3177-097-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2760316
BLAST score
                   315
                   1.0e-177
E value
Match length
                   460
                  100
% identity
                  The sequence of BAC F1N21 from Arabidopsis thaliana
NCBI Description
                  chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166079
Seq. ID
                  LIB3177-098-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g584794
BLAST score
                  527
E value
                  7.0e-54
Match length
                  135
% identity
                  81
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
NCBI Description
                  >gi 282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35)
```

curled-leaved tobacco >gi_170289 (M80489) plasma membrane

BLAST score

789

H+ ATPase [Nicotiana plumbaginifolia]

```
Seq. No.
                   166080
Seq. ID
                   LIB3177-098-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q421826
BLAST score
                   523
E value
                   2.0e-53
Match length
                   123
% identity
NCBI Description
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                   >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   166081
Seq. No.
Seq. ID
                   LIB3177-098-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2388578
BLAST score
                   562
                   4.0e-58
E value
Match length
                   114
% identity
                   99
                   (AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs
NCBI Description
                   gb_T75785,gb_R30580,gb_T04698 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   166082
Seq. ID
                   LIB3177-098-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g132102
BLAST score
                   710
E value
                   3.0e-75
Match length
                   136
                   98
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1}.1.39) small chain
                   B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   166083
                   LIB3177-098-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3335378
BLAST score
                   299
E value
                   4.0e-27
Match length
                   66
% identity
                   (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   166084
                  LIB3177-098-P1-K1-A3.
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2335100
```

Match length

```
E value
                   2.0e-84
Match length
                   152
% identity "
                   97
NCBI Description
                  (AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.
                   166085
                  LIB3177-098-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g417148
BLAST score
                   422
E value
                   2.0e-41
                   144
Match length
% identity
                   56
NCBI Description
                  PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
                   (G2-4) >gi 99912 pir A33654 heat shock protein 26A -
                   soybean >g\bar{i} 1699\bar{8}1 (M20363) Gmhsp26-A [Glycine max]
Seq. No.
                   166086
Seq. ID
                  LIB3177-098-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g3122753
BLAST score
                   539
E value
                   3.0e-55
Match length
                  104
                   95
% identity
                  60S RIBOSOMAL PROTEIN L44 >gi 2244789 emb_CAB10211.1_
NCBI Description
                   (297336) ribosomal protein [Arabidopsis thaliana]
                  166087
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  g3885511
BLAST score
                  504
E value
                  4.0e-51
                  127
Match length
% identity
NCBI Description
                   (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
                  166088
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-B10
                  BLASTX
Method
NCBI GI
                  g4454036
BLAST score
                  754
                  2.0e-80
E value
                  139
Match length
                  99
% identity
NCBI Description
                  (AL035394) putative major latex protein [Arabidopsis
                  thaliana]
Seq. No.
                  166089
Seq. ID
                  LIB3177-098-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1076287
BLAST score
                  570
E value
                  6.0e-59
```

```
% identity
                   85
NCBI Description
                   amine acid permease - Arabidopsis thaliana
                   >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                   [Arabidopsis thaliana]
Seq. No.
                   166090
Seq. ID
                 --LIB3177-098-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q4218123
BLAST score
                   165
                   2.0e-31
E value
Match length
                   95
% identity
                   82
                   (AL035353) photosystem I subunit PSI-E-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  166091
Seq. ID
                  LIB3177-098-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g4106388
BLAST score
                  249
                  3.0e-21
E value
Match length
                  154
% identity
                  44
NCBI Description
                  (AF074849) unknown [Arabidopsis thaliana]
Seq. No.
                  166092
Seq. ID
                  LIB3177-098-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g2651314
BLAST score
                  384
E value
                  5.0e-37
Match length
                  110
% identity
NCBI Description
                  (AC002336) putative ribosomal protein S26 [Arabidopsis
                  thaliana]
Seq. No.
                  166093
Seq. ID
                  LIB3177-098-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g3355463
BLAST score
                  66
E value
                  1.0e-28
Match length
                  134
% identity
                  87
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166094
Seq. ID
                  LIB3177-098-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q266463
BLAST score
                  644
E value
                  1.0e-67
Match length
                  137
% identity
                  91
                  3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM
NCBI Description
```

BLAST score

634

DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_82259_pir_S25670 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi_445064_prf_1908380A beta isopropylmalate dehydrogenase [Solanum tuberosum]

```
Seq. No.
                   166095
 Seq. ID
                   LIB3177-098-P1-K1-B8
Method
                   BLASTN
NCBI GI
                   g2351070
BLAST score
                   34
E value
                   2.0e-09
Match length
                   58
% identity
                   90
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MTH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166096
Seq. ID
                   LIB3177-098-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2392021
BLAST score
                   522
E value
                   3.0e-53
Match length
                   147
% identity
                   63
NCBI Description
                  (D63425) phopholipid hydroperoxide glutathione
                   peroxidase-like protein [Spinacia oleracea]
Seq. No.
                   166097
                   LIB3177-098-P1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3935164
BLAST score
                   72
E value
                   4.0e-17
Match length
                   82
% identity
NCBI Description
                  (AC004557) F17L21.7 [Arabidopsis thaliana]
Seq. No.
                   166098
Seq. ID
                   LIB3177-098-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g585536
BLAST score
                   707
E value
                   5.0e-75
Match length
                  129
% identity
                  100
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
NCBI Description
                  >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
                   [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)
                  thioglucosidase [Arabidopsis thaliana]
Seq. No.
                  166099
Seq. ID
                  LIB3177-098-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3482975
```

NCBI Description

```
E value
                   2.0e-66
Match length
                   146
% identity
                   87
NCBI Description
                  (AL031369) putative protein [Arabidopsis thaliana]
Seq. No.
                   166100
Seq. ID
                   LIB3177-098-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q4741952
BLAST score
                   798
E value
                   1.0e-85
Match length
                   147
% identity
                   65
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  166101
Seq. ID
                  LIB3177-098-P1-K1-C2
Method
                   BLASTX
NCBI GI
                  q421826
BLAST score
                   770
                   2.0e-82
E value
Match length
                   149
                  100
% identity
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
Seq. No.
                  166102
Seq. ID
                  LIB3177-098-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  q4159704
BLAST score
                  200
E value
                  1.0e-108
Match length
                  425
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
Seq. No.
                  166103
Seq. ID
                  LIB3177-098-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q4741952
BLAST score
                  709
E value
                  4.0e-75
Match length
                  131
% identity
                  77
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  166104
Seq. ID
                  LIB3177-098-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g2244800
BLAST score
                  553
E value
                  5.0e-57
Match length
                  112
% identity
                  96
```

(Z97336) carnitine racemase homolog [Arabidopsis thaliana]

```
Seq. No.
                   166105
 Seq. ID
                   LIB3177-098-P1-K1-C6
 Method
                   BLASTX
 NCBI GI
                   g2062158
 BLAST score
                   677
 E value
                   2.0e-71
 Match length
                   143
 % identity
                   47
 NCBI Description
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
                   thaliana)
 Seq. No.
                   166106
 Seq. ID
                   LIB3177-098-P1-K1-C7
 Method
                   BLASTX
 NCBI GI
                   g2832641
BLAST score
                   358
E value
                   5.0e - 34
Match length
                   124
 % identity
                   54
NCBI Description
                  (AL021710) glycolate oxidase - like protein [Arabidopsis
                   thaliana]
Seq. No. 🦿
                   166107
                   LIB3177-098-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2290528
BLAST score
                   451
E value
                   4.0e-45
Match length
                   114
% identity
                   77
NCBI Description (U94746) ATAN11 [Arabidopsis thaliana]
Seq. No.
                   166108
Seq. ID
                   LIB3177-098-P1-K1-C9
Method
                   BLASTN
NCBI GI
                   g4159704
                  95
BLAST score
E value
                   6.0e-46
Match length
                   306
% identity
                   92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MCB17, complete sequence
Seq. No.
                  166109
Seq. ID
                  LIB3177-098-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2529229
BLAST score
                  510
E value
                  8.0e-52
Match length
                  120
% identity
                  78
                 (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                  166110
Seq. ID
                  LIB3177-098-P1-K1-D11
Method
```

BLASTX

E value

1.0e-129

```
NCBI GI
                  q3688799
BLAST score
                   637
                  1.0e-66
E value -
Match length
                  .129
% identity
                   98
NCBI Description
                  (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
                  thaliana]
Seq. No.
                  166111
Seq. ID
                  LIB3177-098-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q3096939
BLAST score
                  539
E value
                  3.0e-55
Match length
                  117
% identity
                  87
NCBI Description
                  (AL023094) putative protein [Arabidopsis thaliana]
Seq. No.
                  166112
Seq. ID
                  LIB3177-098-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2462741
BLAST score
                  664
E value
                  6.0e-70
Match length
                  133
% identity
                  98
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                  (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  166113
Seq. ID
                  LIB3177-098-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q4662609
BLAST score
                  150
E value
                  1.0e-78
Match length
                  469
% identity
                  100
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
                  complete sequence
Seq. No.
                  166114
Seq. ID
                  LIB3177-098-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4006858
BLAST score
                  390
E value
                  9.0e-38
Match length
                  132
% identity
NCBI Description
                  (299707) cold acclimation protein homolog [Arabidopsis
                  thaliana]
Seq. No.
                  166115
Seq. ID
                  LIB3177-098-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  q14342
BLAST score
                  234
```

Seq. ID

```
Match length
                  332
% identity
                  99
NCBI Description A.thaliana mRNA for carbonic anhydrase
Seq. No.
                  166116
Seq. ID
                  LIB3177-098-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                  632
E value
                  4.0e-66
Match length
                  119
                  97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi 68060 pir RKMUB3
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  166117
Seq. ID
                  LIB3177-098-P1-K1-D8
                  BLASTX
Method
NCBI GI
                  g3879734
BLAST score
                  158
E value
                  1.0e-10
Match length
                  89
                  47
% identity
                  (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912
NCBI Description
                  comes from this gene; cDNA EST EMBL: D73452 comes from this
                  gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST
                  EMBL:D74229 comes from this gene; cDNA EST EMBL:D727
                  166118
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3236237
BLAST score
                  417
E value
                  6.0e-41
Match length
                  137
% identity
NCBI Description
                  (AC004684) putative ribotol dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  166119
Seq. ID
                  LIB3177-098-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q2501188
BLAST score
                  633
E value
                  3.0e-66
Match length
                  144
                  89
% identity
NCBI Description
                  THIAZOLE BIOSYNTHETIC ENZYME >gi 2129750 pir S71191 TH14
                  protein homolog - Arabidopsis thaliana >gi_1113783 (U17589)
                  Thil protein [Arabidopsis thaliana]
Seq. No.
                  166120
```

LIB3177-098-P1-K1-E11

Seq. ID

```
Method
                   BLASTX
NCBI GI
                   q4585882
BLAST score
                   394
E value
                   2.0e-38
Match length
                   79
% identity
                   97
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  166121
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-E12
                  BLASTX
Method
NCBI GI
                  q99735
                   384
BLAST score
                   5.0e-37
E value
                  108
Match length
% identity
                  72
NCBI Description
                  L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                  Arabidopsis thaliana (fragment)
                  166122
Seq. No.
                  LIB3177-098-P1-K1-E2
Seq. ID
                 BLASTX
Method
NCBI GI
                  g132074
BLAST score
                  673
E value
                  5.0e-71
Match length
                  122
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  166123
Seq. ID
                  LIB3177-098-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q4008012
BLAST score
                  494
E value
                  6.0e-50
Match length
                  154
                  68
% identity
NCBI Description
                  (AF084037) receptor-like protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  166124
Seq. ID
                  LIB3177-098-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  q4589444
BLAST score
                  313
E value
                  1.0e-176
Match length
                  328
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWF20, complete sequence
Seq. No.
                  166125
```

LIB3177-098-P1-K1-E5

E value

1.0e-66

```
Method
                   BLASTX
NCBI GI
                   g3201613
BLAST score
                   52
                   1.0e-40
E value
Match length
                   89
% identity
                   93
NCBI Description
                  (AC004669) glutathione S-transferase [Arabidopsis thaliana]
Seq. No.
                   166126
                  LIB3177-098-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4204274
BLAST score
                   708
E value
                   5.0e-75
Match length
                   128
% identity
NCBI Description
                   (ACO04146) ribulose bisphosphate carboxylase, small subunit
                   [Arabidopsis thaliana]
Seq. No.
                  166127
                  LIB3177-098-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2842482
BLAST score
                  310
E value
                  2.0e-28
Match length
                  96
% identity
                   61
NCBI Description
                   (AL021749) protein phosphatase 2C-like protein [Arabidopsis
                  thaliana]
                  166128
Seq. No.
                  LIB3177-098-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3341698
BLAST score
                  594
                  1.0e-61
E value
Match length
                  125
% identity
NCBI Description
                  (AC003672) blue copper-binding protein II [Arabidopsis
                  thaliana]
Seq. No.
                  166129
Seq. ID
                  LIB3177-098-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q2832625
BLAST score
                  439
E value
                  2.0e-43
Match length
                  135
% identity
                  63
NCBI Description
                  (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  166130
Seq. ID
                  LIB3177-098-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q3599491
BLAST score
                  637
```

% identity

```
Match length
                   150
% identity
NCBI Description
                  (AF085149) putative aminotransferase [Capsicum chinense]
Seq. No.
                   166131
                   LIB3177-098-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3142295
BLAST score
                   412
                   2.0e-40
E value
Match length
                   110
% identity
                   68
NCBI Description
                   (AC002411) Strong similarity to phosphoribosylanthranilate
                   transferase gb D86180 from Pisum sativum. [Arabidopsis
                   thaliana]
Seq. No.
                   166132
Seq. ID
                   LIB3177-098-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q4678328
BLAST score
                   385
                   4.0e-37
E value
Match length
                   127
% identity
NCBI Description
                   (AL049658) aldehyde dehydrogenase (NAD+)-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   166133
Seq. ID
                   LIB3177-098-P1-K1-F3
Method
                   BLASTX
                   g4371284
NCBI GI
BLAST score
                   69
E value
                   4.0e-64
Match length
                   127
% identity
                   99
                   (AC006260) putative plasma membrane intrinsic protein 2B
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   166134
Seq. ID
                  LIB3177-098-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  q4662640
BLAST score
                   402
                  0.0e + 00
E value
Match length
                  414
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K19 genomic
                  sequence, complete sequence
Seq. No.
                  166135
Seq. ID
                  LIB3177-098-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g1350720
BLAST score
                  553
                  7.0e-57
E value
Match length
                  111
```

Match length

```
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No.
                    166136
Seq. ID
                    LIB3177-098-P1-K1-F6
Method
                    BLASTX
NCBI GI
                    g132074
BLAST score
                   -741
                    6.0e-79
E value
Match length
                    135
% identity
                    100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                    (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir RKMUA1
                    ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                    166137
Seq. ID
                   LIB3177-098-P1-K1-F7
Method
                   BLASTN
NCBI GI
                   q4757401
BLAST score
                    302
                   1.0e-169
E value
Match length
                   448
% identity
                   98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MGH6, complete sequence
Seq. No.
                   166138
Seq. ID
                   LIB3177-098-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   q1169861
BLAST score
                   470
E value
                   4.0e-47
Match length
                   112
                   79
% identity
NCBI Description G-BOX BINDING FACTOR 2 >gi_81616_pir__ S20884 G-box-binding factor 2 - Arabidopsis thaliana >gi_16288_emb_CAA45357_
                   (X63895) G-box binding factor 2 [Arabidopsis thaliana]
                   >gi_3319286 (AF053228) G-box binding factor 2 [Arabidopsis
                   thaliana]
Seq. No.
                   166139
                   LIB3177-098-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2980770
BLAST score
                   681
E value
                   5.0e-73
Match length
                   141
% identity
NCBI Description
                   (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   166140
Seq. ID
                   LIB3177-098-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q4455253
BLAST score
                   685
E value
                   2.0e-72
```

```
% identity
                   88
NCBI Description (AL035523) superoxide dismutase (EC 1.15.1.1)
                   (Fe) (fragment) [Arabidopsis thaliana]
Seq. No.
                  166141
Seq. ID
                  LIB3177-098-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g3695023
BLAST score
                   472
E value
                   4.0e-64
Match length
                  144
% identity
                  89
NCBI Description (AF055850) unknown [Arabidopsis thaliana]
Seq. No.
                  166142
Seq. ID
                  LIB3177-098-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3927830
BLAST score
                  583
E value
                  2.0e-60
                  150
Match length
                  25
% identity
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  166143
                  LIB3177-098-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2809253
BLAST score
                  662
E value
                  9.0e-70
Match length
                  127
% identity
                  98
NCBI Description (AC002560) F21B7.22 [Arabidopsis thaliana]
Seq. No.
                  166144
Seq. ID
                  LIB3177-098-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3386597
BLAST score
                  576
E value
                  1.0e-59
Match length
                  109
% identity
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3702347 (AC005397) putative permease [Arabidopsis
                  thaliana]
Seq. No.
                  166145
Seq. ID
                  LIB3177-098-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1707412
BLAST score
                  367
E value
                  5.0e-35
Match length
                  152
% identity
                  48
NCBI Description
                  (X95906) Cleavage and Polyadenylation Specifity Factor
```

protein [Bos taurus]

```
166146
Seq. No.
Seq. ID
                   LIB3177-098-P1-K1-G4
Method
                   BLASTN ···
NCBI GI
                   g2351063
BLAST score
                   208
E value
                   1.0e-113
                   454
Match length
% identity
                   96
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCL19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166147
Seq. ID
                   LIB3177-098-P1-K1-G5
Method
                   BLASTX ·
NCBI GI
                   g2864617
BLAST score
                   523
                   2.0e-53
E value
Match length
                   132
                   82
% identity
NCBI Description
                   (AL021811) H+-transporting ATP synthase chain9 - like
                   protein [Arabidopsis thaliana]
Seq. No.
                   166148
Seq. ID
                   LIB3177-098-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q544018
BLAST score
                   613
E value
                   7.0e-64
Match length
                   153
% identity
                   78
NCBI Description
                   NITRATE/CHLORATE TRANSPORTER >gi_1076359_pir__A45772
                   nitrate-inducible nitrate transporter - Arabidopsis
                   thaliana >gi_166668 (L10357) CHL1 [Arabidopsis thaliana]
                   >gi 3157921 (AC002131) Identical to nitrate/chlorate
                   transporter cDNA gb_L10357 from A. thaliana. ESTs gb_H37533 and gb_R29790, gb_T46117, gb_T46068, gb_T75688,
                   gb_R29817, gb_R29862, gb Z34634 and gb Z34258 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   166149
Seq. ID
                   LIB3177-098-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q512400
BLAST score
                   562
                   6.0e - 58
E value
Match length
                   153
% identity
                   71
NCBI Description (X74947) annexin [Medicago sativa]
Seq. No.
                   166150
Seq. ID
                   LIB3177-098-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g3915847
BLAST score
                   293
E value
                   1.0e-26
Match length
                   76
% identity
                 . 80
```

Seq. No.

Seq. ID

166155

LIB3177-098-P1-K1-H2

```
NCBI Description
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  166151
Seq. ID
                  LIB3177-098-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  748
E value
                  1.0e-79
Match length
                  136
% identity .
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  166152
Seq. ID
                  LIB3177-098-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q3643610
BLAST score
                  520
E value
                  5.0e-53
Match length
                  103
% identity
                  (AC005395) putative serine/threonine protein kinase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  166153
Seq. ID
                  LIB3177-098-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q1710530
BLAST score
                  331
E value
                  3.0e - 31
Match length
                  83
% identity
                  75
NCBI Description
                  60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi 1107487 emb CAA63025_ (X91959) 60S ribosomal protein
                  L27a [Arabidopsis thaliana]
Seq. No.
                  166154
Seq. ID
                  LIB3177-098-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q99696
BLAST score
                  490
E value
                  1.0e-49
Match length
                  117
% identity
                  glutamate--ammonia ligase (EC 6.3.1.2) precursor,
NCBI Description
                  chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                  >gi_240070_bbs_69728 (S69727) light-regulated glutamine
                  synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                  aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln
                  synthetase [Arabidopsis thaliana]
```

```
Method
                  BLASTX
NCBI GI
                  g1732572
BLAST score
                  601
E value
                  2.0e-66
Match length
                  133
% identity
                  92
NCBI Description (U72154) beta-glucosidase [Brassica nigra]
Seq. No.
                  166156
                  LIB3177-098-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2392762
BLAST score
                  147
                  4.0e-77
E value
                  294
Match length
% identity
NCBI Description
                  Arabidopsis thaliana BAC T32N15 from chromsome III near 54
                  cM, complete sequence
Seq. No.
                  166157
                  LIB3177-098-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499810
BLAST score
                  684
E value
                  3.0e-72
Match length
                  131
                  99
% identity
                  PROFILIN 1 >gi_2981657_pdb_1A0K Profilin I From
NCBI Description
                  Arabidopsis Thaliana >gi 1353763 (U43322) profilin 1
                  [Arabidopsis thaliana] >gi 1353770 (U43325) profilin 1
                  [Arabidopsis thaliana] >gi 1835878 bbs 179026 (S82691)
                  profilin isoform 1 [Arabidopsis thaliana, Columbia,
                  flowers, Peptide, 131 aa] [Arabidopsis thaliana]
                  >gi 3687242 (AC005169) profilin 1 [Arabidopsis thaliana]
                  166158
Seq. No.
                  LIB3177-098-P1-K1-H5
Seq. ID
Method
                  BLASTX
                  g3913525
NCBI GI
BLAST score
                  120
                  1.0e-26
E value
Match length
                  110
                  71
% identity
                  DNA POLYMERASE DELTA CATALYTIC CHAIN >qi 2895198 (AF020193)
NCBI Description
                  DNA polymerase delta [Glycine max]
                  166159
Seq. No.
Seq. ID
                  LIB3177-098-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  g3757516
BLAST score
                  405
                  2.0e-39
E value
Match length
                  143
% identity
NCBI Description
                  (AC005167) putative TMV resistance protein [Arabidopsis
```

thaliana]

```
Seq. No.
                   166160
Seq. ID
                   LIB3177-098-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q4490737
BLAST score
                   516
E value
                   3.0e-60
Match length
                   140
% identity
                   86
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   166161
Seq. ID
                   LIB3177-098-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g3834302
BLAST score
                   57
                   6.0e-52
E value
Match length
                  113
% identity
                   93
                  (AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase
NCBI Description
                   from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  166162
                  LIB3177-099-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3193311
BLAST score
                  259
E value
                  1.0e-144
Match length
                  453
% identity
                  100
NCBI Description Arabidopsis thaliana BAC F6N15
Seq. No.
                  166163
Seq. ID
                  LIB3177-099-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2983203
BLAST score
                  145
E value
                  5.0e-09
Match length
                  57
% identity
                  42
NCBI Description
                  (AE000696) polypeptide deformylase [Aquifex aeolicus]
Seq. No.
                  166164
                  LIB3177-099-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4056477
BLAST score
                  555
                  4.0e-57
E value
Match length
                  127
% identity
                  (AC005896) putative RNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166165
Seq. ID
                  LIB3177-099-P1-K1-A2
Method
```

BLASTX

q3386609

NCBI GI

```
BLAST score
                   190
                   1.0e-14
E value
Match length
                   90
% identity
                   49
NCBI Description
                   (AC004665) putative DNA-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   166166
Seq. ID
                   LIB3177-099-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g2443751
BLAST score
                   677
E value
                   2.0e-71
Match length
                   135
                   99
% identity
NCBI Description
                   (AF020303) fumarase [Arabidopsis thaliana] >gi 2529676
                   (AC002535) putative fumarase [Arabidopsis thaliana]
Seq. No.
                   166167
Seq. ID
                   LIB3177-099-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g2160182
BLAST score
                   160
E value
                   8.0e-11
Match length
                   129
% identity
                   36
NCBI Description
                   (AC000132) ESTs gb ATTS1236, gb T43334, gb N97019, qb AA395203
                   come from this gene. [Arabidopsis thaliana]
Seq. No.
                   166168
                  LIB3177-099-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2462840
BLAST score
                   168
                   5.0e-12
E value
Match length
                   34
                   97
% identity
NCBI Description
                  (AF000657) cytochrome C [Arabidopsis thaliana]
Seq. No.
                   166169
Seq. ID
                  LIB3177-099-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   q1934741
BLAST score
                   73
E value
                   9.1e-01
Match length
                   55
% identity
                  11
                  (Y10013) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166170
Seq. ID
                  LIB3177-099-P1-K1-A8
Method .
                  BLASTX
NCBI GI
                  q4512655
BLAST score
                  363
E value
                  5.0e-35
Match length
                  69
```

```
% identity
NCBI Description
                    (AC007048) putative protein phosphatase 2C [Arabidopsis
                    thaliana]
Seq. No.
                    166171
Seq. ID
                    LIB3177-099-P1-K1-A9
Method
                    BLASTX
NCBI GI
                    g2118220
BLAST score
                    244
                    6.0e-21
E value
                    68
Match length
                    76
% identity
NCBI Description
                    H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                    (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581)
                    vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                    thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16
                    kDa proteolipid [Arabidopsis thaliana]
                    >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar
H+-transporting ATPase 16K chain [Arabidopsis thaliana]
>gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
                    ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
                    >gi 4589976 gb_AAD26493.1_AC007195_7 (AC007195) vacuolar
                    H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.
                    166172
                    LIB3177-099-P1-K1-B1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2982464
BLAST score
                    240
E value
                    3.0e-20
Match length
                    130
% identity
                    41
                   (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    166173
                    LIB3177-099-P1-K1-B10
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115783
BLAST score
                    618
E value
                    2.0e-64
Match length
                    116
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                    (CAB-140) (LHCP) >gi_16376_emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thalianal
Seq. No.
                   166174
Seq. ID
                   LIB3177-099-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q166410
BLAST score
                   220
E value
                   6.0e-18
Match length
                   85
% identity
                   52
```

NCBI Description (L07291) Alfin-1 [Medicago sativa]

BLAST score

```
Seq. No.
                   166175
Seq. ID
                  LIB3177-099-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g4741950
BLAST score
                   738
E value
                   1.0e-78
Match length
                   138
% identity
                   100
NCBI Description
                  (AF134125) Lhcb2 protein [Arabidopsis thaliana]
                   166176
Seq. No.
Seq. ID
                  LIB3177-099-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3288823
BLAST score
                   676
                   3.0e-71
E value
Match length
                  133
                  100
% identity
NCBI Description
                  (AF063852) FUS5 [Arabidopsis thaliana]
                  166177
Seq. No.
Seq. ID
                  LIB3177-099-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  q2645198
BLAST score
                  45
                  5.0e-16
E value
                  162
Match length
                  83
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T26J12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166178
Seq. ID
                  LIB3177-099-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  g4490324
BLAST score
                  115
E value
                  4.0e-58
Match length
                  131
                  97
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
                  (ESSA project)
Seq. No.
                  166179
Seq. ID
                  LIB3177-099-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q3549669
BLAST score
                  677
                  2.0e-71
E value
Match length
                  136
                  98
% identity
NCBI Description
                  (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                  166180
Seq. ID
                  LIB3177-099-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  q2564050
```

Method

BLASTX

```
E value
                   0.0e + 00
Match length
                   428
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MUA22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166181
Seq. ID
                  LIB3177-099-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2507281
BLAST score
                   702
E value
                  2.0e-74
Match length
                  129
% identity
                  98
NCBI Description
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb CAA66048
                   (X97380) atran2 [Arabidopsis thaliana]
Seq. No.
                  166182
                  LIB3177-099-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3355480
BLAST score
                  325
E value
                  3.0e-30
Match length
                  100
% identity
                  59
                  (AC004218) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
                  thaliana}
Seq. No.
                  166183
Seq. ID
                  LIB3177-099-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  348
E value
                  3.0e-33
Match length
                  74
                  88
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  166184
Seq. ID
                  LIB3177-099-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3318617
BLAST score
                  742
E value
                  4.0e-79
Match length
                  139
% identity
                  100
NCBI Description
                  (AB016066) mitochondrial phosphate transporter [Arabidopsis
                  thaliana]
Seq. No.
                  166185
Seq. ID
                  LIB3177-099-P1-K1-C5
```

Method

BLASTN

```
NCBI GI
                   g3445209
BLAST score
                   787
E value
                   2.0e-84
Match length
                   148
% identity
                   99
NCBI Description
                   (AC004786) putative serine carboxypeptidase I [Arabidopsis
                   thaliana]
Seq. No.
                   166186
Seq. ID
                   LIB3177-099-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   q2088638
BLAST score
                   422
                   0.0e + 00
E value
                   446
Match length
% identity
                   36
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T28M21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166187
                   LIB3177-099-P1-K1-C7
Seq. ID
                   BLASTX
Method
                   q4455253
NCBI GI
                  . 368
BLAST score
                   3.0e-35
E value
                   87
Match length
% identity
                   80
NCBI Description
                   (AL035523) superoxide dismutase (EC 1.15.1.1)
                   (Fe)(fragment) [Arabidopsis thaliana]
Seq. No.
                   166188
Seq. ID
                   LIB3177-099-P1-K1-C8
Méthod
                   BLASTX
NCBI GI
                   a585536
BLAST score
                   51
E value
                   3.0e-79
Match length
                   146
% identity
NCBI Description
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
                  >gi 1362006 pir S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
                   [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)
                  thioglucosidase [Arabidopsis thaliana]
Seq. No.
                  166189
Seq. ID
                  LIB3177-099-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g441490
BLAST score
                  80
E value
                  3.0e-37
Match length
                  80
                  100
% identity
NCBI Description
                  S.alba chloroplast trnR gene
Seq. No.
                  166190
Seq. ID
                  LIB3177-099-P1-K1-D1
```

Match length

```
NCBI GI
                   g2828182
BLAST score
                   370
                   0.0e+00
E value
Match length
                   374
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166191
                  LIB3177-099-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729479
BLAST score
                   394
E value
                   3.0e-38
Match length
                  100
                  73
% identity
NCBI Description
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >qi 551131
                   (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
Seq. No.
Seq. ID
                  LIB3177-099-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  q1946354
BLAST score
                  165
E value
                   5.0e-88
Match length
                  169
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  166193
Seq. ID
                  LIB3177-099-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q1769968
BLAST score
                  217
E value
                  1.0e-17
Match length
                  84
% identity
                  56
NCBI Description
                  (Y10156) myrosinase-associated protein [Brassica napus]
Seq. No.
                  166194
Seq. ID
                  LIB3177-099-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q4741954
BLAST score
                  561
E value
                  6.0e-58
Match length
                  119
% identity
NCBI Description
                  (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
Seq. No.
                  166195
                  LIB3177-099-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4337175
BLAST score
                  669
                  2.0e-70
E value
```

Seq. No.

```
% identity
NCBI Description
                     (AC006416) ESTs gb T20589, gb_T04648, gb_AA597906,
                     gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                     166196
                     LIB3177-099-P1-K1-D5
Seq. ID
Method
                     BLASTX
NCBI GI
                     q2119846
BLAST score
                     731
E value
                     9.0e-78
Match length
                     139
                     99
% identity
NCBI Description
                     chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                     Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                     photosystem II type I chlorophyll a /b binding protein
                     [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                     II type I chlorophyll a/b binding protein [Arabidopsis
                     thaliana] >gi 3337371 (AC004481) photosystem II type I
                     chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                     166197
Seq. ID
                     LIB3177-099-P1-K1-D6
Method
                     BLASTN
NCBI GI
                     q4490324
BLAST score
                     222
E value
                     1.0e-121
Match length
                     455
% identity
                    Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
NCBI Description
                     (ESSA project)
Seq. No.
                    166198
Seq. ID
                    LIB3177-099-P1-K1-D7
Method
                    BLASTX
NCBI GI
                    g4218123
BLAST score
                    239
E value
                    3.0e-20
Match length
                    101
% identity
                    52
                    (AL035353) photosystem I subunit PSI-E-like protein
NCBI Description
                     [Arabidopsis thaliana]
Seq. No.
                    166199
Seq. ID
                    LIB3177-099-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g2130028
BLAST score
                    352
E value
                    2.0e-33
                    86
Match length
% identity
                    73
                    B12D protein - barley >gi 471319 emb CAA54065.1 (X76604)
NCBI Description
                    HvB12D [Hordeum vulgare] \overline{>}gi_344\overline{5}292\overline{=}emb_CAA709\overline{3}6 (Y09805)
                    B12Dg1 [Hordeum vulgare]
```

```
Seq. ID
                   LIB3177-099-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q4454036
BLAST score
                   514
E value
                   2.0e-52
Match length
                   94...
% identity
                   100
NCBI Description
                   (AL035394) putative major latex protein [Arabidopsis
                   thalianal
Seq. No.
                   166201
Seq. ID
                   LIB3177-099-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g2920839
BLAST score
                   299
E value
                   4.0e-27
Match length
                   101
% identity
                   53
NCBI Description
                  (U95136) Os-FIERG2 gene product [Oryza sativa]
Seq. No.
                   166202
Seq. ID
                   LIB3177-099-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   q3885943
BLAST score
                   483
E value
                   7.0e-49
Match length
                   98
                   98
% identity
                   (AF095455) PII protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4558559_gb_AAD22652.1_AC007138_16 (AC007138) P II
                   nitrogen sensing protein GLB I [Arabidopsis thaliana]
Seq. No.
                   166203
Seq. ID
                   LIB3177-099-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   g3386593
BLAST score
                   155
E value
                   1.0e-81
Match length
                   452
% identity
                   97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166204
Seq. ID
                  LIB3177-099-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2213595
BLAST score
                   535
                   7.0e-55
E value
Match length
                   121
% identity
                   87
NCBI Description
                   (AC000348) T7N9.15 [Arabidopsis thaliana]
Seq. No.
                   166205
Seq. ID
                  LIB3177-099-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q2446981
```

4.

```
BLAST score
                   167
E value
                   4.0e-54
Match length
                   126
% identity
                   83
NCBI Description
                   (AB005560) AtGDI2 [Arabidopsis thaliana]
                   >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis
                   thaliana]
Seq. No.
                   166206
Seq. ID
                   LIB3177-099-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   q3257003
BLAST score
                   170
E value
                   6.0e-12
Match length
                   88
% identity
                   39
NCBI Description
                   (AP000002) 376aa long hypothetical dehydrogenase
                   [Pyrococcus horikoshii]
Seq. No.
                   166207
Seq. ID
                  LIB3177-099-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g1169278
BLAST score
                   305
E value
                   7.0e-28
Match length
                  75
% identity
                  84
NCBI Description
                  DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14
                  protein [Arabidopsis thaliana]
Seq. No.
                   166208
Seq. ID
                  LIB3177-099-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q544134
BLAST score
                  191
E value
                  7.0e-16
Match length
                  77
% identity
                  57
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
                  >gi_99720_pir__S22863 hypothetical protein - Arabidopsis
                  thaliana >gi_421844_pir__A46260 RecA functional analog
                  DRT100 - Arabidopsis thaliana (fragment)
Seq. No.
                  166209
                  LIB3177-099-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  621
E value
                  6.0e-65
Match length
                  122
% identity
                  98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
```

E value

Match length

NCBI Description

% identity

3.0e-72

147

99

protein (LHCP AB 180) [Arabidopsis thaliana] Seq. No. 166210 Seq. ID LIB3177-099-P1-K1-F1 Method BLASTX NCBI GI g1702986 BLAST score · 533 E value 1.0e-54 Match length 125 % identity 86 NCBI Description 14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana] Seq. No. 166211 Seq. ID LIB3177-099-P1-K1-F10 Method BLASTN NCBI GI g2351073 BLAST score 291 E value 1.0e-163 Match length 450 % identity 100 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MYJ24, complete sequence [Arabidopsis thaliana] Seq. No. 166212 Seq. ID LIB3177-099-P1-K1-F11 Method BLASTX NCBI GI g2497886 BLAST score 300 E value 3.0e-27 Match length 54 100 % identity NCBI Description METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana] Seq. No. 166213 LIB3177-099-P1-K1-F12 Seq. ID Method BLASTX NCBI GI g2286069 BLAST score 547 E value 3.0e-56 Match length 118 % identity 88 NCBI Description (U72155) beta-glucosidase [Arabidopsis thaliana] Seq. No. 166214 Seq. ID LIB3177-099-P1-K1-F2 Method BLASTX NCBI GI g3953473 BLAST score 49

(AC002328) F2202.18 [Arabidopsis thaliana]

Match length

```
Seq. No.
                  166215
Seq. ID
                  LIB3177-099-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2129533
                  710
BLAST score
                 3.0e-75
E value
Match length
                  146
                   96
% identity
                  adenine nucleotide translocase - Arabidopsis thaliana
NCBI Description
                  >gi 1051109 emb CAA89201 (Z49227) adenine nucleotide
                  translocase [Arabidopsis thaliana]
Seq. No.
                  166216
                  LIB3177-099-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267136
BLAST score
                  442
E value
                  6.0e-44
                  117
Match length
                  74
% identity
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED
                  TONOPLAST INTRINSIC PROTEIN) (WSI-TIP)
                  >gi_217869_dbj_BAA02520_ (D13254) transmembrane channel
                  protein [Arabidopsis thaliana] >gi 4371283 gb AAD18141
                   (AC006260) putative plasma membrane intrinsic protein 2C
                   [Arabidopsis thaliana] >gi 384324 prf 1905411A
                  transmembrane channel [Arabidopsis thaliana]
Seq. No.
                  166217
Seq. ID
                  LIB3177-099-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  q4589440
BLAST score
                  431
E value
                  0.0e + 00
Match length
                  452
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSD21, complete sequence
Seq. No.
                  166218
Seq. ID
                  LIB3177-099-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g4741962
BLAST score
                  328
E value
                  6.0e-39
Match length
                  125
% identity
                  57
NCBI Description
                  (AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.
                  166219
Seq. ID
                  LIB3177-099-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1769905
BLAST score
                  504
E value
                  4.0e-51
```

```
% identity
                   72
 NCBI Description
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana].
 Seq. No.
                   166220
                   LIB3177-099-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q99688
BLAST score
                   317
E value
                   2.0e-55
Match length
                   147
% identity
                   80
NCBI Description
                   translation elongation factor eEF-1 alpha chain (gene A4) -
                   Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)
                   elongation factor 1-alpha [Arabidopsis thaliana]
Seq. No.
                   166221
Seq. ID
                   LIB3177-099-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g4263712
BLAST score
                   453
E value
                   3.0e-45
Match length
                   121
% identity
NCBI Description
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
                  thaliana]
Seq. No.
                  166222
Seq. ID
                  LIB3177-099-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g3763935
BLAST score
                   46
E value
                  3.0e-72
Match length
                  136
% identity
                 - 99
NCBI Description (AC004450) putative myb-related transcription factor
                   [Arabidopsis thaliana]
Seq. No.
                  166223
Seq. ID
                  LIB3177-099-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g1914683
BLAST score
                  281
E value
                  5.0e-25
Match length
                  75
% identity
                  73
NCBI Description
                  (Y12013) RAD23, isoform I [Daucus carota]
Seq. No.
                  166224
Seq. ID
                  LIB3177-099-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1710780
BLAST score
                  384
                  4.0e-37
E value
Match length
                  106
% identity
                  72
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_
```

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```
anserina]
                   166225
 Seq. No.
Seq. ID
                   LIB3177-099-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   q2493318
BLAST score
                   339
E value
                   8.0e-32
Match length
                   138
% identity
                   52
NCBI Description
                   BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
                   (Z25471) blue copper protein [Pisum sativum]
                   >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]
Seq. No.
                   166226
Seq. ID
                   LIB3177-099-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q4204268
BLAST score
                   790
E value
                   1.0e-84
Match length
                   145
% identity
                   99
                  (AC005223) 62134 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   166227
Seq. ID
                   LIB3177-099-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g3201633
BLAST score
                   342
E value
                   8.0e-33
Match length
                   70
% identity
                   100
NCBI Description
                   (AC004669) putative cell division protein [Arabidopsis
                   thaliana]
Seq. No.
                   166228
Seq. ID
                  LIB3177-099-P1-K1-G8
Method
                  BLASTN
NCBI GI
                   g4469002
BLAST score
                   422
E value
                   0.0e + 00
Match length
                   445
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                   (ESSA project)
Seq. No.
                  166229
Seq. ID
                  LIB3177-099-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3024434
BLAST score
                  464
E value
                  2.0e-46
Match length
                  113
% identity
                  84
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
                  PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951
```

(X96613) cytoplasmic ribosomal protein S7 [Podospora





(D88663) Tat binding protein 1 [Brassica rapa]

```
Seq. No.
                   166230
 Seq. ID
                   LIB3177-099-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g2446981
BLAST score
                   758
E value
                   6.0e-81
Match length
                   147
% identity
                   99
NCBI Description
                   (AB005560) AtGDI2 [Arabidopsis thaliana]
                   >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis
                   thaliana]
Seq. No.
                   166231
Seq. ID
                   LIB3177-099-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g1053047
BLAST score
                   582
E value
                   3.0e-60
Match length
                   116
% identity
                   100
NCBI Description
                   (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
                   histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                   [Glycine max]
Seq. No.
                   166232
Seq. ID
                   LIB3177-099-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g4539316
BLAST score
                   392
E value
                   5.0e-38
Match length
                   81
% identity
                   100
                   (AL035679) putative fructose-bisphosphate aldolase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   166233
Seq. ID
                   LIB3177-099-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   g2618602
BLAST score
                   167
E value
                   7.0e-89
Match length
                   446
% identity
                   98 ·
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166234
Seq. ID
                  LIB3177-099-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g4006885
BLAST score
                  318
E value
                  1.0e-179
Match length
                  411
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
```

fragment No Seq. No. 166235 Seq. ID LIB3177-099-P1-K1-H5 Method BLASTX NCBI GI ' g541799 BLAST score 197 E value 1.0e-15 Match length 38 % identity NCBI Description light-harvesting chlorophyll a/b-binding protein - ginkgo >gi_349443 (L23107) light-harvesting chlorophyll a/b binding protein of photosystem II [Ginkgo biloba] Seq. No. 166236 Seq. ID LIB3177-099-P1-K1-H7 Method BLASTN NCBI GI q3550981 BLAST score 148 E value 2.0e-77 Match length 400 % identity 100 NCBI Description Arabidopsis thaliana mutM homologue gene, complete cds Seq. No. 166237 Seq. ID LIB3177-099-P1-K1-H8 Method BLASTX NCBI GI q132074 BLAST score 730 E value 1.0e-77 Match length 140 % identity 97 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain Al precursor - Arabidopsis thaliana Seq. No. 166238 Seq. ID LIB3234-001-P1-K1-A10 Method BLASTN NCBI GI g1313927 BLAST score 55 E value 5.0e-22 Match length 219 % identity 82 NCBI Description B.oleracea mRNA for IFA binding protein (sp10) ·Seq. No. 166239 Seq. ID LIB3234-001-P1-K1-A11 Method BLASTN NCBI GI g2645198 BLAST score 45 E value 5.0e-16 Match length 162 % identity

Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

83

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NCBI Description

```
Seq. No.
                    166240
 Seq. ID
                    LIB3234-001-P1-K1-A12
 Method
                    BLASTX
 NCBI GI
                    g4204298
 BLAST score
                    565
 E value
                    3.0e-58-
 Match length
                    145
 % identity
                    77
 NCBI Description
                    (AC003027) lcl_prt_seq No definition line found
                    [Arabidopsis thaliana]
 Seq. No.
                    166241
 Seq. ID
                    LIB3234-001-P1-K1-A2
 Method
                    BLASTX
 NCBI GI
                    g3983125
 BLAST score
                    665
 E value
                    5.0e-70
Match length
                    145
 % identity
                    (AF097648) phosphate/triose-phosphate translocator
NCBI Description
                    precursor [Arabidopsis thaliana]
Seq. No.
                    166242
Seq. ID
                    LIB3234-001-P1-K1-A3
Method
                    BLASTN
NCBI GI
                    g4510360
BLAST score
                    89
E value
                    2.0e-42
Match length
                    326
% identity
                   88
NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic
                   sequence, complete sequence
Seq. No.
                   166243
Seq. ID
                   LIB3234-001-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   g135858
BLAST score
                   353
E value
                   2.0e-33
Match length
                   69
% identity
                   100
NCBI Description
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
                   >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
                   thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                   [Arabidopsis thaliana] >gi_445128_prf _1908432A tonoplast
                   intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.
                   166244
Seq. ID
                   LIB3234-001-P1-K1-A5
Method
                   BLASTN
NCBI GI
                   g4220628
BLAST score
                   457
E value
                   0.0e+00
Match length
                   461
```

% identity

```
% identity
                   77
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                   K24C1, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   166245
                   LIB3234-001-P1-K1-A6
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   q3172156
 BLAST score
                   393
 E value
                   0.0e + 00
 Match length
                   449
 % identity
 NCBI Description
                   Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,
                   complete sequence [Arabidopsis thaliana]
                   166246
 Seq. No.
 Seq. ID
                   LIB3234-001-P1-K1-A7
                   BLASTN
 Method
 NCBI GI
                   q4006885
 BLAST score
                   312
                   1.0e-175
 E value
 Match length
                   393
                   99
 % identity
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                   fragment No
 Seq. No.
                   166247
 Seq. ID
                   LIB3234-001-P1-K1-A9
 Method
                   BLASTX
 NCBI GI
                   g3335169
 BLAST score
                   221
                   8.0e-18
 E value
Match length
                   84
 % identity
NCBI Description
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                   >gi_4455197_emb CAB36520.1 (AL035440) embryo-specific
                   protein 1 (ATS1) [Arabidopsis thaliana]
 Seq. No.
                   166248
Seq. ID
                   LIB3234-001-P1-K1-B10
Method
                   BLASTN
NCBI GI
                   q2828180
BLAST score
                   190
E value
                   1.0e-102
Match length
                   264
 % identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MDK4, complete sequence [Arabidopsis thaliana]
                   166249
Seq. No.
Seq. ID
                   LIB3234-001-P1-K1-B12
Method
                   BLASTX
.NCBI GI
                   q4506223
BLAST score
                   191
E value
                   2.0e-14
Match length
                   99
```

```
NCBI Description
                  proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
                   >gi_3618343_dbj_BAA33214_ (AB009398) 26S proteasome subunit
                  p40.5 [Homo sapiens]
Seq. No.
                   166250
Seq. ID
                  LIB3234-001-P1-K1-B2
Method
                   BLASTX
                  q3236248
NCBI GI
BLAST score
                   535
E value
                   9.0e-55
Match length
                   140
                  77
% identity
NCBI Description
                  (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166251
Seq. ID
                  LIB3234-001-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3914002
BLAST score
                  701
                  3.0e-74
E value
Match length
                  154
% identity
NCBI Description
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >qi 2935279
                   (AF033862) Lon protease [Arabidopsis thaliana]
Seq. No.
                  166252
                  LIB3234-001-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709379
BLAST score
                  489
E value
                  2.0e-49
Match length
                  115
                  78
% identity
NCBI Description
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
                  >gi 881441 (U27653) NADH-plastoquinone oxidoreductase
                  [Lupinus luteus]
Seq. No.
                  166253
Seq. ID
                  LIB3234-001-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2459446
BLAST score
                  626
E value
                  2.0e-65
Match length
                  137
% identity
                  89
                  (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166254
Seq. ID
                  LIB3234-001-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  q4519195
BLAST score
                  434
E value
                  0.0e + 00
Match length
                  438
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
```

MQC12, complete sequence

```
Seq. No.
                   166255
Seq. ID
                   LIB3234-001-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   q3335171
BLAST score
                   674
E value
                   5.0e-71
Match length
                   151
% identity
                   84
NCBI Description
                   (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
Seq. No.
                   166256
Seq. ID
                   LIB3234-001-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   q3540210
BLAST score
                   344
                   0.0e + 00
E value
Match length
                   428
% identity
                   97
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F5A8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166257
Seq. ID
                   LIB3234-001-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g3025445
BLAST score
                   164
E value
                   3.0e-11
Match length
                  123
% identity
                  25
NCBI Description
                  (AC004528) R32184 1 [Homo sapiens]
Seq. No.
                  166258
                  LIB3234-001-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935149
BLAST score
                  408
E value
                  7.0e-40
Match length
                  144
                  56
% identity
NCBI Description
                  (AC005106) T25N20.13 [Arabidopsis thaliana]
Seq. No.
                  166259
Seq. ID
                  LIB3234-001-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g131286
BLAST score
                  552
E value
                  9.0e-57
Match length
                  133
% identity
                  80
NCBI Description
                  PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN PRECURSOR (P6
                  PROTEIN) (CP43) >gi_2144937_pir__F2SP44 photosystem II
                  chlorophyll a-binding protein psbC - spinach chloroplast
                  >gi_12281_emb_CAA25864 (X01724) 44 kd reaction-centre
                  protein [Spinacia oleracea] >gi 343362 (M36833) 44 kD
```

chlorophyll a apoprotein [Spinacia oleracea]

Method

BLASTX

```
Seq. No.
                  166260
Seq. ID
                  LIB3234-001-P1-K1-C4
Method
                  BLASTN
NCBI GI
                   g4589420
BLAST score
                   377
E value
                   0.0e + 00
Match length
                   413
% identity
                   92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K3G17, complete sequence
Seq. No.
                   166261
Seq. ID
                  LIB3234-001-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1418990
BLAST score
                  217
                  2.0e-17
E value
Match length
                  99
% identity
                   42
NCBI Description (275524) unknown [Lycopersicon esculentum]
Seq. No.
                  166262
Seq. ID
                  LIB3234-001-P1-K1-C6
Method ·
                  BLASTX
NCBI GI
                  g2194126
BLAST score
                   515
                  2.0e-52
E value
Match length
                  118
% identity
                  86
NCBI Description
                  (AC002062) EST gb_T43335 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  166263
Seq. ID
                  LIB3234-001-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g4467131
BLAST score
                  439
E value
                  0.0e+00
Match length
                  4.55
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
                  (ESSA project)
Seq. No.
                  166264
                  LIB3234-001-P1-K1-D1
Seq. ID
                                                                      4. ...
Method
                  BLASTX
NCBI GI
                  g3461848
BLAST score
                  111
E value
                  2.0e-19
Match length
                  106
% identity
                  58
NCBI Description
                  (AC005315) putative ATPase [Arabidopsis thaliana]
Seq. No.
                  166265
Seq. ID
                  LIB3234-001-P1-K1-D10
```

```
NCBI GI
                   q4204299
 BLAST score
                    646
 E value
                   8.0e-68
Match length
                   143
 % identity
                   88
NCBI Description
                    (AC003027) lcl_prt_seq No definition line found
                    [Arabidopsis thaliana]
 Seq. No.
                   166266
                   LIB3234-001-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2062164
BLAST score
                   333
E value
                   4.0e-31
Match length
                   125
% identity
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   166267
Seq. ID
                   LIB3234-001-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g421929
BLAST score
                   516
E value
                   1.0e-52
Match length
                   110
% identity
                   14
                   ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156)
NCBI Description
                   ubiquitin [Lycopersicon esculentum]
Seq. No.
                   166268
Seq. ID
                   LIB3234-001-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g2462744
BLAST score
                   237
E value
                   8.0e-20
Match length
                   149
% identity
                   34
NCBI Description
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   166269
Seq. ID
                   LIB3234-001-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g2244792
BLAST score
                   237
E value
                   8.0e-20
Match length
                   66
% identity
                   70
NCBI Description
                  (Z97336) ankyrin homolog [Arabidopsis thaliana]
Seq. No.
                   166270
Seq. ID
                   LIB3234-001-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   q4558586
BLAST score
                   55
E value
                   5.0e-22
Match length
                   71
```

% identity

```
% identity
                   61
NCBI Description
                   Arabidopsis thaliana chromosome 1 BAC T518 sequence,
                   complete sequence
Seq. No.
                   166271
Seq. ID
                   LIB3234-001-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g4585990
BLAST score
                   124
E value
                   1.0e-06
                   139
Match length
% identity
NCBI Description
                   (AC005287) Very similar to disease resistance proteins
                   [Arabidopsis thaliana]
Seq. No.
                   166272
Seq. ID
                   LIB3234-001-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q3297819
BLAST score
                   323
                   7.0e-30
E value
                  104
Match length
% identity
                   65
NCBI Description
                  (AL031032) protein kinase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                   166273
Seq. ID
                  LIB3234-001-P1-K1-E1
Method
                  BLASTN
NCBI GI
                  g4220643
BLAST score
                   226
E value
                   1.0e-124
Match length
                   230
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166274
Seq. ID
                  LIB3234-001-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1169598
BLAST score
                  155
E value
                  2.0e-81
Match length
                  149
% identity
                  100
NCBI Description
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  166275
                  LIB3234-001-P1-K1-E11
Seq. ID
Method -
                  BLASTX
NCBI GI
                  q3273743
BLAST score
                  620
E value
                  9.0e-65
Match length
                  118
```



```
NCBI Description (AF057357) lipid transfer protein 2 precursor [Arabidopsis
                   thaliana] >gi 3786019 (AC005499) unknown protein
                   [Arabidopsis Thaliana]
Seq. No.
                   166276
                   LIB3234-001-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4115915
BLAST score
                   266
E value
                   3.0e-23
Match length
                   112
% identity
                   47
NCBI Description
                   (AF118222) contains similarity to Helix pomatia br-1
                   protein (GB: X96994) [Arabidopsis thaliana]
Seq. No.
                   166277
Seq. ID
                   LIB3234-001-P1-K1-E2
Method
                   BLASTN
NCBI GI
                   q4063737
BLAST score
                   415
                   0.0e + 00
E value
Match length
                   423
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC F24D13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166278
Seq. ID
                   LIB3234-001-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q4163997
BLAST score
                   747
E value
                   1.0e-79
Match length
                   138
% identity
                   99
                   (AF087483) alpha-xylosidase precursor [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   166279
Seq. ID
                  LIB3234-001-P1-K1-E5
Method
                  BLASTX
NCBI GI
                   g3935158
BLAST score
                   401
E value
                   5.0e-39
Match length
                  100
% identity
                  83
NCBI Description
                  (AC004557) F17L21.1 [Arabidopsis thaliana]
Seq. No.
                  166280
Seq. ID
                  LIB3234-001-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2129641
BLAST score
                  164
E value
                  2.0e-79
Match length
                  147
% identity
                  99
NCBI Description
                  major latex protein type 1 - Arabidopsis thaliana
```

>gi_1107493_emb_CAA63026 (X91960) major latex protein

typel [Arabidopsis thaliana]

```
Seq. No.
                   166281
Seq. ID
                   LIB3234-001-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q2281082
BLAST score
                   324
                                     est.
E value
                   5.0e-30
Match length
                   80
% identity
                   80
NCBI Description
                   (AC002333) polygalacturonase isolog, 3' partial
                   [Arabidopsis thaliana]
Seq. No.
                  166282
Seq. ID
                  LIB3234-001-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  337
E value
                  2.0e-35
Match length
                  94
% identity
                  80
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  166283
Seq. ID
                  LIB3234-001-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g4678299
BLAST score
                  711
E value
                  2.0e-75
Match length
                  140
% identity
                  99
NCBI Description
                  (AL049655) cysteine proteinase precursor-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  166284
Seq. ID
                  LIB3234-001-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  g4756963
BLAST score
                  100
E value
                  3.0e-49
Match length
                  140
                  93
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                  (ESSA project)
Seq. No.
                  166285
Seq. ID
                  LIB3234-001-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g4557060
```

NCBI GI

g131360

```
BLAST score
                     146
 E value
                     9.0e-46
 Match length
                     107
 % identity
                     93
                     (AC007154) putative chromosome-associated polypeptide, 5'
 NCBI Description
                     partial [Arabidopsis thaliana]
 Seq. No.
                     166286
 Seq. ID
                     LIB3234-001-P1-K1-F2
 Method
                     BLASTX
 NCBI GI
                     g2245109
 BLAST score
                     668
                     2.0e-70
 E value
 Match length
                     130
 % identity
                     99
                     (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis
 NCBI Description
                     thaliana]
 Seq. No.
                     166287
 Seq. ID
                     LIB3234-001-P1-K1-F4
 Method
                     BLASTN
 NCBI GI
                     g3047100
 BLAST score
                     392
~ E value
                     0.0e+00
 Match length
                     408
 % identity
                     99
 NCBI Description
                    Arabidopsis thaliana BAC F6N23
 Seq. No.
                     166288
 Seq. ID
                    LIB3234-001-P1-K1-F5
 Method
                    BLASTN
 NCBI GI
                    g3309259
 BLAST score
                    215
 E value
                    1.0e-117
 Match length
                    398
 % identity
                    87
 NCBI Description
                    Arabidopsis thaliana BAC F4H6, chromosome IV, complete
                    sequence
                    166289
 Seq. No.
 Seq. ID
                    LIB3234-001-P1-K1-F7
 Method
                    BLASTX
 NCBI GI
                    g1703108
 BLAST score
                    520
 E value
                    5.0e-53
 Match length
                    97
 % identity
                    98
                    ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
 NCBI Description
                    thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                    thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                    thaliana]
 Seq. No.
                    166290
                    LIB3234-001-P1-K1-F8
 Seq. ID
 Method
                    BLASTX
```

Seq. No.

```
BLAST score
                   241
 E value
                   3.0e-20
 Match length
                   61
 % identity
                   80
 NCBI Description
                   PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
                   >gi_81727_pir__S02115 photosystem II protein psbK precursor
                   - white mustard chloroplast >gi_12209_emb_CAA31909
                   (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
 Seq. No.
                   166291
                   LIB3234-001-P1-K1-F9
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g266693
 BLAST score
                   593
 É value
                   1.0e-61
Match length
                   141
 % identity
                   84
                   OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis
NCBI Description
                   thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin
                   [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
                   (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
Seq. No.
                   166292
                   LIB3234-001-P1-K1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4757403
BLAST score
                   258
E value
                   1.0e-143
Match length
                   459
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
Seq. No.
                  166293
Seq. ID
                  LIB3234-001-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  g4263813
BLAST score
                  344
E value
                  0.0e+00
Match length
                  360
% identity
                  41
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T13P21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166294
Seq. ID
                  LIB3234-001-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g4538963
BLAST score
                  557
E value
                  2.0e-57
Match length
                  137
% identity
                  62
NCBI Description
                  (AL049488) chlorophyll a/b-binding protein-like
                  [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                  (AF134129) Lhcb5 protein [Arabidopsis thaliana]
```

E value

Match length

0.0e + 00

```
Seq. ID
                    LIB3234-001-P1-K1-G2
 Method
                    BLASTX
 NCBI GI
                    g2664214
 BLAST score
                    764
 E value
                    1.0e-81
 Match length
                    149
 % identity
                    99
 NCBI Description (AJ222646) G2484-1 [Arabidopsis thaliana]
 Seq. No.
                    166296
 Seq. ID
                    LIB3234-001-P1-K1-G3
 Method
                    BLASTX
 NCBI GI
                    g399013
 BLAST score
                    642
 E value
                    3.0e-67
 Match length
                    126
 % identity
                    100
 NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                    (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                    >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                    thaliana (fragment) >gi_16175 emb CAA46518 (X65549)
                    adenylate translocator [Arabidopsis thaliana]
                    >gi_445607_prf__1909354A adenylate translocator
                    [Arabidopsis thaliana]
                    166297
 Seq. No.
 Seq. ID
                    LIB3234-001-P1-K1-G4
 Method
                    BLASTX
 NCBI GI
                    g112682
 BLAST score
                    656
                    6.0e-69
 E value
 Match length
                    149
 % identity
                    83
 NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                    cruciferin precursor (CRB) - Arabidops\overline{i}s tha\overline{l}ian\overline{a}
                    >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                    thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                    storage protein [Arabidopsis thaliana]
Seq. No.
                    166298
 Seq. ID
                    LIB3234-001-P1-K1-G5
 Method
                    BLASTX
 NCBI GI
                    q3402696
 BLAST score
                    436
 E value
                    4.0e-43
 Match length
                    120
 % identity
                    77
                   (AC004261) putative ferrodoxin-dependent glutamate
 NCBI Description
                    synthase, 3' partial [Arabidopsis thaliana]
 Seq. No.
                    166299
 Seq. ID
                    LIB3234-001-P1-K1-G6
 Method
                    BLASTN
 NCBI GI
                    g4159705
 BLAST score
                    382
```

```
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                   MGD8, complete sequence
 Seq. No.
                   166300
 Seq. ID
                   LIB3234-001-P1-K1-G7
 Method
                   BLASTN
 NCBI GI
                   g2656028
 BLAST score
                   440
                   0.0e+00
 E value
 Match length
                   456
 % identity
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MNF13
Seq. No.
                   166301
Seq. ID
                   LIB3234-001-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g1931639
BLAST score
                   185
E value
                   1.0e-13
Match length
                   62
% identity
                   58
NCBI Description
                  (U95973) lysophospholipase isolog [Arabidopsis thaliana]
Seq. No.
                   166302
Seq. ID
                   LIB3234-001-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g2244884
BLAST score
                   376
E value
                   4.0e-36
Match length
                   138
% identity
                   55
NCBI Description
                  (Z97338) glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                   166303
Seq. ID
                  LIB3234-001-P1-K1-H2
Method
                   BLASTN
NCBI GI
                   g2842474
BLAST score
                   71
E value
                   3.0e - 32
Match length
                  113
% identity
                   97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                   (ESSAII project)
Seq. No.
                  166304
                  LIB3234-001-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4375831
BLAST score
                  625
E value
                  3.0e-65
Match length
                  152
% identity
NCBI Description
                  (AJ006960) peroxidase [Arabidopsis thaliana]
Seq. No.
                  166305
```

Method

BLASTX

```
Seq. ID
                   LIB3234-001-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q112737
BLAST score
                   380
E value
                   9.0e-37
Match length
                   110
% identity
                   73
NCBI Description
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68853_pir NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi 4490710 emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
Seq. No.
                   166306
Seq. ID
                   LIB3234-001-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q1170503
BLAST score
                   584
E value
                   2.0e-60
Match length
                   113
% identity
                   100
NCBI Description
                   EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
                   >gi_322503_pir__JC1452 translation initiation factor
                   eIF-4A1 - Arabidopsis thaliana >gi 16554 emb CAA46188
                   (X65052) eukaryotic translation in \overline{1} tiation factor 4A-\overline{1}
                   [Arabidopsis thaliana]
Seq. No.
                   166307
Seq. ID
                   LIB3234-001-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q231586
BLAST score
                   289
E value
                   6.0e-26
Match length
                   118
% identity
                   56
NCBI Description
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi 82027 pir _S20504 H+-transporting ATP synthase (EC
                   3.6.1.34) beta chain, mitochondrial - Para rubber tree
                   >gi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase
                  beta-subunit [Hevea brasiliensis]
Seq. No.
                  166308
Seq. ID
                  LIB3234-001-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4539293
BLAST score
                  481
E value
                  2.0e-48
Match length
                  151
% identity
                  69
NCBI Description
                  (AL049480) putative membrane transporter [Arabidopsis
                  thaliana]
Seq. No.
                  166309
Seq. ID
                  LIB3234-001-P1-K1-H9
```

Match length

```
NCBI GI
                   q4678299
BLAST score
                   697
                   9.0e-74
E value
Match length
                   140
% identity
                   98
                   (AL049655) cysteine proteinase precursor-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  166310
Seq. No.
                  LIB3234-003-P1-K1-A2
Seq. ID
Method
                   BLASTN
NCBI GI
                  g2924651
BLAST score
                   37
                   2.0e-11
E value
Match length
                   312
% identity
                   95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166311
                  LIB3234-003-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415909
BLAST score
                  504
                  3.0e-51 ~
E value
                  122
Match length
                  27
% identity
NCBI Description
                  (AC006282) LEA protein AtECP63 [Arabidopsis thaliana]
Seq. No.
                  166312
Seq. ID
                  LIB3234-003-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q4415909
BLAST score
                  91
E value
                  6.0e-03
Match length
                  96
% identity
                  (AC006282) LEA protein AtECP63 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166313
Seq. ID
                  LIB3234-003-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2651299
BLAST score
                  370
E value
                  1.0e-35
Match length
                  119
% identity
                  64
NCBI Description
                  (AC002336) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  166314
Seq. ID
                  LIB3234-003-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  q4220627
BLAST score
                  111
E value
                  1.0e-55
```

E value

```
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K20J1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166315
Seq. ID
                   LIB3234-003-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   q2494261
BLAST score
                   182
E value
                   2.0e-13
Match length
                   35
% identity
                   100
NCBI Description
                  ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                   >gi_99903_pir__S21567 translation elongation factor Tu
                   precursor - soybean chloroplast >gi_18776_emb_CAA46864_
                   (X66062) EF-Tu [Glycine max] >gi_448921_prf_\overline{1}918220A
                   elongation factor Tu [Glycine max]
Seq. No.
                   166316
                  LIB3234-003-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2656026
BLAST score
                   334
E value
                   0.0e+00
                   359
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDF20
Seq. No.
                   166317
Seq. ID
                   LIB3234-003-P1-K1-C3
Method
                   BLASTN
NCBI GI
                  q4263694
BLAST score
                   44
E value
                   2.0e-15
Match length
                  165
                  85
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
                  sequence, complete sequence [Arabidopsis thaliana].
Seq. No.
                  166318
Seq. ID
                  LIB3234-003-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q2088638
BLAST score
                  280
E value
                  1.0e-156
Match length
                  280
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166319
Seq. ID
                  LIB3234-003-P1-K1-C5
Method
                  BLASTN 
NCBI GI
                  g4199934
BLAST score
                  273
```

1.0e-152

BLAST score

```
Match length
                   347
% identity .
                   92
                   Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   166320
Seq. ID
                  LIB3234-003-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   532
E value
                   1.0e-54
                  104
Match length
                   97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  166321
Seq. No.
Seq. ID
                  LIB3234-003-P1-K1-C8
                  BLASTN
Method
NCBI GI
                  g12218
BLAST score
                  229
                  1.0e-126
E value
Match length
                  360
% identity
                  91
NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly
Seq. No.
                  166322
Seq. ID
                  LIB3234-003-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2499236
BLAST score
                  356
E value
                  6.0e - 34
Match length
                  90
% identity
                  82
NCBI Description
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST
                  >gi_1419474_emb_CAA66944 (X98298) ndhA [Arabidopsis
                  thaliana]
Seq. No.
                  166323
Seq. ID
                  LIB3234-003-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1084336
BLAST score
                  234
E value
                  1.0e-19
Match length
                  44
                  98
% identity
                  chlorophyll a/b-binding protein type II - Arabidopsis
NCBI Description
                  thaliana >gi_541565 (U03395) PSI type II chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  166324
Seq. ID
                  LIB3234-003-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q3643588
```

% identity

```
E value
                   3.0e-31
Match length
                   133
% identity
                   88
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F17H15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166325
Seq. ID
                   LIB3234-003-P1-K1-D4
Method
                   BLASTN
NCBI GI
                   q2842474
BLAST score
                   348
E value
                   0.0e+00
Match length
                   368
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                   (ESSAII project)
Seq. No.
                   166326
Seq. ID
                   LIB3234-003-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   g3063438
BLAST score
                   95
E value
                   6.0e-46
Match length
                   251
% identity
                   84
NCBI Description
                   Complete sequence of Arabidopsis F22013, complete sequence
                   [Arabidopsis thaliana]
Seq. No.
                   166327
Seq. ID
                   LIB3234-003-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   g2281648
BLAST score
                   203
E value
                   1.0e-110
Match length
                   207
% identity
NCBI Description
                   Arabidopsis thaliana AP2 domain containing protein RAP2.12
               ... mRNA, partial cds
Seq. No.
                   166328
Seq. ID
                   LIB3234-003-P1-K1-D7
Method
                   BLASTN
NCBI GI
                   q972918
BLAST score
                   160
E value
                   9.0e-85
Match length
                   256
% identity
                   91
NCBI Description
                  Arabidopsis thaliana IAA8 (IAA8) gene complete cds
Seq. No.
                   166329
Seq. ID
                   LIB3234-003-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q132074
BLAST score
                   576
E value
                   1.0e-59
Match length
                   117
```

```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   166330
Seq. ID
                   LIB3234-003-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q4678285
BLAST score
                   195
E value
                   5.0e-15
Match length
                   113
% identity
                   42
NCBI Description (AL049660) putative protein [Arabidopsis thaliana]
Seq. No.
                   166331
Seq. ID
                   LIB3234-003-P1-K1-E11
Method
                   BLASTN
                   q4056476
NCBI GI
BLAST score
                   79
E value
                   2.0e-36
Match length
                   259
% identity
                   83
NCBI Description Arabidopsis thaliana chromosome II BAC F3G5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166332
Seq. ID
                  LIB3234-003-P1-K1-E12 .
Method
                  BLASTX
NCBI GI
                  g140292
BLAST score
                  387
                  1.0e-37
E value
Match length
                  88
% identity
                  86
NCBI Description
                  HYPOTHETICAL 21.5 KD PROTEIN (ORF 184)
                  >gi 82208 pir A05197 hypothetical protein 184 - common
                  tobacco chloroplast >gi 11843 emb CAA77363 (Z00044)
                  hypothetical protein [Nicotiana tabacum]
                  >gi 225211_prf__1211235AR ORF 184 [Nicotiana tabacum]
Seq. No.
                  166333
Seq. ID
                  LIB3234-003-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2288887
BLAST score
                  214
E value
                  3.0e-17
Match length
                  87
% identity
NCBI Description
                  (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
                  thaliana] >gi 3250736 emb CAA76803 (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                  >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                  [Arabidopsis thaliana]
Seq. No.
                  166334
Seq. ID
                  LIB3234-003-P1-K1-E4
Method
                  BLASTX
```

```
NCBI GI
                   g4138179
BLAST score
                   439
                   1.0e-43
E value
Match length
                   99
% identity
                   86
                   (AJ223969) elongation factor 1 alpha subunit [Malus
NCBI Description
                   domestica]
Seq. No.
                   166335
Seq. ID
                   LIB3234-003-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g4001805
BLAST score
                   180
                   3.0e-13
E value
                   99
Match length
% identity
                   40
NCBI Description
                  (AF041476) BAF53a [Mus musculus]
Seq. No.
                   166336
                   LIB3234-003-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4001805
BLAST score
                   142
E value
                   9.0e-09
                   57
Match length
% identity
                   51
NCBI Description
                  (AF041476) BAF53a [Mus musculus]
Seq. No.
                   166337
Seq. ID
                   LIB3234-003-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q4582787
BLAST score
                   149
E value
                   9.0e-10
Match length
                   74
                   45
% identity
                  (AJ012281) adenosine kinase [Zea mays]
NCBI Description
Seq. No.
                  166338
Seq. ID
                  LIB3234-003-P1-K1-F12
Method
                  BLASTN
NCBI GI
                   q4589446
BLAST score
                   44
E value
                   1.0e-15
Match length
                  192
% identity
                  81
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  T12B11, complete sequence
Seq. No.
                  166339
Seq. ID
                  LIB3234-003-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  q3176693
BLAST score
                  258
E value
                  1.0e-143
Match length
                  338
% identity
                  94
```

Seq. ID

```
NCBI Description Arabidopsis thaliana chromosome I BAC T27I1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                 . 166340
                  LIB3234-003-P1-K1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1109698
BLAST score
                  55
E value
                  3.0e-22
                  210
Match length
                  85
% identity
NCBI Description A.thaliana mRNA for gibberellin 20-oxidase (1425 bp)
Seq. No.
                  166341
Seq. ID
                  LIB3234-003-P1-K1-F8
                  BLASTN
Method
NCBI GI
                  a1109698
                  32
BLAST score
E value
                  1.0e-08
                  88
Match length
                  84
% identity
                  A.thaliana mRNA for gibberellin 20-oxidase (1425 bp)
NCBI Description
Seq. No.
                  166342
Seq. ID
                  LIB3234-003-P1-K1-G7
Method
                  BLASTX
                  g3023217
NCBI GI
                  357
BLAST score
E value
                  5.0e-34
Match length
                  93
                  84
% identity
                  14-3-3-LIKE PROTEIN GF14 NU >qi 1531631 (U60445) GF14 nu
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  166343
Seq. ID
                  LIB3234-003-P1-K1-H2
                  BLASTN
Method
                  q12218
NCBI GI
                  212
BLAST score
E value
                  1.0e-116
                  320
Match length
% identity
                  91
NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly
                  166344
Seq. No.
Seq. ID
                  LIB3234-003-P1-K1-H4
Method
                  BLASTN
                  q3335170
NCBI GI
BLAST score
                  199
                  1.0e-108
E value
Match length
                  367
% identity
NCBI Description Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene,
                 -complete cds
Seq. No.
                  166345
```

LIB3234-004-P1-K1-A1

NCBI GI

```
Method
                   BLASTX
 NCBI GI
                   g419757
 BLAST score
                    613
 E value
                    6.0e-64
 Match length
                   146
 % identity
                   84
NCBI Description
                   ketol-acid reductoisomerase (EC 1.1.1.86) precursor -
                   Arabidopsis thaliana
 Seq. No.
                   166346
                   LIB3234-004-P1-K1-A10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2702279
 BLAST score
                   125
                   1.0e-63
 E value
 Match length
                   129
                   99
 % identity
 NCBI Description
                   (AC003033) putative phosphate transporter [Arabidopsis
                   thaliana] >gi_2780345_dbj BAA24280 (AB000093) inorganic
                   phosphate transporter [Arabidopsis thaliana] >qi 2914691
                    (AC003974).putative phosphate transporter [Arabidopsis
                   thaliana]
 Seq. No.
                  · 166347
 Seq. ID
                   LIB3234-004-P1-K1-A11
 Method
                   BLASTX
                   g4539005
 NCBI GI
 BLAST score
                   125
 E value
                   2.0e-22
 Match length
                   116
 % identity
                   44
 NCBI Description
                   (AL049481) putative oxidoreductase [Arabidopsis thaliana]
 Seq. No.
                   166348
 Seq. ID
                   LIB3234-004-P1-K1-A12
 Method
                   BLASTX
 NCBI GI
                   g2500378
 BLAST score
                   445
 E value
                   4.0e-44
Match length
                   89
 % identity
                   93
NCBI Description
                  60S RIBOSOMAL PROTEIN L37
 Seq. No.
                   166349
Seq. ID
                   LIB3234-004-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g1657268
BLAST score
                   610
E value
                   2.0e-63
Match length
                   165
% identity
                   68
                   (Y07701) aminopeptidase [Homo sapiens]
NCBI Description
Seq. No.
                   166350
Seq. ID
                   LIB3234-004-P1-K1-A3
Method
                   BLASTN
```

g4580386

E value

6.0e-25

```
BLAST score
                   36
E value
                   5.0e-11
Match length
                   60
% identity
                   90
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T8018 genomic
                  sequence, complete sequence
Seq. No.
                  166351
Seq. ID
                  LIB3234-004-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q1262171
BLAST score
                  689
E value
                  9.0e-73
Match length
                  138
% identity
                  99
                  (U21557) phosphoprotein phosphatase 2A, regulatory subunit
NCBI Description
                  A [Arabidopsis thaliana]
Seq. No.
                  166352
                  LIB3234-004-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2864614
BLAST score
                  188
E value
                  5.0e-14
Match length
                  140
                  66
% identity
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                  166353
Seq. ID
                  LIB3234-004-P1-K1-A6
Method
                  BLASTN '
NCBI GI
                  q4006885
BLAST score
                  154
                  5.0e-81
E value
Match length
                  505
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  166354
                  LIB3234-004-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169598
BLAST score
                  414
E value
                  9.0e-41
Match length
                  90
                  84
% identity
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  166355
                  LIB3234-004-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4580386
BLAST score
                  60
```

BLAST score

```
Match length
                   159
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T8018 genomic
                  sequence, complete sequence
Seq. No.
                  166356
Seq. ID
                  LIB3234-004-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  q3522932
BLAST score
                  212
E value
                  1.0e-115
Match length
                  516
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166357
Seq. ID
                  LIB3234-004-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q127041
BLAST score
                  542
                  1.0e-55
E value
                  109
Match length
% identity
                  95
NCBI Description
                 S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_81647_pir__JN0131 methionine adenosyltransferase (EC
                  2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077)
                  S-adenosylmethionine synthetase [Arabidopsis thaliana]
Seq. No.
                  166358
Seq. ID
                  LIB3234-004-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g3421102
BLAST score
                  77
E value
                  4.0e-44
Match length
                  91
% identity
                  95
NCBI Description
                  (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
                  thaliana]
Seq. No.
                  166359
Seq. ID
                  LIB3234-004-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  q4539402
BLAST score
                  292
E value
                  1.0e-163
Match length
                  477
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13
                  (ESSA project)
Seq. No.
                  166360
Seq. ID
                  LIB3234-004-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q118926
```

```
E value
                   3.0e-45
Match length
                   167
 % identity
                   55
NCBI Description
                   DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
                   >gi_320600_pir__E45509 desiccation-related protein (clone
                   PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                   dessication-related protein [Craterostigma plantagineum]
                   >gi 227781_prf _1710351E abscisic acid responsive protein E
                   [Craterostigma plantagineum]
Seq. No.
                   166361
Seq. ID
                   LIB3234-004-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g1345967
BLAST score
                   360
                   3.0e-34
E value
Match length
                   112
% identity
                   64
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (VERSION 2) >gi_322649_pir A44227 omega-3 fatty acid
                   desaturase (EC 1.14.99.-) - rape >gi 167148 (L01418)
                   linoleic acid desaturase [Brassica napus]
Seq. No.
                   166362
Seq. ID
                   LIB3234-004-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   q1477480
BLAST score
                   164
E value
                   2.0e-27
Match length
                   88
% identity
                   78
NCBI Description
                   (U40341) carbamoyl phosphate synthetase large chain
                   [Arabidopsis thaliana]
Seq. No.
                   166363
Seq. ID
                  LIB3234-004-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g4490734
BLAST score
                  279
E value
                  1.0e-155
Match length
                  451
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
NCBI Description
                  project)
Seq. No.
                  166364
Seq. ID
                  LIB3234-004-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3695396
BLAST score
                  305
E value
                  2.0e-35
                  97
Match length
% identity
                  81
NCBI Description
                  (AF096372) contains similarity to Arabidopsis thaliana
                  retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]
```

166365

Seq. No.

Method

BLASTN

```
Seq. ID
                   LIB3234-004-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   q1657268
BLAST score
                   621
E value
                   8.0e-65
Match length
                   164
% identity
                   70
                  (Y07701) aminopeptidase [Homo sapiens]
NCBI Description
Seq. No.
                   166366
Seq. ID
                   LIB3234-004-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q4581146
BLAST score
                   615
E value
                   4.0e-64
Match length
                   136
% identity
                   90
                   (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                   cytoplasmic [Arabidopsis thaliana]
Seq. No.
                   166367
Seq. ID
                   LIB3234-004-P1-K1-C12
. Method
                   BLASTN
NCBI GI
                   q4589437
BLAST score
                   153
E value
                   2.0e-80
Match length
                   440
                   97
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MPN9, complete sequence
Seq. No.
                   166368
Seq. ID
                   LIB3234-004-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g1169476.
BLAST score
                   733
E value
                   6.0e-78
Match length
                   143
% identity
                   99
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                   ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                   vitronectin-like adhesion protein [Nicotiana tabacum]
Seq. No.
                   166369
Seq. ID
                   LIB3234-004-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   g3702724
BLAST score
                   81
E value
                   1.0e-37
Match length
                   421
% identity
                   86
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166370
Seq. ID
                   LIB3234-004-P1-K1-C7
```

NCBI GI

```
NCBI GI
                  q3128142
BLAST score
                  396
E value
                  0.0e+00
                                         Match length
                  479
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQN23, complete sequence [Arabidopsis thaliana]
                  166371
Seq. No.
                  LIB3234-004-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  396
E value
                  5.0e-39
Match length
                  74
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  166372
Seq. ID
                  LIB3234-004-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q3953473
BLAST score
                  702 ·
                  3.0e-74
E value
                  145
Match length
% identity
                  96
NCBI Description
                  (AC002328) F2202.18 [Arabidopsis thaliana]
Seq. No.
                  166373
Seq. ID
                  LIB3234-004-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q3273743
BLAST score
                  354
E value
                  3.0e-54
Match length
                  116
% identity
NCBI Description
                  (AF057357) lipid transfer protein 2 precursor [Arabidopsis
                  thaliana] >gi 3786019 (AC005499) unknown protein
                  [Arabidopsis thaliana]
Seq. No.
                  166374
Seq. ID
                  LIB3234-004-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  q4159706
BLAST score
                  50
E value
                  5.0e-19
Match length
                  114
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGL6, complete sequence
Seq. No.
                  166375
Seq. ID
                  LIB3234-004-P1-K1-D4
                  BLASTX
Method
```

q2213597

Match length

```
BLAST score
                   112
                   2.0e-35 .
E value
Match length
                   85
% identity
                   92
NCBI Description
                  (AC000348) T7N9.17 [Arabidopsis thaliana]
Seq. No.
                   166376
Seq. ID
                   LIB3234-004-P1-K1-E1
Method
                   BLASTN
NCBI GI
                   q4371278
BLAST score
                   307
                   1.0e-172
E value
Match length
                   431
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC T2N18 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166377
Seq. ID
                  LIB3234-004-P1-K1-E10
Method
                  BLASTN
                   q2760165
NCBI GI
                   66
BLAST score
                   7.0e-29
E value
Match length
                  185
% identity
                  86
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166378
                  LIB3234-004-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245136
BLAST score
                  141
                  1.0e-50
E value
Match length
                  156
% identity
                   (Z97344) trehalose-6-phosphate synthase homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  166379
Seq. ID
                  LIB3234-004-P1-K1-E3
Method
                  BLASTN
                  g3128166
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  192
% identity
                  84
                  Arabidopsis thaliana chromosome II BAC F4I1 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166380
                  LIB3234-004-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3540208
BLAST score
                  220
                  9.0e-18
E value
```

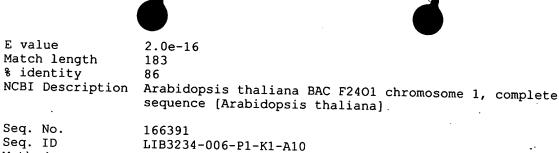
```
% identity
NCBI Description
                   (AC004260) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   166381
Seq. ID
                   LIB3234-004-P1-K1-F11
Method
                   BLASTX
NCBI GI ..
                   g2160133
BLAST score
                   138
                   3.0e-25
E value
Match length
                   143
                   50
% identity
                  (AC000375) Strong similarity to Arabidopsis
NCBI Description
                   gb_X91953,F19K23.3,F19K23.15. ESTs
                   gb T21984, gb ATTS0219, gb ATTS0207, gb T21984 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   166382
Seq. ID
                   LIB3234-004-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q167367
BLAST score
                   225
E value
                   2.0e-36
Match length
                   100
% identity
                   74
NCBI Description
                  (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   166383
Seq. ID
                  LIB3234-004-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  q3366536
BLAST score
                   461
                   0.0e + 00
E value
Match length
                   477
% identity
                   99
                  Genomic sequence for Arabidopsis thaliana BAC T25N2O,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166384
Seq. ID
                  LIB3234-004-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  g4079614
BLAST score
                  381
E value
                  0.0e+00
Match length
                  492
% identity
                  96
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166385
Seq. ID
                  LIB3234-004-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  g4586098
BLAST score
                  262
E value
                  1.0e-145
Match length
                  306
                  96
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
```

BLAST score

45

(ESSA project)

```
Seq. No.
                   166386
Seq. ID
                   LIB3234-004-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   q4262221
BLAST score
                   105
                   5.0e-52
E value
Match length
                   289
% identity
                   88
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F10A8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3234-004-P1-K1-H11
Method
                   BLASTN
NCBI GI
                   q4678705
BLAST score
                   370
E value
                   0.0e + 00
Match length
                   461
                   95
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                   (ESSA project)
Seq. No.
                   166388
Seq. ID
                   LIB3234-004-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g416911
BLAST score
                   88
E value
                   5.0e-11
Match length
                   90
% identity
                   DIPHTERIA TOXIN RESISTANCE PROTEIN 2 >gi 419830 pir S34679
NCBI Description
                   diphthamide synthesis protein DPH2 - yeast (Saccharomyces cerevisiae) >gi_296987_emb_CAA49420_ (X69765) diphtheria
                   toxin resistance [Saccharomyces cerevisiae]
                   >gi 395234 emb CAA52247 (X74151) orf1 [Saccharomyces
                   cerevisiae] >gi_486339_emb_CAA82035_ (Z28191) ORF YKL191w
                   [Saccharomyces cerevisiae] >gi 765109 (L01424) diphthamide
                   [Saccharomyces cerevisiae]
Seq. No.
                   166389
Seq. ID
                   LIB3234-004-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q2129659
BLAST score
                   213
E value
                   5.0e-17
Match length
                   146
                   36
% identity
NCBI Description
                   oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
                   (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                   166390
Seq. ID
                   LIB3234-004-P1-K1-H5
Method
                   BLASTN
NCBI GI
                   q2689438
```



Method BLASTX NCBI GI q66179 BLAST score 532 E value 2.0e-54 Match length 119 82

% identity NCBI Description

Seq. No.

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - common tobacco chloroplast >gi_225255_prf__1211235CP NADH

dehydrogenase 4-like ORF 509B [Nicotiana tabacum]

Seq. ID LIB3234-006-P1-K1-A11 Method BLASTN NCBI GI g4159712 BLAST score 114 E value 2.0e-57

166392

Match length 230 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:

MWI23, complete sequence

Seq. No. 166393 Seq. ID LIB3234-006-P1-K1-A2 Method BLASTX NCBI GI g3063449 BLAST score 451 E value 3.0e-45

Match length 98 % identity 92

NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]

Seq. No. 166394 Seq. ID

LIB3234-006-P1-K1-A4 Method

BLASTN NCBI GI g4539378 BLAST score 230 E value 1.0e-126 Match length 384 % identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21

(ESSA project)

Seq. No. 166395

Seq. ID LIB3234-006-P1-K1-A5

Method BLASTX NCBI GI g131336 BLAST score 330 E value 8.0e-31 Match length 72

% identity

```
% identity
                   92
NCBI Description PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P
                   photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD
                   phosphoprotein [Nicotiana tabacum]
                   .>gi_225225_prf 1211235BG photosystem II 10kD
                   phosphoprotein [Nicotiana tabacum]
Seq. No.
                   166396
Seq. ID
                   LIB3234-006-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g4056502
BLAST score
                   586
                   7.0e-61
E value
Match length
                   126
% identity
                   95
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.
                   166397
Seq. ID
                   LIB3234-006-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   q3063449
BLAST score
                   582
                   2.0e-60
E value
Match length
                   124
                   94
% identity
NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]
Seq. No.
                . 166398
Seq. ID
                  LIB3234-006-P1-K1-A8
Method
                   BLASTN
NCBI GI
                   g3063438
BLAST score
                   105
                   2.0e-52
E value
Match length
                   140
% identity
NCBI Description Complete sequence of Arabidopsis F22013, complete sequence
                   [Arabidopsis thaliana]
Seq. No.
                   166399
Seq. ID
                   LIB3234-006-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   q1695717
BLAST score
                   492
E value
                   7.0e-50
Match length
                   123
% identity
                   81
NCBI Description (D89341) luminal binding protein [Arabidopsis thaliana]
Seq. No.
                   166400
Seq. ID
                   LIB3234-006-P1-K1-B1
Method
                   BLASTN
NCBI GI
                   q4006815
BLAST score
                   67
E value
                   3.0e-29
Match length
                   141
```

```
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T6P5 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166401
                   LIB3234-006-P1-K1-B10
Seq. ID
Method .
                   BLASTN
NCBI GI
                   q511598
BLAST score
                   122
E value
                   4.0e-62
Match length
                   301
% identity
                   64
NCBI Description
                   Arabidopsis thaliana cell wall protein (APTR-1) gene,
                   complete cds
Seq. No.
                   166402
Seq. ID
                   LIB3234-006-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g625977
BLAST score
                   424
E value
                   7.0e-42
Match length
                   94
% identity
                   85
NCBI Description
                   p40 protein homolog - Arabidopsis thaliana >gi_402904
                   (U01955) laminin receptor-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   166403
Seq. ID
                   LIB3234-006-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q4091806
BLAST score
                   95
E value
                   2.0e-03
                   86
Match length
                   27
% identity
NCBI Description
                  (AF052585) CONSTANS-like protein 2 [Malus domestica]
Seq. No.
                   166404
Seq. ID
                   LIB3234-006-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   g4490734
                   36
BLAST score
E value
                   4.0e-11
Match length
                   206
                   80
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
                                                                       (ESSA
                  project)
Seq. No.
                  166405
                  LIB3234-006-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263771
BLAST score
                   227
E value
                  9.0e-19
Match length
                  64
% identity
                  66
NCBI Description
                  (AC006218) putative nonspecific lipid-transfer protein
                  precursor [Arabidopsis thaliana]
```

```
>gi_4726121_gb_AAD28321.1_AC006436 12 (AC006436) putative
                  nonspecific lipid-transfer protein precursor [Arabidopsis
                  thaliana]
Seq. No.
                  166406.
Seq. ID
                  LIB3234-006-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  g3510336
BLAST score
                  207
E value
                  1.0e-113
Match length
                  388
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18J17, complete sequence [Arabidopsis thaliana]
```

 Seq. No.
 166407

 Seq. ID
 LIB3234-006-P1-K1-B6

 Method
 BLASTX

 NCBI GI
 g2160164

 BLAST score
 209

E value 1.0e-16
Match length 125
% identity 48

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

 Seq. No.
 166408

 Seq. ID
 LIB3234-006-P1-K1-B7

 Method
 BLASTN

 NCBI GI
 94159701

NCBI GI g4159701 BLAST score 152 E value 6.0e-80 Match length 330 % identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22G18, complete sequence

Seq. No. 166409

Seq. ID LIB3234-006-P1-K1-B8

Method BLASTX
NCBI GI 9730645
BLAST score 396
E value 1.0e-38
Match length 93
% identity 87

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal

protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_(Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_(AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 166410

Seq. ID LIB3234-006-P1-K1-C10

Method BLASTX NCBI GI g2129659

E value

4.0e-17

cı.

```
BLAST score
                   358
E value
                   4.0e-34
Match length
                   118
% identity
NCBI Description
                   oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
                   (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                   166411
Seq. ID
                   LIB3234-006-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g1109600
BLAST score
                   657
E value
                   3.0e-69
Match length
                   123
                   100
% identity
NCBI Description
                   (D16628) ATsEH [Arabidopsis thaliana] >gi 2760840
                   (AC003105) soluble epoxide hydrolase [Arabidopsis thaliana]
Seq. No.
                   166412
Seq. ID
                   LIB3234-006-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   g2618600
BLAST score
                   265
E value
                   1.0e-147
Match length
                   382
                   92
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MDC12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166413
                   LIB3234-006-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2160186
BLAST score
                   332
E value
                   4.0e-31
Match length
                   77
% identity
                   87
                   (AC000132) Identical to A. thaliana HEMA2 (gb_U27118).
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   166414
Seq. ID
                   LIB3234-006-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   g511598
BLAST score
                   342
E value
                  0.0e+00
Match length
                   358 -
% identity
                   32
NCBI Description
                  Arabidopsis thaliana cell wall protein (APTR-1) gene,
                   complete cds
Seq. No.
                   166415
Seq. ID
                  LIB3234-006-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  212
```

BLAST score

```
Match length
                   47
 % identity
 NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
 Seq. No.
                   166416
                   LIB3234-006-P1-K1-C6
 Seq. ID
Method
                   BLASTN
NCBI GI
                   q3241927
BLAST score
                   211
E value
                   1.0e-115
Match length
                   381
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166417
                   LIB3234-006-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1346263
BLAST score
                   400
                   5.0e-39
E value
Match length
                   82
% identity
                   98
NCBI Description
                  GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR)
                   >gi_2146736_pir__S65773 glutamyl-tRNA reductase 2 precursor
                   - Arabidopsis thaliana >gi_1049057 (U27118) glutamyl-tRNA
                   reductase [Arabidopsis thaliana]
Seq. No.
                  166418
Seq. ID
                  LIB3234-006-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  161
E value
                  1.0e-85
Match length
                  180
% identity
                  97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                  (ESSAII project)
Seq. No.
                  166419
Seq. ID
                  LIB3234-006-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g2656025
BLAST score
                  149
E value
                  3.0e-78
Match length
                  201
% identity
                  94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
Seq. No.
                  166420
Seq. ID
                  LIB3234-006-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g4773906
```

% identity

```
E value
                   1.0e-41
Match length
                   92
                   89
% identity
                   (AF074021) putative symbiosis-related protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   166421
Seq. ID
                   LIB3234-006-P1-K1-D4
Method
                   BLASTN
NCBI GI
                   q4580381
BLAST score
                   181
E value
                   2.0e-97
Match length
                   305
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T11P11 genomic
                   sequence, complete sequence
                   166422
Seq. No.
Seq. ID
                   LIB3234-006-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   q2924729
BLAST score
                   40
                   4.0e-13
E value
Match length
                   72
% identity
                   89
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MNA5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166423
Seq. ID
                   LIB3234-006-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q2330885
BLAST score
                   205
E value
                   3.0e-16
Match length
                   123
% identity
                  (AJ000486) methionine gamma-lyase [Trichomonas vaginalis]
NCBI Description
Seq. No.
                   166424
Seq. ID
                   LIB3234-006-P1-K1-E1
Method
                   BLASTN
NCBI GI
                   q4756963
BLAST score
                   318
E value
                   1.0e-179
Match length
                   338
% identity
                   99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                   (ESSA project)
Seq. No.
                  166425
Seq. ID
                  LIB3234-006-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1172498
BLAST score
                  655
E value
                  6.0e-69
Match length
                  126
```

```
NCBI Description
                  PHYTOCHROME E >gi 1076376 pir S46313 phytochrome E -
                   Arabidopsis thaliana >gi 452817 emb CAA54075 (X76610)
                   phytochrome E [Arabidopsis thaliana]
Seq. No.
                   166426
Seq. ID
                   LIB3234-006-P1-K1-E2
Method
                   BLASTN
NCBI GI
                   q2213606
BLAST score
                   372
E value
                   0.0e + 00
Match length
                   380
                   99
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F21J9,
                   complete sequence [Arabidopsis thaliana]
                   166427
Seq. No.
Seq. ID
                   LIB3234-006-P1-K1-E5
Method
                   BLASTN
NCBI GI
                   q2673901
BLAST score
                   337
E value
                   0.0e + 00
Match length
                   353
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T24P15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166428
Seq. ID
                  LIB3234-006-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q3808062
BLAST score
                  155
E value
                  3.0e-10
Match length
                  64
% identity
                  45
NCBI Description
                  (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  166429
Seq. ID
                  LIB3234-006-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g4510397
BLAST score
                  662
E value
                  9.0e-70
Match length
                  126
% identity
                  99
                  (ACO06587) putative preproMP27-MP32 [Arabidopsis thaliana]
NCBI Description
                  166430
Seq. No.
Seq. ID
                  LIB3234-006-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g3449326
BLAST score
                  34
                  1.0e-09
E value
Match length
                  54
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19M22, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                   166431
 Seq. ID
                   LIB3234-006-P1-K1-F10
 Method
                   BLASTX
 NCBI GI
                   g2894574
 BLAST score
                   623
                   3.0e-65
 E value
Match length
                   127
 % identity
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
 NCBI Description
                   >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
Seq. No.
                   166432
                   LIB3234-006-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3169175
BLAST score
                   153
E value
                   5.0e-10
Match length
                   41
% identity
                   (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   166433
Seq. ID
                   LIB3234-006-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g2129658
BLAST score
                   319
E value
                   1.0e-29
Match length
                   116
% identity
                   56
NCBI Description
                  oleosin type 2 - Arabidopsis thaliana
                   >gi_1107497_emb_CAA63022_ (X91956) oleosin type2
                   [Arabidopsis thaliana]
Seq. No.
                  166434
Seq. ID
                  LIB3234-006-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4325282
BLAST score
                  290
E value
                   4.0e-26
Match length
                  56
% identity
                  93
NCBI Description
                  (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
                  >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
Seq. No.
                  166435
Seq. ID
                  LIB3234-006-P1-K1-G1
                  BLASTX
Method
NCBI GI
                  g226996
BLAST score
                  330
E value
                  7.0e-31
Match length
                  61
% identity
                  100
NCBI Description petB2 gene [Pisum sativum]
```

```
Seq. No.
                   166436
 Seq. ID
                   LIB3234-006-P1-K1-G11
 Method
                   BLASTX
 NCBI GI
                   g4204299
 BLAST score
                   629
 E value
                   7.0e-66
 Match length
                   125
 % identity
 NCBI Description
                   (AC003027) lcl prt_seq No definition line found
                   [Arabidopsis thaliana]
 Seq. No.
                   166437
                   LIB3234-006-P1-K1-G12
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q4150874
BLAST score
                   145
 E value
                   1.0e-09
Match length
                   69
 % identity
                   39
NCBI Description
                  (AJ011848) ndhD gene product [Hordeum vulgare]
Seq. No.
                   166438
Seq. ID
                   LIB3234-006-P1-K1-G2
Method
                   BLASTN
NCBI GI
                   g4589439
BLAST score
                   144
E value
                   3.0e-75
Match length
                   304
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MQM1, complete sequence
Seq. No.
                   166439
Seq. ID
                   LIB3234-006-P1-K1-G3
Method
                   BLASTN
NCBI GI
                   g12279
BLAST score
                   34
E value
                   1.0e-09
Match length
                   42
% identity
                   95
NCBI Description
                   Spinach chloroplast genes for the D2 and 44 kd reaction
                   centre, chlorophyll a-binding protein and for tRNA-Ser
                   (UGA)
Seq. No.
                   166440
Seq. ID
                  LIB3234-006-P1-K1-G7
Method
                  BLASTX
NCBI GI
                   g4455342
BLAST score
                   360
E value
                  2.0e-34
Match length
                  122
% identity
                  58
                  (AL035522) O-methyltransferase-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166441
Seq. ID
                  LIB3234-006-P1-K1-H1
```

E value

2.0e-61

```
Method
                   BLASTX
NCBI GI
                   g3935149
BLAST score
                   627
E value
                   1.0e-65
Match length
                   127
% identity
NCBI Description
                   (AC005106) T25N20.13 [Arabidopsis thaliana]
Seq. No.
                   166442
Seq. ID
                   LIB3234-006-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g4587532
BLAST score
                   333
E value
                   4.0e-31
Match length
                   113
% identity
                   57
NCBI Description
                   (AC007060) Strong similarity to F19I3.2 gi_3033375 putative
                   berberine bridge enzyme from Arabidopsis thaliana BAC
                   gb_AC004238. This gene
Seq. No.
                   166443
Seq. ID
                   LIB3234-006-P1-K1-H11
Method
                   BLASTN
NCBI GI
                   g2924651
BLAST score
                   131
E value
                   2.0e-67
Match length
                   329
% identity
                 .. 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166444
Seq. ID
                   LIB3234-006-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g4406775
BLAST score
                   190
E value
                   2.0e-14
Match length
                   106
% identity
                   35
NCBI Description
                  (AC006836) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166445
                  LIB3234-006-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1109699
BLAST score
                  530
E value
                  3.0e-54
Match length
                  101
% identity
                  100
                  (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166446
Seq. ID
                  LIB3234-006-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  591
```

BLAST score

```
Match length
                   118
 % identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
 NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana) >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
 Seq. No.
                   166447
Seq. ID
                   LIB3234-006-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   g2827538
BLAST score
                   370
E value
                   0.0e + 00
Match length
                   390
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17
                   (ESSAII project)
Seq. No.
                   166448
Seq. ID
                   LIB3234-006-P1-K1-H5
Method
                   BLASTN
NCBI GI
                   g408482
BLAST score
                   44
E value
                   2.0e-15
Match length
                   195
% identity
                   90
NCBI Description Arabidopsis thaliana chloroplast omega-r fatty acid
                   desaturase gene, complete cds
Seq. No.
                   166449
Seq. ID
                   LIB3234-006-P1-K1-H7
Method
                   BLASTN
NCBI GI
                   g4733953
BLAST score
                   226
E value
                  1.0e-124
Match length
                  304
% identity
                   95
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
                  sequence, complete sequence
Seq. No.
                  166450
Seq. ID
                  LIB3234-006-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1076632
BLAST score
                  544
E value
                  6.0e-56
Match length
                  126
% identity
                  81
NCBI Description
                  protein kinase - common tobacco >gi 506534 emb CAA50374
                  (X71057) protein kinase [Nicotiana tabacum]
Seq. No.
                  166451
Seq. ID
                  LIB3234-006-P1-K1-H9
Method
                  BLASTN
```

g2160689

```
E value
                   1.0e-175
Match length
                   320
% identity
                   99
                   Arabidopsis thaliana B' regulatory subunit of PP2A
NCBI Description
                   (AtB'alpha) mŖNA, complete cds
Seq. No.
                   166452
Seq. ID
                   LIB3234-008-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g633890
BLAST score
                   241
E value
                   9.0e-21
Match length
                   75
% identity.
NCBI Description
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                   vulgare]
Seq. No.
                   166453
Seq. ID
                   LIB3234-008-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   q3600045
BLAST score
                   121
E value
                   2.0e-61
Match length
                   370
% identity
                   94
NCBI Description Arabidopsis thaliana BAC F2P3
Seq. No.
                   166454
Seq. ID
                   LIB3234-008-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g3860247
BLAST score
                   558
E value
                   1.0e-57
Match length
                  107
% identity
                   96
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166455
Seq. ID
                  LIB3234-008-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1419388
BLAST score
                  340
E value
                  5.0e-32
Match length
                  75
% identity
                  84
NCBI Description
                  (X98925) stromal ascorbate peroxidase [Arabidopsis
                  thaliana]
Seq. No.
                  166456
Seq. ID
                  LIB3234-008-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g116527
BLAST score
                  460
E value
                  4.0e-46
Match length
                  97
% identity
                  88
NCBI Description
                  PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)
```

>gi_1143166 (U32397) ClpP protease [Nicotiana tabacum]
>gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease proteolytic subuni [Nicotiana tabacum]

Seq. No. 166457 Seg. ID LIB3234-008-P1-K1-A5 Method BLASTX NCBI GI g2245006 BLAST score 218 E value 1.0e-17 Match length 87 49 % identity NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana] Seq. No. 166458 Seq. ID LIB3234-008-P1-K1-A6 Method BLASTX NCBI GI g2577957 BLAST score 448 E value 1.0e-44 Match length 122 % identity 73 NCBI Description (AJ002473) ABI3 protein [Arabidopsis thaliana] Seq. No. 166459 Seq. ID LIB3234-008-P1-K1-A7 Method BLASTX NCBI GI g1345973 BLAST score 425 E value 5.0e-42 Match length ' 96 % identity 81 NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana] Seq. No. 166460 Seq. ID LIB3234-008-P1-K1-A8 Method BLASTX NCBI GI q3002603 BLAST score 238

2.0e-30 E value Match length 86 % identity 79

NCBI Description (AF033679) histone H3 [Bellamya heudi guangdungensis]

Seq. No. 166461

LIB3234-008-P1-K1-A9 Seq. ID

Method BLASTN NCBI GI g3176695 BLAST score 315

```
E value
                     1.0e-177
  Match length
                     331
  % identity
                     52
  NCBI Description
                     Arabidopsis thaliana chromosome I BAC F14J9 genomic
                     sequence contains phyA marker, complete sequence
                     [Arabidopsis thaliana]
  Seq. No.
                     166462
                     LIB3234-008-P1-K1-B10
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g3047100
  BLAST score
                     325
  E value
                     0.0e+00
  Match length
                     359
                     97
  % identity
  NCBI Description Arabidopsis thaliana BAC F6N23
  Seq. No.
                     166463
  Seq. ID
                     LIB3234-008-P1-K1-B12
  Method
                     BLASTN
  NCBI GI
                     g3241916
  BLAST score
                     346
  E value
                     0.0e + 00
  Match length
                     .374
  % identity
                     98
  NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                     K15N18, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     166464
  Seq. ID
                     LIB3234-008-P1-K1-B4
  Method
                     BLASTX
  NCBI GI
                     g112682
  BLAST score
                     641
  E value
                     2.0e-67
  Match length
                     122
  % identity
                     98
  NCBI Description
                     12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                     cruciferin precursor (CRB) - Arabidops\overline{i}s tha\overline{l}ian\overline{a}
                     >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                     thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                     storage protein [Arabidopsis thaliana]
  Seq. No.
                     166465
  Seq. ID
                    LIB3234-008-P1-K1-B5
  Method
                    BLASTN
  NCBI GI
                    g4006815
  BLAST score
                    87
  E value
                    3.0e-41
  Match length
                    250
  % identity
                    97
  NCBI Description
                    Arabidopsis thaliana chromosome II BAC T6P5 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    166466
 Seq. ID
                    LIB3234-008-P1-K1-B6
 Method
                    BLASTN
 NCBI GI
                    g2252848
```

% identity

```
BLAST score
                   34
E value
                   1.0e-09
Match length
                   165
                                                ...
% identity
                   85
NCBI Description Arabidopsis thaliana BAC TM018A10
Seq. No.
                   166467
Seq. ID
                   LIB3234-008-P1-K1-B9
Method
                   BLASTN
NCBI GI
                   g2244870
BLAST score
                   364
E value
                   0.0e+00
Match length
                   376
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  166468
Seq. ID
                  LIB3234-008-P1-K1-C1
Method
                  BLASTX
                  g2959734
NCBI GI
BLAST score
                   345
E value
                  1.0e-32
Match length
                  88
% identity
                  - 78
NCBI Description (Y13650) homologous to GATA-binding transcription factors
                   [Arabidopsis thaliana]
Seq. No.
                  166469
Seq. ID
                  LIB3234-008-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g12216
BLAST score
                  240
E value
                  1.0e-132
Match length
                  316
% identity
                  94
NCBI Description Sinapis alba chloroplast rps16 gene
Seq. No.
                  166470
Seq. ID
                  LIB3234-008-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  q4699904
BLAST score
                  320
E value
                  1.0e-180
Match length
                  374
% identity
                  90
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F1E22,
                  complete sequence
Seq. No.
                  166471
Seq. ID
                  LIB3234-008-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  q4581161
BLAST score
                  75
E value
                  4.0e-34
Match length
                  242
```

E value

1.0e-35

```
NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic
                   sequence, complete sequence
Seq. No.
                   166472
Seq. ID
                   LIB3234-008-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   q4510360
BLAST score
                   352
E value
                   0.0e + 00
Match length
                   368
                   88
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F11F19 genomic
                   sequence, complete sequence
Seq. No.
                   166473
Seq. ID
                   LIB3234-008-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1107501
BLAST score
                   386
                   2.0e-37
E value
Match length
                   99
% identity
NCBI Description
                   (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
                   Match to gb_X91954 orf gene product from A. thaliana. ESTs
                   gb Z17604, gb H76594, gb AA597972 and gb AA394824 come from
                   th\overline{i}s gene. [Arabidopsis \overline{t}haliana]
Seq. No.
                   166474
Seq. ID
                   LIB3234-008-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q112740
BLAST score
                   236
E value
                   8.0e-20
Match length
                   112
% identity
                   50
NCBI Description
                  NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)
                   >gi 81691 pir A25997 napin precursor (napA) - rape
                   >gi_167153 (J02586) prepronapin [Brassica napus] >gi 167155
                   (J02798) napin [Brassica napus]
Seq. No.
                   166475
Seq. ID
                  LIB3234-008-P1-K1-C9
Method
                  BLASTX
NCBI GI
                   q4204299
BLAST score
                   629
E value
                   6.0e-66
Match length
                  124
% identity
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  166476
Seq. ID
                  LIB3234-008-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g1107501
BLAST score
                  371
```

```
Match length
                  111
% identity
                   68
                  (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
NCBI Description
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb AA597972 and gb AA394824 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  166477
Seq. ID
                  LIB3234-008-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  q4519195
BLAST score
                  339
E value
                  0.0e + 00
Match length
                  355
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MQC12, complete sequence
Seq. No.
                  166478
Seg. ID
                  LIB3234-008-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  590
E value
                  2.0e-61
Match length
                  117
% identity
                  96
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  166479
Seg. ID
                  LIB3234-008-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q3808062
BLAST score
                  155
E value
                  3.0e-10
Match length
                  64
% identity
NCBI Description
                  (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  166480
Seq. ID
                  LIB3234-008-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2459417
BLAST score
                  626
                  1.0e-65
E value
                  125
Match length
% identity
NCBI Description
                  (AC002332) putative pre-mRNA splicing factor PRP19
                  [Arabidopsis thaliana]
Seq. No.
                  166481
Seq. ID
                  LIB3234-008-P1-K1-D4
Method
                  BLASTX
```

q3068713

```
BLAST score
                   44
                   6.0e-24
E value
Match length
                   113
% identity
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   166482
                   LIB3234-008-P1-K1-D5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3510337
BLAST score
                   74
E value
                   2.0e-33
Match length
                   234
% identity
                   83
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19E20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166483
Seq. ID
                   LIB3234-008-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   q2342727
BLAST score
                   357
E value
                   5.0e - 34
Match length
                   92
% identity
                   75
NCBI Description
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   166484
Seq. ID
                   LIB3234-008-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   g2264306
BLAST score
                   366
                   0.0e+00
E value
Match length
                   374
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166485
                  LIB3234-008-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q207905
BLAST score
                  171
E value
                  3.0e-12
Match length
                  122
% identity
                  34
NCBI Description
                  (M18027) alpha globulin B [Artificial gene]
Seq. No.
                  166486
                  LIB3234-008-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266693
BLAST score
                  367
                  2.0e-35
E value
Match length
                  96
                  79
% identity
NCBI Description
                  OLEOSIN >gi 282875 pir S22538 oleosin - Arabidopsis
```

BLAST score

```
(AL035523) oleosin, 18.5K [Arabidopsis thaliana]
Seq. No.
                   166487
Seq. ID
                   LIB3234-008-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   q480450
BLAST score
                   329
E value
                   9.0e-31
Match length
                   80
% identity
                   86
                   ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                   thaliana >gi_402552_emb_CAA49506 (X69880) ketol-acid
                   reductoisomerase [Arabidopsis thaliana]
Seq. No.
                   166488
Seq. ID
                  LIB3234-008-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q477280
BLAST score
                  169
E value
                   6.0e-12
Match length
                  59
% identity
                  58
NCBI Description
                  mitochondrial processing peptidase (EC 3.4.99.41) 55K
                  protein precursor - potato >gi_410633 bbs 136740 cytochrome
                  c reductase-processing peptidase subunit I, MPP subunit I,
                  P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  534 aa]
Seq. No.
                  166489
                  LIB3234-008-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  289
                  4.0e-26
E value
Match length
                  92
% identity
                  63
NCBI Description
                  oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
                  (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  166490
Seq. ID
                  LIB3234-008-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  q4263694
BLAST score
                  365
E value
                  0.0e + 00
Match length
                  369
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                 .166491
Seq. ID
                  LIB3234-008-P1-K1-E6
Method
                  BLASTX
```

thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_

q2191176

Seq. ID

```
E value
                   4.0e-49
Match length
                   107
                   90
% identity
NCBI Description
                   (AF007270) Similar to SRF-type transcription factor
                   [Arabidopsis thaliana]
Seq. No.
                   166492
Seq. ID
                   LIB3234-008-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   q4757390
BLAST score
                   357
                   0.0e + 00
E value
Match length
                   377
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   F24B18, complete sequence
Seq. No.
                   166493
Seq. ID
                   LIB3234-008-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q1176658
BLAST score
                   242
                   2.0e-20
E value
Match length
                   101
% identity
                   47
                  HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
NCBI Description
                   >gi_726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
Seq. No.
                   166494
Seq. ID
                  LIB3234-008-P1-K1-F1
Method
                   BLASTX
NCBI GI
                  q544415
BLAST score
                   292
E value
                   2.0e-26
Match length
                  109
% identity
                   54
NCBI Description
                  GLYCEROL-3-PHOSPHATE DEHYDROGENASE MITOCHONDRIAL PRECURSOR
                   (GPD-M) (GPDH-M) >gi_627996 pir A54051
                  glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) precursor
                  - rat >gi_493022 (U08027) glycerolphosphate dehydrogenase
                   [Rattus norvegicus] >gi_603583 emb CAA55329 (X78593)
                  glycerol-3-phosphate dehydrogenase [Rattus norvegicus]
Seq. No.
                  166495
                  LIB3234-008-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g419757
BLAST score
                  491
E value
                  9.0e-50
Match length
                  119
% identity
                  83
NCBI Description
                  ketol-acid reductoisomerase (EC 1.1.1.86) precursor -
                  Arabidopsis thaliana
Seq. No.
                  166496
```

LIB3234-008-P1-K1-F11

q421836

```
Method
                   BLASTX
NCBI GI
                   g3915961
BLAST score
                   273
E value
                   1.0e-24
Match length
                   57
% identity
                   95
NCBI Description
                   HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
                   >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana
                   tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
                   protein [Nicotiana tabacum]
Seq. No.
                   166497
Seq. ID
                   LIB3234-008-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g3063706
BLAST score
                   342
E value
                   3.0e-32
Match length
                   78
% identity
                   82
NCBI Description
                  (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                   166498
Seq. ID
                   LIB3234-008-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g2499964
BLAST score
                   690
E value
                   4.0e-73
Match length
                   123
% identity
                   99
                   PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2
NCBI Description
                   >gi_669096_emb_CAA58958_ (X84153) photosystem I subunit
                   [Antirrhinum majus]
Seq. No.
                   166499
Seq. ID
                   LIB3234-008-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   g1916613
BLAST score
                   462
E value
                   2.0e-46
Match length
                   96
% identity
                   100
NCBI Description
                  (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]
Seq. No.
                   166500
Seq. ID
                  LIB3234-008-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g4539421
BLAST score
                   368
E value
                  3.0e-35
Match length
                  97
% identity
                  72
NCBI Description
                  (AL049171) putative protein [Arabidopsis thaliana]
Seq. No.
                  166501
Seq. ID
                  LIB3234-008-P1-K1-F9
Method
                  BLASTX
```

```
BLAST score
                   454
E value
                   2.0e-45
Match length
                   92
                   100
% identity
NCBI Description
                  G-box-binding factor GF14 - Arabidopsis thaliana >qi 553040
                   (M96855) GF14 [Arabidopsis thaliana]
Seq. No.
                  166502
Seq. ID
                  LIB3234-008-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g544424
BLAST score
                   423
E value
                   9.0e-42
Match length
                  89
                   93
% identity
NCBI Description
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir $30147
                  glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                  >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
                   [Arabidopsis thaliana] >gi 166837 (L00648) RNA-binding
                  protein [Arabidopsis thaliana]
                  >gi 4567224 gb AAD23639.1 AC007119 5 (AC007119)
                  glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                  166503
Seq. ID
                  LIB3234-008-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  g4733953
BLAST score
                  311
E value
                  1.0e-175
Match length
                  369
% identity
                  96
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
                  sequence, complete sequence
Seq. No.
                  166504
Seq. ID
                  LIB3234-008-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3925239
BLAST score
                  407
E value
                  7.0e-40
Match length
                  105
% identity
                  76
NCBI Description
                  (AF037037) 6-phosphogluconate dehydrogenase isoenzyme A
                  [Zea mays]
Seq. No.
                  166505
Seq. ID
                  LIB3234-008-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2605714
BLAST score
                  447
                  1.0e-44
E value
                  110
Match length
% identity
                  81
NCBI Description
                  (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                  thaliana]
```

166506

Seq. No.

```
LIB3234-008-P1-K1-G2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g135858
BLAST score
                    276
E value
                    2.0e-24
Match length
                    56
% identity
                    98
NCBI Description
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
                    >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114 (X63551)
                    tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                    [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast
                    intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.
                   166507
Seq. ID
                   LIB3234-008-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g3023848
BLAST score
                    531
E value
                   2.0e-54
Match length
                   105
% identity
                   56
NCBI Description
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                   >gi 2289095 (U77381) WD-40 repeat protein [Arabidopsis
                   thaliana]
Seq. No.
                   166508
Seq. ID
                   LIB3234-008-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   q3063706
BLAST score
                   345
E value
                   1.0e-32
Match length
                   79
% identity
NCBI Description
                   (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                   166509
Seq. ID
                   LIB3234-008-P1-K1-G5
Method
                   BLASTN
NCBI GI
                   g2924653
BLAST score
                   98
E value
                   4.0e-48
Match length
                   134
% identity
                   93
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166510
Seq. ID
                   LIB3234-008-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g2505874
BLAST score
                   194
E value
                   6.0e-15
Match length
                   57
                   74
% identity
```

```
NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]
Seq. No.
                   166511
Seq. ID
                   LIB3234-008-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   q3080406
BLAST score
                   59
E value
                   5.0e-25
Match length
                   99
% identity
                   90
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12
                   (ESSA project)
Seq. No.
                   166512
Seq. ID
                   LIB3234-008-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g2781394
BLAST score
                   386
E value
                   1.0e-37
Match length
                   82
% identity
                   99
NCBI Description
                  (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
Seq. No.
                   166513
Seq. ID
                   LIB3234-008-P1-K1-H11
Method
                   BLASTN
NCBI GI
                   g2656025
BLAST score
                   342
E value
                   0.0e+00
Match length
                   370
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
Seq. No.
                  166514
Seq. ID
                  LIB3234-008-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2832777
                  272
BLAST score
E value
                  5.0e-24
Match length
                  123
                  50
% identity
NCBI Description
                  (AL021086) /prediction=(method:; /prediction=(method:;
                   /match=(desc:; /match=(desc:; /match=(desc:; /match=(desc:;
                  EST embl AA735498 AA735498 comes from the 5' UTR
                  [Drosophila melanogaster]
Seq. No.
                  166515
                  LIB3234-008-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2979541
BLAST score
                 661
E value
                  1.0e-69
Match length
                  124
% identity
                  97
NCBI Description
                  (AC003680) hypothetical protein, 5' partial [Arabidopsis
                  thaliana]
```

% identity

```
Seq. No.
                   166516
Seq. ID
                   LIB3234-008-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g118926
BLAST score
                   251
E value
                   1.0e-21
Match length
                   96
% identity
                   54
NCBI Description
                   DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
                   >gi 320600_pir_ E45509 desiccation-related protein (clone
                   PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                   dessication-related protein [Craterostigma plantagineum]
                   >qi 227781 prf 1710351E abscisic acid responsive protein E
                   [Craterostigma plantagineum]
Seq. No.
                   166517
Seq. ID
                   LIB3234-008-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g625977
BLAST score
                   555
E value
                   3.0e-57
Match length
                   108
% identity
                   100
NCBI Description
                  p40 protein homolog - Arabidopsis thaliana >gi 402904.
                   (U01955) laminin receptor-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   166518
Seq. ID
                   LIB3234-008-P1-K1-H6
Method
                   BLASTN
NCBI GI
                   q4006815
BLAST score
                   92
E value
                   4.0e-44
Match length
                   186
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC T6P5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166519
Seq. ID
                  LIB3234-008-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q2618688
BLAST score
                  191
E value
                  2.0e-26
Match length
                  76
                  78
% identity
NCBI Description
                  (AC002510) putative esterase D [Arabidopsis thaliana]
Seq. No.
                  166520
Seq. ID
                  LIB3234-008-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q1592677
BLAST score
                  202
E value
                  7.0e-16
Match length
                  113
```

```
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.
                   166521
Seq. ID
                  LIB3234-008-P1-K1-H9
Method :
                  BLASTN
NCBI GI
                   g3985949
BLAST score
                   286
E value
                   1.0e-160
Match length
                   358
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166522
Seq. ID
                  LIB3234-009-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  q4757392
BLAST score
                  323
E value
                  0.0e+00
Match length
                  374
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14A17, complete sequence
Seq. No.
                  166523
                  LIB3234-009-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2961390
BLAST score
                  559
E value
                  1.0e-57
Match length
                  103
% identity
                  100
NCBI Description
                  (AL022141) beta-galactosidase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  166524
Seq. ID
                  LIB3234-009-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3123279
BLAST score
                  309
E value
                  2.0e-28
Match length
                  72
% identity
                  83
NCBI Description
                  40S RIBOSOMAL PROTEIN S26 >gi 2651298 (AC002336) putative
                  ribosomal protein S26 [Arabidopsis thaliana]
Seq. No.
                  166525
Seq. ID
                  LIB3234-009-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g3953471
BLAST score
                  106
E value
                  1.0e-56
Mátch length
                  119
% identity
                  92
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                  166526
```

```
LIB3234-009-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  g585165
NCBI GI
BLAST score
                   304
E value
                  1.0e-27
Match length
                  78
                  76
% identity
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                   (G6PD) >gi_2129985 pir S60287 glucose-6-phosphate
                  1-dehydrogenase (EC 1.1.1.49) - potato
                  >gi_471345_emb_CAA52442 (X74421) glucose-6-phosphate
                  1-dehydrogenase [Solanum tuberosum]
                  166527
Seq. No.
Seq. ID
                  LIB3234-009-P1-K1-B3
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  79
E value
                  2.0e-61
Match length
                  123
                  92
% identity
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  166528
Seq. ID
                  LIB3234-009-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q2388571
BLAST score
                  472
E value
                  1.0e-47
Match length
                  93
                  98
% identity
NCBI Description
                  (AC000098) Strong similarity to Arabidopsis peroxidase
                  ATPEROX7A (gb X98321). [Arabidopsis thaliana] >qi 2738254
                  (U97684) peroxidase precursor [Arabidopsis thaliana]
Seq. No.
                  166529
                  LIB3234-009-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q231586
BLAST score
                  589
                  3.0e-61
E value
Match length
                  126
% identity
NCBI Description
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi 82027 pir S20504 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >gi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase
                  beta-subunit [Hevea brasiliensis]
Seq. No.
                  166530
Seq. ID
                  LIB3234-009-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q3775987
BLAST score
                  557
E value
                  2.0e-57
```

BLAST score

```
120
 Match length
 % identity
                   93
 NCBI Description
                  (AJ010457) RNA helicase [Arabidopsis thaliana]
 Seq. No.
                   166531
 Seq. ID
                   LIB3234-009-P1-K1-B8
Method
                   BLASTX
 NCBI GI
                   g3763916
BLAST score
                   291
E value
                   2.0e-26
Match length
                   88
 % identity
                   60
NCBI Description
                   (AC004450) unknown protein [Arabidopsis thaliana]
                   >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   166532
Seq. ID
                   LIB3234-009-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g3461850
BLAST score
                   329
E value
                   1.0e-30
Match length
                   92
% identity
                   (AC005315) putative ligand-gated ionic channel [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   166533
Seq. ID
                   LIB3234-009-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g2239083
BLAST score
                   287
E value
                   8.0e-26
Match length
                   118
% identity
                   53
                   (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385)
                   anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus]
Seq. No.
                  166534
Seq. ID
                  LIB3234-009-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1076442
BLAST score
                  611
E value
                  8.0e-64
Match length
                  119
% identity
                  90
NCBI Description
                  beta-glucosidase (EC 3.2.1.21) - rape
                  >gi_757740_emb_CAA57913 (X82577) beta-glucosidase
                  [Brassica napus]
Seq. No.
                  166535
Seq. ID
                  LIB3234-009-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q3063472
```

```
E value
                   2.0e-52
Match length
                   99
                   97
% identity
NCBI Description
                  (AC003981) F22013.34 [Arabidopsis thaliana]
Seq. No.
                   166536
Seq. ID
                   LIB3234-009-P1-K1-C3
Method .
                   BLASTN
NCBI GI
                   g2760167
BLAST score
                   34
                   2.0e-10
E value
                   50
Match length
                   92
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCO15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166537
                   LIB3234-009-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2062167
BLAST score
                   239
                   4.0e-20
E value
                   60
Match length
% identity .
                   72
NCBI Description
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
                   thaliana]
                                                                       ς.
                   166538
Seq. No.
Seq. ID
                  LIB3234-009-P1-K1-C8
Method
                   BLASTN
NCBI GI
                   g3687221
BLAST score
                   57
                   2.0e-23
E value
                   206
Match length
% identity
                   94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6F22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166539
Seq. ID
                  LIB3234-009-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g4210331
BLAST score
                  195
E value
                  1.0e-106
Match length
                  259
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for 2-oxoglutarate dehydrogenase
                  E2 subunit
Seq. No.
                  166540
Seq. ID
                  LIB3234-009-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  q4757662
BLAST score
                  76
E value
                  1.0e-34
Match length
                  252
% identity
                  83
```

··· :

Seq. No.

```
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F10B6 from
                   chromosome I, complete sequence
Seq. No.
                   166541
Seq. ID
                   LIB3234-009-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   q2264315
BLAST score
                   286
                   1.0e-160
E value
                   358
Match length
% identity
                   95
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRN17, complete sequence [Arabidopsis thaliana]
                   166542
Seq. No.
                  LIB3234-009-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                  g1731324
BLAST score
                  164
                  7.0e-13
E value
Match length
                   57
% identity
                  74
                  HYPOTHETICAL PROTEIN >gi_166306 (M23451) steroid receptor
NCBI Description
                   [Achlya ambisexualis]
Seq. No.
                  166543
                  LIB3234-009-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4587584
BLAST score
                  358
E value
                  3.0e - 34
Match length
                  109
% identity
                  71
NCBI Description
                  (AC007232) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166544
Seq. ID
                  LIB3234-009-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g82228
BLAST score
                  247
E value
                  4.0e-21
Match length
                  78
% identity
                  69
                  hypothetical protein 77 - common tobacco chloroplast
NCBI Description
                  >gi_225199_prf__1211235AD ORF 77 [Nicotiana tabacum]
                  166545
Seq. No.
Seq. ID
                  LIB3234-009-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g2252823
BLAST score
                  174
E value
                  2.0e-93
Match length
                  178
                  99
% identity
NCBI Description
                  Arabidopsis thaliana BAC IG005I10
```

Method

BLASTX

```
Seq. ID
                   LIB3234-009-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g266410
BLAST score
                   348
                   5.0e-33
E value
Match length
                   120
% identity ·
                   60
NCBI Description CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi 82507 pir S13934
                   protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog - rice >gi_20194_emb_CAA41172_ (X58194) cdc2+/CDC28-related
                   protein kinase [Oryza sativa]
                   166547
Seq. No.
Seq. ID
                   LIB3234-009-P1-K1-D7
Method
                   BLASTN
NCBI GI
                   g3687221
BLAST score
                   280
E value
                   1.0e-156
Match length
                   384
% identity
                   94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6F22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166548
Seq. ID
                   LIB3234-009-P1-K1-D8
Method
                   BLASTN
NCBI GI
                   g2160132
BLAST score
                   100
                   6.0e-49
E value
Match length
                   164
% identity
                   90
                   Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166549
                   LIB3234-009-P1-K1-D9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1448916
BLAST score
                   155
E value
                   7.0e-82
Match length
                   283
% identity
                   89
NCBI Description Arabidopsis thaliana threonine synthase mRNA, 3' end of cds
Seq. No.
                   166550
Seq. ID
                   LIB3234-009-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   q2191126
BLAST score
                   190
E value
                   1.0e-102
Match length
                   384
                   97
% identity
NCBI Description
                  Arabidopsis thaliana BAC IG002N01
Seq. No.
                   166551
Seq. ID
                   LIB3234-009-P1-K1-E2
```

```
NCBI GI
                   g1931647
BLAST score
                   352
                   2.0e-33
E value
Match length
                   78
% identity
                   85
                   (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   166552
Seq. ID
                   LIB3234-009-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g1418323
BLAST score
                   438
E value
                   2.0e-43
Match length
                   122
% identity
                   68
NCBI Description
                   (X98671) zinc finger protein [Arabidopsis thaliana]
                   >gi_1418333_emb_CAA67228_ (X98670) zinc finger protein
                   [Arabidopsis thaliana]
Seq. No.
                   166553
Seq. ID
                  LIB3234-009-P1-K1-E4
Method
                   BLASTN
NCBI GI
                   g4469002
BLAST score
                   255
E value
                   1.0e-141
Match length
                   382
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                   (ESSA project)
Seq. No.
                  166554
Seq. ID
                  LIB3234-009-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  155
E value
                   9.0e-82
Match length
                  293
% identity
                  85
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
Seq. No.
                  166555
Seq. ID
                  LIB3234-009-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g16473
BLAST score
                  159
E value
                  4.0e-84
Match length
                  711
% identity
                  17
NCBI Description
                  Arabidopsis thaliana 25S-18S ribosomal DNA spacer
Seq. No.
                  166556
Seq. ID
                  LIB3234-009-P1-K1-E8
Method
                  BLASTX
NCBI GI
```

g112682

272

BLAST score

```
E value
                   1.0e-24
Match length
                   58
% identity
                   93
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   166557
Seq. ID
                   LIB3234-009-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g1345973
BLAST score
                   406
                   9.0e-40
E value
Match length
                   93
% identity
                   81
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                   1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj BAA05514 (D26508)
                   microsomal omega-3 fatty \overline{\text{acid}} desaturase [Arabidopsis
                   thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
Seq. No.
                   166558
Seq. ID
                   LIB3234-009-P1-K1-F11 ···
Method
                   BLASTX
NCBI GI
                   q2648032
BLAST score
                   292
E value
                   2.0e-26
Match length
                   128
% identity
                  45
NCBI Description
                  (AJ001374) alpha-glucosidase [Solanum tuberosum]
Seq. No.
                  166559
Seq. ID
                  LIB3234-009-P1-K1-F12.
Method
                  BLASTN
NCBI GI
                  g4159709
BLAST score
                  203
E value
                  1.0e-110
Match length
                  312
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLN21, complete sequence
Seq. No.
                  166560
Seq. ID
                  LIB3234-009-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2245019
BLAST score
                  630
E value
                  5.0e-66
Match length
                  123
% identity
                  98
NCBI Description
                  (Z97341) proteinase homolog [Arabidopsis thaliana]
```

```
Seq. No.
                  166561
Seq. ID
                  LIB3234-009-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  g3449331
BLAST score
                  370
E value
                  0.0e+00
Match length
                  374
% identity
                  27
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166562
Seq. ID
                  LIB3234-009-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1616787
BLAST score
                  600
E value
                  2.0e-62
Match length
                  117
% identity
                  97
NCBI Description
                  (U71122) pyruvate decarboxylase [Arabidopsis thaliana]
                  166563
Seq. No.
                  LIB3234-009-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454028
BLAST score
                  264
E value
                  4.0e-23
Match length
                  55
% identity
NCBI Description
                  (AL035394) tyrosine transaminase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  166564
Seq. ID
                  LIB3234-009-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g119194
BLAST score
                  349
E value
                  5.0e-33
Match length
                  123
% identity
                  59
                  ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
NCBI Description
                  >gi_81607_pir__S09152 translation elongation factor Tu
                  precursor, chloroplast - Arabidopsis thaliana
                  >qi 22565 emb CAA36498 (X52256) elongation factor Tu
                  precursor [Arabidopsis thaliana] >gi_226817_prf_ 1607332A
                  elongation factor Tu [Arabidopsis thaliana]
Seq. No.
                  166565
Seq. ID
                  LIB3234-009-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  q3449312
BLAST score
                  114
E value
                  2.0e-57
Match length
                  216
% identity
                  100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
```

```
Seq. No.
                   166566
Seq. ID
                   LIB3234-009-P1-K1-G10
Method
                   BLASTN
NCBI GI
                   g4512656
BLAST score
                   147
E value
                   5.0e-77
Match length
                   303 .
% identity
                   89
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F7D19 genomic
                   sequence, complete sequence
Seq. No.
                   166567
Seq. ID
                   LIB3234-009-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   g4220640
BLAST score
                   349
E value
                   0.0e + 00
Match length
                   373
% identity
                   98
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166568
Seq. ID
                   LIB3234-009-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   g3366536
BLAST score
                   137
E value
                   3.0e-71
Match length
                   193
% identity
                   95
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC T25N2O,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   166569
Seq. ID
                   LIB3234-009-P1-K1-G2
Method
                   BLASTN
NCBI GI
                   q4159712
BLAST score
                   105
E value
                   6.0e-52
Match length
                   353
% identity
                   78
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MWI23, complete sequence
                   166570
Seq. No.
Seq. ID
                  LIB3234-009-P1-K1-G3
Method
                   BLASTX
NCBI GI
                  g267073
BLAST score
                   561
E value
                   6.0e-58
Match length
                  102
% identity
                  100
                  TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi \overline{166898} (M84700)
```

K16L22, complete sequence [Arabidopsis thaliana]

beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

```
Seq. No.
                   166571
Seq. ID
                  LIB3234-009-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g2160158
BLAST score
                   676
E value
                   2.0e-71
Match length
                   126
% identity
                   99
NCBI Description
                   (AC000132) Similar to elongation factor 1-gamma
                   (gb_EF1G_XENLA). ESTs gb T20564, gb T45940, gb T04527 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                  166572
Seq. ID
                  LIB3234-009-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3738257
BLAST score
                  149
E value
                  5.0e-10
Match length
                  50
% identity
                  66
NCBI Description
                   (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
                  nigra]
Seq. No.
                  166573
                  LIB3234-009-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2062167
BLAST score
                  234
                  1.0e-19
E value
Match length
                  87
% identity
                  51
NCBI Description
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
                  thaliana]
Seq. No.
                  166574
Seq. ID
                  LIB3234-009-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q207905
BLAST score
                  141
E value
                  1.0e-08
Match length
                  64
% identity
                  41
NCBI Description
                  (M18027) alpha globulin B [Artificial gene]
Seq. No.
                  166575
                  LIB3234-009-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1616787
BLAST score
                  515
E value
                  1.0e-52
Match length
                  114
% identity
NCBI Description
                 (U71122) pyruvate decarboxylase [Arabidopsis thaliana]
Seq. No.
                  166576
```

Seq. No.

```
Seq. ID
                    LIB3234-009-P1-K1-H11
 Method
                    BLASTN
 NCBI GI
                    g4159705
 BLAST score
                    183
 E value
                    9.0e-99
 Match length
                    207
 % identity
                    97
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                   MGD8, complete sequence
 Seq. No.
                   166577
 Seq. ID
                   LIB3234-009-P1-K1-H12
 Method
                   BLASTX
 NCBI GI
                   q2465923
 BLAST score
                   258
 E value
                   2.0e-22
 Match length
                   74
 % identity
                   65
 NCBI Description
                   (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
 Seq. No.
                   166578
 Seq. ID
                   LIB3234-009-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   g3885325
BLAST score
                   284
E value
                   1.0e-159
Match length
                   372
% identity
                   94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20P8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166579
Seq. ID
                   LIB3234-009-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g131360
BLAST score
                   241
E value
                   2.0e-20
Match length
                   61
% identity
                   80
NCBI Description
                   PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
                  >gi_81727_pir__S02115 photosystem II protein psbK precursor
                   - white mustard chloroplast >gi_12209_emb_CAA31909
                   (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
Seq. No.
                  166580
Seq. ID
                  LIB3234-009-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  526
E value
                  7.0e-54
Match length
                  100
% identity
                  100
NCBI Description
                  (AC003027) lcl_prt_seq No definition line found
                  [Arabidopsis thaliana]
```

```
Seq. ID
                   LIB3234-010-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g2262167
BLAST score
                   514
E value
                   2.0e-52
Match length
                   98
% identity
                   100
NCBI Description
                   (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
Seq. No.
                   166582
Seq. ID
                   LIB3234-010-P1-K1-A12
Method
                  BLASTN
NCBI GI
                   q4510323
BLAST score
                   348
E value
                   0.0e+00
Match length
                   360
                   99
% identity
NCBI Description Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
                  cM, complete sequence
Seq. No.
                  166583
Seq. ID
                  LIB3234-010-P1-K1-A3 -
Method
                  BLASTN
NCBI GI
                  q3402747
BLAST score
                  351
E value
                  0.0e+00
Match length
                  351
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22
                  (ESSAII project)
Seq. No.
                  166584
Seq. ID
                  LIB3234-010-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g3540210
BLAST score
                  314
E value
                  1.0e-176
Match length
                  346
% identity
                  98
NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166585
Seq. ID
                  LIB3234-010-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3785989
BLAST score
                  413
E value
                  1.0e-40
Match length
                  80
% identity
                  100
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166586
Seq. ID
                  LIB3234-010-P1-K1-A9
Method
                  BLASTN
```

q3985950

Match length

```
BLAST score
                   131
E value
                   1.0e-67
Match length
                   251
% identity
                   96
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MPI10, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166587
Seq. ID
                   LIB3234-010-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g2914700
BLAST score
                   431
E value
                   1.0e-42
Match length
                   86
% identity
                   99
NCBI Description
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
                   thaliana]
Seq. No.
                   166588
Seq. ID
                   LIB3234-010-P1-K1-B10
Method
                   BLASTN
NCBI GI
                   q4159712
BLAST score
                   185
E value
                   1.0e-99
Match length
                  ·289
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MWI23, complete sequence
Seq. No.
                   166589
Seq. ID
                   LIB3234-010-P1-K1-B11
Method
                   BLASTN
NCBI GI
                   q4467131
BLAST score
                   192
E value
                   1.0e-104
Match length
                   315
% identity
                   97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
                   (ESSA project)
Seq. No.
                  166590
Seq. ID
                  LIB3234-010-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4582436
BLAST score
                  482
E value
                  1.0e-48
Match length
                  115
% identity
                  79
NCBI Description
                  (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166591
Seq. ID
                  LIB3234-010-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  378
E value
                  1.0e-36
```

NCBI Description

```
% identity
                   81
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   166592
Seq. ID
                   LIB3234-010-P1-K1-B4
Method
                   BLASTN
                   g2760170
NCBI GI
BLAST score
                   363
E value
                   0.0e + 00
Match length
                   367
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MIO24, complete sequence [Arabidopsis thaliana]
                   166593
Seq. No.
Seq. ID
                   LIB3234-010-P1-K1-B5
Method
                   BLASTN
NCBI GI
                   g4220643
BLAST score
                   347
E value
                   0.0e + 00
Match length
                   367
                   99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166594
                   LIB3234-010-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   554
                   4.0e-57
E value
Match length
                   105
                   100
% identity
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
Seq. -No.
                  166595
Seq. ID
                  LIB3234-010-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g1872522
BLAST score
                  119
E value
                  3.0e-60
Match length
                  119
% identity
                  100
                  Arabidopsis thaliana zinc-finger protein Lsd1 (LSD1) gene,
NCBI Description
                  complete cds
Seq. No.
                  166596
Seq. ID
                  LIB3234-010-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3335171
BLAST score
                  557
E value
                  2.0e-57
Match length
                  121
% identity
                  88
```

(AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

BLAST score

```
Seq. No.
                    166597
Seq. ID
                    LIB3234-010-P1-K1-C2
Method
                    BLASTX
NCBI GI
                    g1173345
BLAST score
                    450
E value
                    6.0e-45
Match length
                    118
% identity
                    78
                   SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase -
                   Arabidopsis thaliana >gi_786466_bbs_159034 (S74719)
                    sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37}
                    [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa]
                    [Arabidopsis thaliana]
Seq. No.
                   166598
Seq. ID
                   LIB3234-010-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g3915961
BLAST score
                   606
E value
                   3.0e-63
Match length
                   122
% identity
                   95
                  HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
NCBI Description
                   >gi_2924274_emb_CAA77427 (Z00044) Ycf2 protein [Nicotiana
                   tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
                   protein [Nicotiana tabacum]
Seq. No.
                   166599
                   LIB3234-010-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3913418
BLAST score
                   · 610
E value
                   1.0e-63
Match length
                   118
% identity
                   98
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1531763_emb CAA69073_ (Y07765)
                   S-adenosylmethionine decarboxylase [Arabidopsis thaliana]
Seq. No.
                   166600
Seq. ID
                   LIB3234-010-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   g4220643
BLAST score
                   319
E value
                   1.0e-179
Match length
                   323
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166601
Seq. ID
                   LIB3234-010-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q4704766
```

```
E value
                   5.0e-38
Match length
                   107
% identity
                   45
NCBI Description
                   (AF131223) protein disulfide isomerase homolog; PDI
                 . [Datisca glomerata]
Seq. No.
                   1,66602
Seq. ID
                   LIB3234-010-P1-K1-C9
Method
                   BLASTN
NCBI GI
                   ġ3402671
BLAST score
                   329
                   0.0e + 00
E value
Match length
                   336
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T16B24 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166603
Seq. ID
                   LIB3234-010-P1-K1-D1
Method
                   BLASTN
                   g3766106
NCBI GI
BLAST score
                   365
E value
                   0.0e+00
Match length
                   373
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   166604
Seq. ID
                  LIB3234-010-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g2583111
BLAST score
                   621
E value
                   5.0e-65
Match length
                   117
% identity
NCBI Description
                   (AC002387) putative dihydrodipicolinate synthase
                   [Arabidopsis thaliana]
Seq. No.
                  166605
Seq. ID
                  LIB3234-010-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  257
E value
                  1.0e-142
Match length
                  281
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  166606
Seq. ID
                  LIB3234-010-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q4099349
BLAST score
                  590
E value
                  2.0e-61
Match length
                  120
```

```
% identity
                   98
NCBI Description
                  (U86394) ATP synthase beta subunit [Papaver orientale]
Seq. No.
                   166607
Seq. ID
                   LIB3234-010-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   q3335169
BLAST score
                   599
E value
                   2.0e-62
Match length
                   116
% identity
                   98
NCBI Description
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                   >gi_4455197 emb CAB36520.1_ (AL035440) embryo-specific
                   protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                   166608
Seq. ID
                   LIB3234-010-P1-K1-D7
Method
                   BLASTN
NCBI GI
                   g4199934
BLAST score
                   321
E value
                   0.0e + 00
Match length
                   325
% identity
                   100
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   166609
Seq. ID
                  LIB3234-010-P1-K1-D8
Method
                   BLASTX
NCBI GI
                  g2499605
BLAST score
                  599
E value
                   2.0e-62
Match length
                  123
% identity
                   93
NCBI Description
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (MAP KINASE 1)
                   (ATMPK1) >gi_533280_dbj BAA03535 (D14713) ATMPK1
                   [Arabidopsis thaliana]
Seq. No.
                  166610
Seq. ID
                  LIB3234-010-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q2597824
BLAST score
                  547
E value
                  3.0e-56
Match length
                  123
% identity
                  85
                  (AJ002532) endo-polygalacturonase [Arabidopsis thaliana]
NCBI Description
                  >gi_4090973 (AF037367) endo-polygalacturonase [Arabidopsis
                  thaliana]
Seq. No.
                  166611
Seq. ID
                  LIB3234-010-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q4586044
BLAST score
                  275
E value
                  2.0e-24
Match length
                  110
```

```
% identity
 NCBI Description
                    (AC007020) putative receptor protein kinase [Arabidopsis
                    thaliana]
 Seq. No.
                   166612
 Seq. ID
                   LIB3234-010-P1-K1-E11
 Method
                   BLASTN
 NCBI GI
                   g3046856
 BLAST score
                   288
 E value
                   1.0e-161
 Match length
                   351
 % identity
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MXI22, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   166613
 Seq. ID
                   LIB3234-010-P1-K1-E12
 Method
                   BLASTN
 NCBI GI
                   q3047060
 BLAST score
                   34
E .value
                   1.0e-09
Match length
                   66
 % identity
                   88
NCBI Description Arabidopsis thaliana BAC F7N22
Seq. No.
                   166614
Seq. ID
                   LIB3234-010-P1-K1-E2
Method
                   BLASTN
NCBI GI
                  -g1279629
BLAST score
                   341
E value
                   0.0e + 00
Match length
                   376
% identity
                   98
NCBI Description
                  O.lamarckiana chloroplast 16S rRNA, trnI, trnA and 23S rRNA
Seq. No.
                   166615
Seq. ID
                   LIB3234-010-P1-K1-E4
Method
                   BLASTN
NCBI GI
                   q4519195
BLAST score
                   72
E value
                   3.0e-32
Match length
                   138
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
Seq. No.
                  166616
Seq. ID
                  LIB3234-010-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3915847
BLAST score
                  333
E value
                  3.0e - 31
Match length
                  75
% identity -
                  88
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
```

```
Seq. No.
                   166617
 Seq. ID
                   LIB3234-010-P1-K1-E7
 Method
                   BLASTN
 NCBI GI
                   g3510339
 BLAST score
                   368
 E value
                   0.0e+00
 Match length
                  368
 % identity
                   100
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K3K7, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   166618
 Seq. ID
                   LIB3234-010-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   g1279629
BLAST score
                   325
E value
                   0.0e+00
Match length
                   360
% identity
                   98
NCBI Description
                   O.lamarckiana chloroplast 16S rRNA, trnI, trnA and 23S rRNA
                   genes
Seq. No.
                   166619
Seq. ID
                   LIB3234-010-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g464986
BLAST score
                   480
E value
                   2.0e-48
Match length
                   89
% identity
                   98
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
                   6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis thaliana]
                  >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                  166620
Seq. ID
                  LIB3234-010-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2583108
BLAST score
                  597
E value
                  3.0e-62
Match length
                  120
% identity
                  100
NCBI Description
                  (AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.
                  166621
Seq. ID
                  LIB3234-010-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2497540
```

```
BLAST score
                   408
 E value
                   3.0e-40
 Match length
                   96
 % identity
                   88
 NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G
 Seq. No.
                   166622
 Seq. ID
                   LIB3234-010-P1-K1-F12
 Method
                   BLASTX
 NCBI GI
                   g3980412
 BLAST score
                   123
 E value
                   6.0e-07
Match length
                   78
 % identity
 NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
 Seq. No.
                   166623
 Seq. ID
                   LIB3234-010-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   g4309719
 BLAST score
                   332
E value
                   0.0e+00
Match length
                   365
% identity
                   97 -
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T30D6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166624
Seq. ID
                   LIB3234-010-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g2583125
BLAST score
                   511
E value
                   4.0e-52
Match length
                   94
% identity
                   100
NCBI Description
                   (AC002387) putative transketolase precursor [Arabidopsis
                   thaliana]
Seq. No.
                   166625
                   LIB3234-010-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                  g2583125
BLAST score
                   450
E value
                   4.0e-45
Match length
                  96
% identity
                  86
NCBI Description
                   (AC002387) putative transketolase precursor [Arabidopsis
                  thaliana]
Seq. No.
                  166626
Seq. ID
                  LIB3234-010-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1864017
BLAST score
                  477 -..
E value
                  4.0e-48
Match length
                  91
% identity
```

```
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   166627
                   LIB3234-010-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832620
BLAST score
                   392
E value
                   3.0e-38
Match length
                   108
% identity
                   69
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   166628
Seq. ID
                  LIB3234-010-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                   46
E value
                   1.0e-16
Match length
                  110
% identity
                  85
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
"Seq. No.
                  166629
                  LIB3234-010-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467139
BLAST score
                  157
E value
                  1.0e-10
Match length
                  43
% identity
                  77
NCBI Description
                  (AL035540) putative protein phosphatase-2c [Arabidopsis
                  thaliana]
Seq. No.
                  166630
                  LIB3234-010-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  644
E value
                  1.0e-67
Match length
                  117
% identity
                  100
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  166631
                  LIB3234-010-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3024871
BLAST score
                  193
E value
                  2.0e-18
Match length
                  107
```

```
% identity
                   50
NCBI Description
                  HYPOTHETICAL 77.3 KD PROTEIN SLL0005
                  >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis
                   sp.]
Seq. No.
                  166632
Seq. ID
                  LIB3234-010-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g137579
BLAST score
                  180
E value
                  3.0e-13
Match length
                  108
                  37
% identity
                  PROVICILIN (TYPE A) >gi 72292 pir FWPMVA vicilin type A
NCBI Description
                  precursor - garden pea (fragment)
Seq. No.
                  166633
Seq. ID
                  LIB3234-010-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g4586053
BLAST score
                  230
E value
                  3.0e-19
Match length
                  117
% identity
                  47
NCBI Description
                  (AC007020) putative lacasse [Arabidopsis thaliana]
Seq. No.
                  166634
Seq. ID
                  LIB3234-010-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g3540196
BLAST score
                  178
                  1.0e-13
E value
                  59
Match length
                  63
% identity
                  (AC004260) Putative amp-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166635
                  LIB3234-010-P1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1070376
BLAST score
                  67
E value
                  3.0e-29
Match length
                  141
% identity
                  91
NCBI Description P.deltoides chloroplast psbT and psbH genes
Seq. No.
                  166636
Seq. ID
                  LIB3234-010-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g4587567
BLAST score
                  552
E value
                  6.0e-57
Match length
                  105
% identity
                  99
NCBI Description (AC006550) F1003.7 [Arabidopsis thaliana]
```

BLAST score

```
166637
Seq. No.
Seq. ID
                  LIB3234-010-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g3850928
BLAST score
                  388
E value
                  1.0e-37
                                                        Match length
                  85
% identity
                  87
NCBI Description
                 (AF060404) ATP synthase beta subunit [Adenanthos obovatus]
Seq. No.
                  166638
Seq. ID
                  LIB3234-010-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2959781
BLAST score
                  604
E value
                  5.0e-63
Match length
                  119
% identity
                  99
NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]
                  166639
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g4679028
BLAST score
                  268
                  1.0e-23
E value
Match length
                  115
% identity
                  48
                  (AF077207) HSPC021 [Homo sapiens]
NCBI Description
Seq. No.
                  166640
Seq. ID
                  LIB3234-011-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g4539309
BLAST score
                  136
E value
                  1.0e-70
Match length
                  188
% identity
NCBI Description
                 Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22
                  (ESSA project)
Seq. No.
                  166641
Seq. ID
                  LIB3234-011-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4056457
BLAST score
                  590
E value
                  2.0e-61
Match length
                  116
% identity
                  100
                  (AC005990) ESTs gb_234051 and gb_F13722 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
Seq. No.
                  166642
Seq. ID
                  LIB3234-011-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  g2914688
```

BLAST score

```
E value
                   2.0e-94
 Match length
                   353
 % identity
                   100
 NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   166643
 Seq. ID
                   -LIB3234-011-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q132074
BLAST score
                   441
E value
                   4.0e-44
Match length
                   87
 % identity
                   94
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   166644
Seq. ID
                   LIB3234-011-P1-K1-B1
Method
                   BLASTN
NCBI GI
                   q4159712
BLAST score
                   297
E value
                   1.0e-166
Match length
                   347
% identity
                   96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
Seq. No.
                   166645
Seq. ID
                  LIB3234-011-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  g2656028
BLAST score
                  161
E value
                  2.0e-85
Match length
                  353
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNF13
Seq. No.
                  166646
Seq. ID
                  LIB3234-011-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  g4558656
BLAST score
                  181
E value
                  2.0e-97
Match length
                  285
% identity
                  92
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T10F5 genomic
                  sequence, complete sequence
Seq. No.
                  166647
Seq. ID
                  LIB3234-011-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g21911
```

```
E value
                    3.0e-15
Match length
                   79
                    46
% identity
NCBI Description
                   (X62625) vicilin [Theobroma cacao]
Seq. No.
                   166648
Seq. ID
                   LIB3234-011-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g544424
BLAST score
                   60
E value
                   8.0e-37
Match length
                   85
                   98
% identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                   166649
Seq. No.
Seq. ID
                   LIB3234-011-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   q166570
BLAST score
                   174
E value
                   1.0e-12
Match length
                   31
% identity
                   100
NCBI Description
                   (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                   166650
Seq. ID
                   LIB3234-011-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   q3851636
BLAST score
                   382
E value
                   5.0e-37
Match length
                   99
% identity
                   71
NCBI Description
                   (AF098519) unknown [Avicennia marina] >gi 4128206
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                   166651
                   LIB3234-011-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464988
BLAST score
                   175
                   1.0e-12
E value
Match length
                   36
% identity
                   83
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 (UBIQUITIN-PROTEIN
                   LIGASE 11) (UBIQUITIN CARRIER PROTEIN 11)
                   >gi_421856_pir__S32673 ubiquitin--protein ligase (EC
                   6.3.2.19) UBC11 - Arabidopsis thaliana (fragment)
                   >gi 297880 emb {
m CAA78716}_{-} (Z14992) ubiquitin conjugating
                   enzyme [Arabidopsis thaliana] >gi 349215 (L00641) ubiquitin
```

conjugating enzyme [Arabidopsis thaliana]

Seq. No.

```
Seq. No.
                   166652
Seq. ID
                  LIB3234-011-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q3269286
BLAST score
                   435
                   3.0e-43
E value
Match length
                   107
% identity
                   88
NCBI Description
                  (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  166653
Seq. ID
                  LIB3234-011-P1-K1-C12
Method
                  BLASTX
                  g3688175
NCBI GI
BLAST score
                   281
E value
                   3.0e-25
Match length
                   91
% identity
                  63
NCBI Description
                   (AL031804) gamma-VPE (vacuolar processing enzyme)
                   [Arabidopsis thaliana]
Seq. No.
                  166654
                  LIB3234-011-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710581
BLAST score
                  483
E value
                  8.0e-49
Match length
                  100
% identity
                  94
NCBI Description
                  60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir_ S71255 ribosomal
                  protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_
                  (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
Seq. No.
                  166655
Seq. ID
                  LIB3234-011-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  g2494110
BLAST score
                  309
E value
                  1.0e-173
Match length
                  309
% identity
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166656
Seq. ID
                  LIB3234-011-P1-K1-C5
Method
                  BLASTN
NCBI GI
                  q4199934
BLAST score
                  291
E value
                  1.0e-163
Match length
                  306
                  99
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
```

NCBI GI

```
Seq. ID
                   LIB3234-011-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   g2494110
BLAST score
                   276
E value
                   1.0e-154
Match length
                   308
                   97 - . . .
% identity
NCBI Description
                   Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
                   166658
Seq. No.
Seq. ID
                   LIB3234-011-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g4567199
BLAST score
                   535
                   6.0e-55
E value
Match length
                   112
                   92
% identity
NCBI Description
                  (AC007168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   166659
Seq. ID
                   LIB3234-011-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   g4544365
BLAST score
                   44
                   1.0e-15
E value
Match length
                   300
% identity
                   91
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F26H6 genomic
                   sequence, complete sequence
Seq. No.
                   166660
                   LIB3234-011-P1-K1-D11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4510392
BLAST score
                   99
E value
                   2.0e-48
Match length
                  103
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T17D12 genomic
                  sequence, complete sequence
Seq. No.
                  166661
Seq. ID
                  LIB3234-011-P1-K1-D2
Method
                  BLASTX
                  q687844
NCBI GI
BLAST score
                  101
E value
                  5.0e-04
Match length
                  78
% identity
NCBI Description
                  (U21320) contains TPR domain-like repeats [Caenorhabditis
                  elegans]
Seq. No.
                  166662
Seq. ID :
                  LIB3234-011-P1-K1-D3
Method
                  BLASTN
```

g3859658

```
BLAST score
                   327
E value
                   0.0e+00
Match length
                   339
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
                   (ESSAII project)
Seq. No.
                  166663
Seq. ID
                  LIB3234-011-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  q3256065
BLAST score
                  272
E value
                  1.0e-151
                  292
Match length
% identity
                  98
NCBI Description
                  Arabidopsis thaliana mRNA for chloroplast NAD-dependent
                  malate dehydrogenase
Seq. No.
                  166664
Seq. ID
                  LIB3234-011-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g2114077
BLAST score
                  188
E value
                  1.0e-101
Match length
                  321
% identity
                  92
NCBI Description
                  Arabidopsis thaliana DNA for larger subunit of Rubisco,
                  beta subunit of coupling factor one, partial cds
Seq. No.
                  166665
Seq. ID
                  LIB3234-011-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  g3256065
BLAST score
                  277
E value
                  1.0e-154
Match length
                  293
% identity
                  99
NCBI Description
                  Arabidopsis thaliana mRNA for chloroplast NAD-dependent
                  malate dehydrogenase
Seq. No.
                  166666
Seq. ID
                  LIB3234-011-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  q2351068
BLAST score
                  231
E value
                  1.0e-127
                  347
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRH10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166667
Seq. ID
                  LIB3234-011-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  50
```

4.0e-19

E value

```
Match length
                   113
% identity
                   86
NCBI Description
                   Tobacco chloroplast genome DNA
Seq. No.
                   166668
Seq. ID
                   LIB3234-011-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   g3869069
BLAST score
                   189
E value
                   1.0e-102
Match length
                   351
                   99
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166669
Seq. ID
                   LIB3234-011-P1-K1-E10
                   BLASTN
Method
NCBI GI
                   g2583106
BLAST score
                   282
                   1.0e-157
E value
Match length
                   347
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4L23 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No...
                   166670
Seq. ID
                  LIB3234-011-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   g2656031
BLAST score
                   302
                   1.0e-169
E value
Match length
                   347
                   99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXC20
Seq. No.
                  166671
Seq. ID
                  LIB3234-011-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q3522946
BLAST score
                  423
E value
                  8.0e-42
Match length
                  92
% identity
                  88
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166672
Seq. ID
                  LIB3234-011-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g4263791
BLAST score
                  298
E value
                  4.0e-27
Match length
                  116 ·
% identity
                  53
NCBI Description
                  (AC006068) putative receptor protein kinase [Arabidopsis
```

thaliana]

```
166673
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-E5
Method
                  BLASTX
NCBI GI
                 g2583125
BLAST score
                  480 <
E value
                  2.0e-48
                  105
Match length
                  95
% identity
                  (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                  thaliana]
                  166674
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g4512646
BLAST score
                  301
                  1.0e-169
E value
Match length
                  348
% identity
                  37
NCBI Description Arabidopsis thaliana chromosome II BAC F23N11 genomic
                  sequence, complete sequence
                  166675
Seq. No.
Seq. ID "
                  LIB3234-011-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g3985952
BLAST score
                  260
                  1.0e-144
E value
Match length
                  346
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MRC8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166676
Seq. ID
                  LIB3234-011-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  363
E value
                  9.0e-35
Match length
                  93
                  77
% identity
NCBI Description
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  166677
Seq. ID
                  LIB3234-011-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q4586249
BLAST score
                  325
                  2.0e-30
E value
Match length
                  103
% identity
NCBI Description
                  (AL049640) putative pollen surface protein [Arabidopsis
                  thaliana]
Seq. No.
                  166678
Seq. ID
                  LIB3234-011-P1-K1-F11
```

E value

2.0e-11

```
Method
                   BLASTN
NCBI GI
                   g2264306
BLAST score
                   331
E value
                   0.0e+00
Match length
                   343
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166679
                   LIB3234-011-P1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4585977
BLAST score
                   194
E value
                   6.0e-15
Match length
                   59
% identity
                   61
NCBI Description
                  (AC005287) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  166680
Seq. ID
                  LIB3234-011-P1-K1-F2
Method
                  BLASTN
NCBI GI
                   g2252823
BLAST score
                   273
E~value
                  1.0e-152
Match length
                   346
% identity
                   98
NCBI Description Arabidopsis thaliana BAC IG005I10
Seq. No.
                  166681
Seq. ID
                  LIB3234-011-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  q4337186
BLAST score
                  196
E value
                  1.0e-106
                  241
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T28I24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166682
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2160144
BLAST score
                  151
E value
                  6.0e-10
                  63
Match length
% identity
NCBI Description
                  (AC000375) Strong similarity to Arabidopsis oligopeptide
                 transporter (gb X77503). [Arabidopsis thaliana]
Seq. No.
                  166683
                  LIB3234-011-P1-K1-F6
Seq. ID
Method.
                  BLASTX
NCBI GI
                  g2160144
BLAST score
                  164
```

```
Match length
                   63
                   44
% identity
NCBI Description
                   (AC000375) Strong similarity to Arabidopsis oligopeptide
                   transporter (gb_X77503). [Arabidopsis thaliana]
Šeq. No.
                  166684
Seq. ID
                  LIB3234-011-P1-K1-F7
Method
                  BLASTX
NCBI GI
                   q3935151
BLAST score
                   535
                   6.0e-55
E value
                  100
Match length
                   99
% identity
NCBI Description
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
Seq. No.
                  166685
Seq. ID
                  LIB3234-011-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g4512666
BLAST score
                   587
E value
                   5.0e-61
                  115
Match length
                  92
% identity
                  (AC006931) putative mei2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166686
Seq. ID
                  LIB3234-011-P1-K1-G1
Method
                  BLASTN
                  g2815404
NCBI GI
BLAST score
                  252
E value
                  1.0e-140
Match length
                  300
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMG4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166687
                  LIB3234-011-P1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220641
BLAST score
                  318
E value
                  1.0e-179
Match length
                  346
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUL3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166688
                  LIB3234-011-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362162
BLAST score
                  262
                  6.0e-23
E value
Match length
                  66
% identity
                  74
NCBI Description
                  beta-glucosidase BGQ60 precursor - barley >gi 804656
                  (L41869) beta-glucosidase [Hordeum vulgare]
```

Method

BLASTX

```
166689
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-G12
                  BLASTN
Method
NCBI GI
                  g2196463
BLAST score
                  341
E value
                  0.0e + 00
                  357
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana chloroplast trnC, rpoB & rpoC1 genes
                  166690
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3327957
BLAST score
                  161
                  4.0e-11
E value
Match length
                  51
                  55
% identity
NCBI Description
                  (AF060490) TLS-associated protein TASR-2 [Mus musculus]
                  >gi 3327976 (AF067730) TLS-associated protein TASR-2 [Homo
                  sapiens]
                  166691
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1592677
BLAST score
                  189
                  2.0e-14
E value
                  38
Match length
% identity
                  97
                 (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166692
Seq. ID
                  LIB3234-011-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score .
                  475
E value
                  6.0e-48-
Match length
                  96
                  99
% identity
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  166693
Seq. ID
                  LIB3234-011-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3941528
BLAST score
                  647
E value
                  4.0e-68
Match length
                  116
                  99
% identity
                  (AF062918) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  166694
Seq. No.
Seq. ID
                  LIB3234-011-P1-K1-G6
```

Match length

```
NCBI GI
                   g2341034
BLAST score
                   464
E value
                  1.0e-46
                   94
Match length
                   99
% identity
                 (AC000104) F19P19.13 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166695
Seq. ID
                  LIB3234-011-P1-K1-G9
Method
                  BLASTN
NCBI ĠI
                  g4510338
BLAST score
                   178
                   2.0e-95
E value
Match length
                   314
                   98
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic
                  sequence, complete sequence
Seq. No.
                  166696
Seq. ID
                  LIB3234-011-P1-K1-H1
Method
                  BLASTX
                  g2921158
NCBI GI
BLAST score
                  533
E value
                  1.0e-54
Match length
                  112
                  97
% identity
NCBI Description (AF022909) ClpC [Arabidopsis thaliana]
Seq. No.
                  166697
                  LIB3234-011-P1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2864607
BLAST score
                  317
E value
                  1.0e-178
Match length
                  341
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                  (ESSAII project)
Seq. No.
                  166698
Seq. ID
                  LIB3234-011-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  q2618683
BLAST score
                  317
E value
                  1.0e-178
Match length
                  345
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166699
Seq. ID
                  LIB3234-011-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2605714
BLAST score
                  103
E value
                  2.0e-40
```

Seq. ID

```
% identity
                    81
NCBI Description
                    (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                    thaliana]
Seq. No.
                    166700
Seq. ID
                    LIB3234-012-P1-K1-A1
Method
                    BLASTX
NCBI GI
                    q2252844
BLAST score
                    354
E value
                    1.0e-33
                    78
Match length
% identity
                    83
NCBI Description
                    (AF013293) belongs to the cytochrome p450 family
                    [Arabidopsis thaliana]
Seq. No.
                    166701
Seq. ID
                    LIB3234-012-P1-K1-A10
Method
                    BLASTX
NCBI GI
                    g1345973
BLAST score
                    52
E value
                    9.0e-21
Match length
                    91
% identity
                    62
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                    omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                    microsomal omega-3 fatty acid desaturase [Arabidopsis
                    thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                    desaturase [Arabidopsis thaliana]
                    166702
Seq. No.
Seq. ID
                    LIB3234-012-P1-K1-A11
Method
                    BLASTN
                   g4006885
NCBI GI
BLAST score
                    312
                    1.0e-175
E value
Match length
                    324
% identity
                    99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                    fragment No
                    166703
Seq. No.
                   LIB3234-012-P1-K1-A2
Seq. ID
Method
                    BLASTN
NCBI GI
                    q4309719
BLAST score
                    24
                    1.0e-03
E value
Match length
                    331
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T30D6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   166704
Seq. No.
```

LIB3234-012-P1-K1-A4

% identity

```
Method
                   BLASTX
NCBI GI
                   g3763916
BLAST score
                   146
                  2.0e-09
E value
Match length
                   50
% identity
                   52
NCBI Description
                   (AC004450) unknown protein [Arabidopsis thaliana]
                  >gi_4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  166705
                  LIB3234-012-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4417264
BLAST score
                  111
                  1.0e-55
E value
Match length
                  302
                  72
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166706
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g1914683
BLAST score
                  240
                  2.0e-20
E value
Match length
                  65
                  72
% identity
NCBI Description
                  (Y12013) RAD23, isoform I [Daucus carota]
Seq. No.
                  166707
Seq. ID
                  LIB3234-012-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q1345973
BLAST score
                  440
                  8.0e-44
E value
Match length
                  94
% identity
                  85
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi 471091 dbj BAA04505 (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  166708
Seq. ID
                  LIB3234-012-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g4159712
BLAST score
                  284
E value
                  1.0e-159
Match length
                  333
```

Seq. ID

Method

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
                  166709
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  629
E value
                  6.0e-66
                  114
Match length
                  100
% identity
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_541882_pir__JQ2335_omega-3_fatty_acid_desaturase_(EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  166710
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g3046856
BLAST score
                  338
                  0.0e+00
E value
                  350
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXI22, complete sequence [Arabidopsis thaliana]
                  166711
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q4512673
BLAST score
                  344
E value
                  1.0e-32
                  67
Match length
                  100
% identity
NCBI Description
                  (AC006931) putative phosphoprotein phosphatase [Arabidopsis
                  thaliana]
Seq. No.
                  166712
Seq. ID
                  LIB3234-012-P1-K1-B12
                  BLASTN
Method
NCBI GI
                  g2864607
BLAST score
                  39
                  2.0e-13
E value
                  67
Match length
                  67
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                  (ESSAII project)
Seq. No.
                  166713
```

LIB3234-012-P1-K1-B4

BLASTN

E value

4.0e-13

```
NCBI GI
                  g4512656
BLAST score
                  301
E value
                  1.0e-169
Match length
                  343
% identity
                  89
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
Seq. No.
                  166714
Seq. ID
                  LIB3234-012-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q4220637
BLAST score
                  318
E value
                  1.0e-179
Match length
                  342
                  89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MIE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166715
Seq. ID
                  LIB3234-012-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  q4335711
BLAST score
                  339
E value
                  0.0e+00
                  347
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F9013 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166716
Seq. ID
                  LIB3234-012-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g4589421
BLAST score
                  99
E value
                  2.0e-48
Match length
                  140
% identity
                  92
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K5K13, complete sequence
Seq. No.
                  166717
                  LIB3234-012-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4325340
BLAST score
                  282
                  1.0e-157
E value
                  350
Match length
% identity
                  95
NCBI Description Arabidopsis thaliana BAC T1J1
Seq. No.
                  166718
Seq. ID
                  LIB3234-012-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2129759
BLAST score
                  179
```

```
Match length
                   42
% identity
                   86
NCBI Description
                  UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana
                  >gi 1143392 emb CAA90941 (Z54214) uridine diphosphate
                  glucose epimerase [Arabidopsis thaliana]
Seq. No.
                  166719
Seq. ID
                  LIB3234-012-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2961390
BLAST score
                  340
                  4.0e-32
E value
Match length
                  98
                  72
% identity
NCBI Description
                  (AL022141) beta-galactosidase like protein [Arabidopsis
                  thaliana]
                  166720
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  g343996
BLAST score
                  41
E value
                  5.0e-14
Match length
                  122
                  88
% identity
NCBI Description
                  Pea chloroplast psbM gene for photosystem II polypeptide M
                  166721
Seq. No.
`Seq. ID
                  LIB3234-012-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g21911
BLAST score
                  187
                  4.0e-14
E value
                  77
Match length
                  44
% identity
NCBI Description
                 (X62625) vicilin [Theobroma cacao]
Seq. No.
                  166722
Seq. ID
                  LIB3234-012-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g4159712
BLAST score
                  48
E value
                  6.0e-18
Match length
                  72
% identity
                  92
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
                  166723
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  g3449326
BLAST score
                  34
E value
                  1.0e-09
Match length
                  54
% identity
                  91
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
```

```
K19M22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166724
Seq. ID
                   LIB3234-012-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g2996096
                   598 -
BLAST score
E value
                   2.0e-62
                   113
Match length
% identity
                   100
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
                   166725
Seq. No.
Seq. ID
                   LIB3234-012-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   g511598
BLAST score
                   313
                   1.0e-176
E value
Match length
                   341
% identity
                   33
NCBI Description
                   Arabidopsis thaliana cell wall protein (APTR-1) gene,
                   complete cds
Seq. No.
                   166726
Seq. ID
                   LIB3234-012-P1-K1-D2
Method
                   BLASTN
NCBI GI
                   g3046853
BLAST score
                   59
                   1.0e-24
E value
Match length
                   136
% identity
                   85
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MRA19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166727
Seq. ID
                   LIB3234-012-P1-K1-D3
Method
                   BLASTN
NCBI GI
                   g3046853
BLAST score
                   40
E value
                   3.0e-13
Match length
                   127
                   90
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MRA19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166728
Seq. ID
                   LIB3234-012-P1-K1-D4
                   BLASTX
Method
NCBI GI
                   q4582436
BLAST score
                   66
E value
                   9.0e-50
Match length
                   112
% identity
                   92
NCBI Description
                  (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166729
```

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```
Seq. ID
                    LIB3234-012-P1-K1-D8
  Method
                    BLASTX
  NCBI GI
                    g4263791
  BLAST score
                    491
· E value
                    8.0e-50
  Match length
                    93
  % identity
                    99
  NCBI Description
                    (AC006068) putative receptor protein kinase [Arabidopsis
                    thaliana]
  Seq. No.
                    166730
  Seq. ID
                    LIB3234-012-P1-K1-E1
  Method
                    BLASTX
  NCBI GI
                    g541847
  BLAST score
                    608
                    2.0e-63
 E value
 Match length
                    114
  % identity
                    100
 NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
  Seq. No.
                    166731
  Seq. ID
                    LIB3234-012-P1-K1-E10
 Method
                    BLASTN
 NCBI GI
                    g4220628
 BLAST score
                    218
 E value
                    1.0e-119
 Match length
                    313
                    100
  % identity
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                    K24C1, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    166732
 Seq. ID
                    LIB3234-012-P1-K1-E2
 Method
                    BLASTN
 NCBI GI
                    q2244747
 BLAST score
                    338
 E value
                    0.0e + 00
 Match length
                    346
                    99
 % identity
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                    fragment No
 Seq. No.
                    166733
                    LIB3234-012-P1-K1-E4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q1351837
 BLAST score
                    522
 E value
                    2.0e-53
 Match length
                    110
 % identity
                    91
                   ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
 NCBI Description
                    BETA >gi_2144155_pir__S66564 acetyl CoA carboxylase type II
                   beta-carboxyltransferase chain - rape chloroplast
                    >gi_1069998_emb_CAA90747_ (Z50868) acetyl CoA carboxylase
                    carboxyltransferase (beta subunit) [Brassica napus]
                    >gi_1589046_prf__2210244G Ac-CoA carboxylase:SUBUNIT=beta
                    [Brassica napus]
```

```
Seq. No.
                  166734
Seq. ID
                  LIB3234-012-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2281085
BLAST score
                  375
E value
                  3.0e-36
                  113
Match length
                  59
% identity
NCBI Description
                  (AC002333) CTR1 protein kinase isolog (Arabidopsis
                  thaliana]
                  166735
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g4165132
BLAST score
                  549
E value
                  1.0e-56
Match length
                  115
% identity
                  84
NCBI Description
                  (AF098292) endo-beta-1,4-D-glucanase [Lycopersicon
                  esculentum]
Seq. No.
                  166736
Seq. ID
                  LIB3234-012-P1-K1-E7
Method
                  BLASTX
                  g1345944
NCBI GI
BLAST score
                  517
                  7.0e-53
E value
                  113
Match length
                  88
% identity
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III PRECURSOR
NCBI Description
                  (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) >gi_598075
                   (L31891) 3-ketoacyl-acyl carrier protein synthase III (KAS
                  III) [Arabidopsis thaliana]
                  166737
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g4582411
BLAST score
                  250
                  1.0e-138
E value
Match length
                  345
                  99
% identity
                  Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,
NCBI Description
                  complete sequence
                  166738
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                  239
E value
                  3.0e-20
                  115
Match length
                  39
% identity
NCBI Description vicilin gene B [Saguinus oedipus]
```

```
166739
Seq. No.
Seq. ID
                   LIB3234-012-P1-K1-F10
Method
                  BLASTN
NCBI GI
                   g1946354
BLAST score
                   342
E value
                   0.0e + 00
Match length
                   342
% identity
                   93
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T06B20 genomic
                   sequence, complete sequence
Seq. No.
                   166740
Seq. ID
                   LIB3234-012-P1-K1-F11
Method
                   BLASTN
NCBI GI
                   g3292807
BLAST score
                   174
                   4.0e-93
E value
Match length
                   334
                   100
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
NCBI Description
                   (ESSAII project)
                   166741
Seq. No.
Seq. ID
                   LIB3234-012-P1-K1-F12
Method
                   BLASTN
NCBI GI
                   q2618683
BLAST score
                   327
                   0.0e+00
E value
Match length
                   331
                   100
% identity
                   Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166742
Seq. ID
                   LIB3234-012-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q2315135
                   214
BLAST score
                   2.0e-17
E value
                   49
Match length
                   88
% identity
NCBI Description
                   (AB003522) beta subunit of coupling factor one [Arabidopsis
                   thaliana]
                   166743
Seq. No.
Seq. ID
                   LIB3234-012-P1-K1-F3
                   BLASTX
Method
NCBI GI
                   q1172704
BLAST score
                   562
E value
                   4.0e-58
Match length
                   105
% identity
                   100
NCBI Description
                  PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN)
                   >gi 633940 (L39082) transport protein [Arabidopsis
                   thaliana] >gi_4406786_gb_AAD20096_ (AC006532) histidine transport protein PTR2-B [Arabidopsis thaliana]
```

Method

BLASTX

```
Seq. No.
                   166744
Seq. ID
                  LIB3234-012-P1-K1-F4
Method
                   BLASTN
NCBI GI
                  q1707006
BLAST score
                   90
E value
                   1.0e-43
Match length
                   90
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T1B8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166745
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  g4589425
BLAST score
                  168
E value
                   1.0e-89
Match length
                   342
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBA10, complete sequence
                  166746
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-F8
Method
                  BLASTN
                  g4079614
NCBI GI
BLAST score
                  77
                  7.0e-36
E value
                  85
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166747
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3935151
BLAST score
                   615 -
                  2.0e-64
E value
Match length
                  113
% identity
                  100
NCBI Description
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
Seq. No.
                  166748
                  LIB3234-012-P1-K1-G1
Seq. ID
Method
                  BLASTN
                  q2570223
NCBI GI
                  78
BLAST score
                  7.0e-36
E value
Match length
                  258
                  84
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166749
Seq. ID
                  LIB3234-012-P1-K1-G2
```

E value

```
NCBI GI
                  q1079280
BLAST score
                   437
E value
                  2.0e-43
                  113
Match length
                  77
% identity
NCBI Description
                  chaperonin containing TCP-1 complex gamma chain - African
                  clawed frog >gi_793886_emb_CAA59350_ (X84990) Cctg [Xenopus
                  laevis]
                  166750
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-G3
                  BLASTX
Method
                  g2494125
NCBI GI
BLAST score
                  375
                  2.0e-36
E value
                  91
Match length
                  86
% identity
                   (AC002376) Strong similarity to Cucumis acetyl-CoA
NCBI Description
                  acyltransferase (gb_D70895). [Arabidopsis thaliana]
Seq. No.
                  166751
                  LIB3234-012-P1-K1-G4
Seq. ID
                  BLASTX
Method
                  g3107931
NCBI GI
                  536
BLAST score
E value
                   4.0e-55
                  115
Match length
                  91
% identity
                  (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
NCBI Description
Seq. No.
                  166752
                  LIB3234-012-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3107931
                  486
BLAST score
                  3.0e-49
E value
                  114
Match length
                  84
% identity
                  (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
NCBI Description
                  166753
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g4204298
                  483
BLAST score
E value
                  7.0e-49
                  111
Match length
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  166754
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g3641835
BLAST score
                  302
```

1.0e-169

```
Match length
                   339
% identity
                   97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
                   (ESSAII project)
                  166755
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-G9
Method
                  BLASTX
                  g3269286
NCBI GI
                   395
BLAST score
E value
                  1.0e-38
Match length
                  98
% identity
                  88
NCBI Description
                  (AL030978) putative protein [Arabidopsis thaliana]
                  166756
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-H1
                  BLASTX
Method
NCBI GI
                  g3688191
BLAST score
                  341
                  3.0e - 32
E value
                  94
Match length
                  71
% identity
                  (AJ010090) MAP3K alpha protein kinase [Arabidopsis
NCBI Description
                 #thaliana]
                  166757
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  g14352
BLAST score
                  215
E value
                  1.0e-117
                  343
Match length
                  91
% identity
NCBI Description
                  N.plumbaginifolia chloroplast 16SrDNA, trnV and trnI genes
                  for 16S ribosomal RNA, transfer RNA-Val and transfer
                  RNA-Ile (5'exon)
Seq. No.
                  166758
Seq. ID
                  LIB3234-012-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  q3869075
BLAST score
                  345
                  0.0e + 00
E value
                  345
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXK3, complete sequence [Arabidopsis thaliana]
                  166759
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  q3402695
BLAST score
                  210
E value
                  1.0e-114
Match length
                  309
% identity
                  94
```

```
NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  1667.60
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                  626
E value
                  1.0e-65
Match length
                  120
% identity
                  100
                  (AC003027) lcl prt_seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  166761
Seq. ID
                  LIB3234-012-P1-K1-H6
Method
                  BLASTX
                  g2894574
NCBI GI
                  524
BLAST score
E value
                  1.0e-53
Match length
                  99
                  100
% identity
                  (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
NCBI Description
                  >gi 2961341 emb CAA18099.1_ (AL022140) peroxidase prxr1
                  [Arabidopsis thaliana]
                  166762
Seq. No.
                  LIB3234-012-P1-K1-H8
Seq. ID
Method 5
                  BLASTN
                  g3108024
NCBI GI
BLAST score
                  325
E value
                  0.0e + 00
                  333
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome 1 BAC T1F15 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  166763
Seq. No.
Seq. ID
                  LIB3234-012-P1-K1-H9
                  BLASTN
Method
NCBI GI
                  g3108024
                  171
BLAST score
E value
                  2.0e-91
                  263
Match length
% identity
                  91
                  Arabidopsis thaliana chromosome 1 BAC T1F15 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  166764
Seq. No.
                  LIB3234-013-P1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204299
BLAST score
                  534
                  1.0e-54
E value
                  109
Match length
% identity
                  93
NCBI Description
                  (AC003027) lcl_prt_seq No definition line found
```

[Arabidopsis thaliana]

```
166765
Seq. No.
Seq. ID
                    LIB3234-013-P1-K1-A11
Method
                    BLASTN
NCBI GI
                    g2760167
BLAST score
                    159
E value
                    2.0e-84
Match length
                    167
% identity
                    34
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MCO15, complete sequence [Arabidopsis thaliana]
                    166766
Seq. No.
Seq. ID
                    LIB3234-013-P1-K1-A12
Method
                    BLASTX
                    g134025
NCBI GI
BLAST score
                    403
                    2.0e-39
E value
Match length
                    96
% identity
                    82
NCBI Description
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi 70913 pir R3NT8
                    ribosomal protein S8 - common tobacco chloroplast >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8 [Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal
                    protein S8 [Nicotiana tabacum]
Seq. No.
                    166767
Seq. ID
                    LIB3234-013-P1-K1-A2
Method
                    BLASTX
NCBI GI
                    q3661595
BLAST score
                    300
E value
                    2.0e-27
Match length
                    54
% identity
                    100
NCBI Description
                    (AF091844) aminoalcoholphosphotransferase [Arabidopsis
                    thaliana]
                    166768
Seq. No.
Seq. ID
                    LIB3234-013-P1-K1-A5
Method
                    BLASTN
NCBI GI
                    g4741797
                    148
BLAST score
                    1.0e-77
E value
Match length
                    302
                    97
% identity
                    Arabidopsis thaliana repeat region IID2-8 sequence
NCBI Description
Seq. No.
                    166769
Seq. ID
                    LIB3234-013-P1-K1-A6
                    BLASTX
Method
NCBI GI
                    g99697
BLAST score
                    667
                    2.0e-70
E value
Match length
                    122
                    98
% identity
                    glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone
NCBI Description
```

lambdaAtgsr2) - Arabidopsis thaliana

```
Seq. No.
                  166770
Seq. ID
                  LIB3234-013-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  q4204299
BLAST score
                  611
                  8.0e-64
E value
Match length
                  122
% identity
                  98
                  (AC003027) lcl prt seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  166771
Seq. ID
                  LIB3234-013-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2104949
BLAST score
                  388
E value
                  1.0e-37
                  95
Match length
% identity
                  80
                  (U96716) MAP kinase-like protein [Selaginella lepidophylla]
NCBI Description
Seq. No.
                  166772
Seq. ID
                  LIB3234-013-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g4678315
BLAST score
                  317
                  1.0e-178
E value
Match length
                  361
% identity
                  97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15
                  (ESSA project)
                  166773
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g4490330
BLAST score
                  328
E value
                  4.0e-31
Match length
                  67
% identity
                  (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  166774
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g132939
BLAST score
                  522
E value
                  2.0e-53
                  107
Match length
% identity
                  92
                  60S RIBOSOMAL PROTEIN L3 >gi 81657 pir JQ0771 ribosomal
NCBI Description
                  protein L3 (ARP1) - Arabidopsis thaliana >gi 166858
```

(M32654) ribosomal protein [Arabidopsis thaliana]

BLAST score

```
Seq. No.
                    166775
Seq. ID
                    LIB3234-013-P1-K1-B5
Method
                    BLASTX
NCBI GI
                    g2244750
BLAST score
                    514
E value
                    2.0e-52
Match length
                    114
                    88
% identity
NCBI Description
                    (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                    >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                    [Arabidopsis thaliana]
                    166776
Seq. No.
                    LIB3234-013-P1-K1-B6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g129871
BLAST score
                    179
E value
                    4.0e-13
Match length
                    36
% identity
                    100
                    CYTOCHROME B6-F COMPLEX SUBUNIT 5 >gi_65644_pir__WMRZ4
NCBI Description
                    cytochrome b6-f complex 4.2K protein - rice chloroplast
                    >gi_100947_pir A32159 plastoquinol--plastocyanin reductase
                    (EC 1.10.99.1) chain V - maize chloroplast
                    >gi_2147243_pir S68166 cytochrome b6-f complex chain 5 -
                    beet chloroplast >gi_12006_emb_CAA33967_ (X15901) cytochrome b /f complex subunit 5 [Oryza sativa] >gi_342588
                    (J04502) cytochrome b6-f complex subunit 5 (petE) [Zea
                    mays] >gi_533296_dbj_BAA07216_ (D38019) cytochrome b6/f
                    complex subunit 5 [Beta vulgaris] >gi_533302_dbj_BAA07222
                    (D38020) cytochrome b6/f complex subunit 5 [Beta trigyna]
                    >gi_533304_dbj_BAA07223_ (D38021) cytochrome b6/f complex
subunit 5 [Beta webbiana] >gi_860888_emb_CAA60964_ (X87636)
                    cytochrome b6-f complex subunit 5 [Beta vulgaris]
                    >gi_860894_emb_CAA60969_ (X87637) petG [Beta vulgaris]
>gi_902240_emb_CAA60304_ (X86563) cytochrome b /f complex
                    subunit 5 [Zea mays] >gi 2612818 emb CAA75627 (Y15429)
                    cytochrome b6/f-complex subunit V [Populus deltoides]
                    >gi_2924268_emb_CAA77420 (Z00044) cytochrome b/f complex
                    subunit V [Nicotiana tabacum] >gi 226628 prf 1603356BB
                    cytochrome b/f complex 5 [Oryza sativa]
Seq. No.
                    166777
Seq. ID
                   LIB3234-013-P1-K1-B7
Method
                    BLASTX
NCBI GI
                    q2076623
BLAST score
                    162
                    4.0e-11
E value
Match length
                    110
% identity
NCBI Description (Z95151) PtrB [Mycobacterium leprae]
Seq. No.
                   166778
Seq. ID
                   LIB3234-013-P1-K1-B8
Method
                   BLASTN
NCBI GI
                   g3193305
```

% identity

```
E value
                   0.0e + 00
Match length
                   361
                   100
% identity
NCBI Description Arabidopsis thaliana BAC F3D13
Seq. No.
                   166779
Seq. ID
                   LIB3234-013-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   g2264303
BLAST score
                   38
                   6.0e-12
E value
Match length
                   66
% identity
                   89
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBB18, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166780
Seq. ID
                   LIB3234-013-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   g4584841
BLAST score
                   157
E value
                   6.0e-83
Match length
                   372
% identity
                   47
                  Genomic sequence for Arabidopsis thaliana BAC T23E23,
NCBI Description
                   complete sequence
Seq. No.
                   166781
Seq. ID
                   LIB3234-013-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   g3241917
BLAST score
                   363
E value
                   0.0e+00
Match length
                   367
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19B1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166782
Seq. ID
                   LIB3234-013-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   g3241917
BLAST score
                  246
E value
                   1.0e-136
Match length
                   330
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19B1, complete sequence [Arabidopsis thaliana]
                  166783
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-C7
Method
                  BLASTX
                  g4679028
NCBI GI
BLAST score .
                  233
E value
                  2.0e-19
Match length
                  74
```

```
NCBI Description (AF077207) HSPC021 [Homo sapiens]
Seq. No.
                  166784
Seq. ID
                  LIB3234-013-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g3046851
BLAST score
                  319
E value
                  1.0e-179
Match length
                  368
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166785
Seq. ID
                  LIB3234-013-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2275202
BLAST score
                  309
                  2.0e-28
E value
                  59
Match length
% identity
                  100
                  (AC002337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                  thaliana]
                  166786
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2970654
BLAST score
                  437
                  2.0e-43
E value
Match length
                  120
% identity
                  71
NCBI Description
                  (AF052058) ferritin subunit cowpea2 precursor [Vigna
                  unguiculata]
                  166787
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2130051
BLAST score
                  348
E value
                  5.0e-33
                  96
Match length
                  68
% identity
                  xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                  >gi_1296807_emb_CAA64544 (X95256) xylose isomerase
                  [Hordeum vulgare] >gi_1588664_prf__2209268A xylose
                  isomerase [Hordeum vulgare]
                  166788
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g82051
BLAST score
                  294
E value
                  1.0e-26
Match length
                  111
% identity
                  55
NCBI Description lipid body-associated membrane protein - carrot
```

E value

```
protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                   180 aa] [Daucus carota]
Seq. No.
                  166789
Seq. ID
                  LIB3234-013-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g1170939
BLAST score
                  372
E value
                  8.0e-36
Match length
                  74
% identity
                   95
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
Seq. No.
                  166790
Seq. ID
                  LIB3234-013-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g4519184
BLAST score
                  207
E value
                  1.0e-113
Match length
                  252 ·
% identity
                  84
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K16F13, complete sequence
Seq. No.
                  166791
Seq. ID
                  LIB3234-013-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g3242700
BLAST score
                  39
E value
                  1.0e-12
Match length
                  107
% identity
                  84
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F26B6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166792
Seq. ID
                  LIB3234-013-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2244800
BLAST score
                  348
E value
                  5.0e-33
                  86
Match length
                  78
% identity
                  (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
NCBI Description
                  166793
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2244800
BLAST score
                  519
```

>gi 259453 bbs 117620 (S47635) lipid body membrane

5.0e-53

```
Match length
                  104
% identity
                  97
                  (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166794
Seq. ID
                  LIB3234-013-P1-K1-E1
                  BLASTX
Method
NCBI GI
                  g541847
BLAST score
                  262
E value
                  3.0e-23
                  54
Match length
                  93
% identity
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
Seq. No.
                  166795
Seq. ID
                  LIB3234-013-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  582
E value
                  2.0e-60
Match length
                  121
% identity
                  91
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  166796
Seq. ID
                  LIB3234-013-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g1402904
BLAST score
                  548
E value
                  2.0e-56
Match length
                  104
% identity
                  100
NCBI Description (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                  166797
Seq. ID
                  LIB3234-013-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q2459432
BLAST score
                  247
E value
                  3.0e-21
Match length
                  49
% identity
                  88
NCBI Description (AC002332) CONSTANS-like protein [Arabidopsis thaliana]
Seq. No.
                  166798
                  LIB3234-013-P1-K1-E5
Seq. ID
Method
                  BLASTN
                  g4757662
NCBI GI
BLAST score
                  145
                  8.0e-76
E value
Match length
                  370
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10B6 from
```

113

chromosome I, complete sequence

```
Seq. No.
                   166799
Seq. ID
                   LIB3234-013-P1-K1-E6
Method
                   BLASTN
NCBI GI
                  . g4220645
                   199
BLAST score
                   1.0e-108
E value
Match length
                   354
% identity
                   97
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MYA6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166800
Seq. ID
                   LIB3234-013-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g115778
BLAST score
                   141
                   5.0e-31
E value
                   90
Match length
% identity
                   78
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-1) (LHCP) >gi_282896_pir__S22511 chlorophyll a/b-binding protein (cab-1) - white mustard
                   >gi_21138_emb_CAA34459_ (X16436) chlorophyll a/b-binding
                   protein (AA 1-266) [Sinapis alba] >gi 21140 emb CAA33903
                   (X15894) chlorophyll a/b-binding polypeptide [Sinapis alba]
Seq. No.
                   166801
Seq. ID
                   LIB3234-013-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   g2618603
BLAST score
                   225
                   1.0e-123
E value
                   345
Match length
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSL3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166802
Seq. ID
                   LIB3234-013-P1-K1-E9
Method
                   BLASTN
NCBI GI
                   g3449334
BLAST score
                   333
E value
                   0.0e+00
Match length
                   358
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MYH9, complete sequence [Arabidopsis thaliana]
                   166803
Seq. No.
Seq. ID
                   LIB3234-013-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2252844
BLAST score
                   594
                   8.0e-62
E value
```

```
100
% identity
                  (AF013293) belongs to the cytochrome p450 family
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  166804
                  LIB3234-013-P1-K1-F10
Seq. ID
Method
                  BLASTN
                  g4199934
NCBI GI
BLAST score
                  277
                  1.0e-154
E value
Match length
                  349
% identity
                  92
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166805
Seq. ID
                  LIB3234-013-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g4262250
                  623
BLAST score
E value
                  3.0e-65
Match length
                  120
% identity
                  100
NCBI Description (AC006200)...putative aldolase [Arabidopsis thaliana]
                 <sup>5</sup> 166806
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  q4199934
BLAST score
                  277
E value
                  1.0e-154
Match length
                  347
                  92
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166807
                  LIB3234-013-P1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
                  399
BLAST score
                  6.0e-39
E value
                  81
Match length
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  166808
Seq. No.
                  LIB3234-013-P1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129659
                  309
BLAST score
                  2.0e-28
E value
                  95
Match length
                  64
% identity
NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
```

Seq. No.

166814

(L40954) oleosin (Arabidopsis thaliana)

```
Seq. No.
                  166809
Seq. ID
                  LIB3234-013-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q4165488
BLAST score
                 ₩583
E value
                  2.0e-60
Match length
                  107
% identity
                  100
NCBI Description
                  (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
                  166810
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  q1490552
BLAST score
                  87
E value
                  3.0e-41
Match length
                  218
% identity
                  Arabidopsis thaliana S-adenosylmethionine decarboxylase
NCBI Description
                  (SAMdc) mRNA, complete cds
Seq. No.
                  166811
Seq. ID
                  LIB3234-013-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  q4581161
BLAST score
                  50
E value
                  5.0e-19
Match length
                  134
                  87
% identity
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  166812
Seq. ID
                  LIB3234-013-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  q3869069
BLAST score
                  274
                  1.0e-153
E value
Match length
                  359
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166813
Seq. ID
                  LIB3234-013-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  q4587986
BLAST score
                  201
E value
                  1.0e-109
Match length
                  328
% identity
                  98
NCBI Description
                  Arabidopsis thaliana ABA-regulated gene cluster, complete
                  sequence
```

```
LIB3234-013-P1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1707657
                  218
BLAST score
                  1.0e-17
E value
                  88
Match length
                  57
% identity
NCBI Description (Z71640) DnaJ homologue [Pisum sativum]
                  166815
Seq. No.
                  LIB3234-013-P1-K1-G2
Seq. ID
                  BLASTN
Method
                  q2894591
NCBI GI
BLAST score
                  366
                  0.0e + 00
E value
                  366
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
NCBI Description
                  (ESSAII project)
Seq. No.
                  166816
                  LIB3234-013-P1-K1-G3
Seq. ID
                  BLASTX
Method
                  g1531762
NCBI GI
                9152
195
BLAST score
                  5.0e-15
E value
Match length
                  51
                  75
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166817
Seq. ID
                  LIB3234-013-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  g4580454
                  353
BLAST score
                  0.0e+00
E value
                  370
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T2G17 genomic
                  sequence, complete sequence
                  166818
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-G6
                  BLASTX
Method
                  g112682
NCBI GI
                  150
BLAST score
                  9.0e-10
E value
                  76
Match length
                  59
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  166819
Seq. No.
```

```
LIB3234-013-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g881615
BLAST score
                  558
                  1.0e-57
E value
Match length
                  118
% identity
                  92
NCBI Description
                   (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
                  >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase
                  1 [Arabidopsis thaliana]
                  166820
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-G9
                  BLASTN
Method
NCBI GI
                  g3789706
                  38
BLAST score
                  6.0e-12
E value
                  106
Match length
                  59
% identity
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166821
Seq. ID
                  LIB3234-013-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  q4406752
BLAST score
                  266
                  1.0e-148
E value
                  340
Match length
                  49
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F19B11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  166822
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  181
                  2.0e-13
E value
Match length
                  58
                  52
% identity
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                  [Nicotiana tabacum]
                  166823
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-H12
Method
                  BLASTN
NCBI GI:
                  q166913
BLAST score
                  192
                  1.0e-104
E value
                  221
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana alpha-2 tubulin (TUA2) gene, exon and
                  5' end
Seq. No.
                  166824
Seq. ID
                  LIB3234-013-P1-K1-H2
```

NCBI GI

```
Method
                  BLASTN
NCBI GI
                  q4455321
BLAST score
                  369
E value
                  0.0e + 00
Match length
                  369
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
NCBI Description
                  (ESSAII project)
                  166825
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-H4
                  BLASTN
Method
NCBI GI
                  q2760165
BLAST score
                  300
                  1.0e-168
E value
                  365
Match length
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC9, complete sequence [Arabidopsis thaliana]
                  166826
Seq. No.
Seq. ID
                  LIB3234-013-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g4432845 .
                  149
BLAST score
                  1.0e-09
E value
                  63
Match length
                  57
% identity
NCBI Description
                  (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166827
Seq. ID
                  LIB3234-015-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q131378
BLAST score
                  210
E value
                  9.0e-17
Match length
                  43
% identity
                  98
NCBI Description
                  PHOTOSYSTEM II REACTION CENTRE N PROTEIN
                  >gi 2924272 emb CAA77424 (Z00044) PSII N-protein
                  [Nicotiana tabacum]
Seq. No.
                  166828
                  LIB3234-015-P1-K1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2114077
BLAST score
                  114
                  2.0e-57
E value
Match length
                  238
% identity
                  89
NCBI Description
                  Arabidopsis thaliana DNA for larger subunit of Rubisco,
                  beta subunit of coupling factor one, partial cds
Seq. No.
                  166829
Seq. ID
                  LIB3234-015-P1-K1-A12
Method
                  BLASTX
```

q4582446

```
BLAST score
                  210
E value
                  8.0e-17
                  87
Match length
% identity
                  55
NCBI Description
                  (AC007071) putative RING finger protein [Arabidopsis
                  thaliana]
Seq. No.
                  166830
Seq. ID
                  LIB3234-015-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  g4558521
                  284
BLAST score
E value
                  1.0e-158
                  332
Match length
                  99
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T10024,
NCBI Description
                  complete sequence
Seq. No.
                  166831
                  LIB3234-015-P1-K1-A6
Seq. ID
Method
                  BLASTN
                  q2213606
NCBI GI
                  351
BLAST score
E value
                  0.0e + 00
                  367
Match length
                  99
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F21J9,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  166832
Seq. ID
                  LIB3234-015-P1-K1-A7
                  BLASTN
Method
NCBI GI
                  q1490552
BLAST score
                  266
E value
                  1.0e-148
Match length
                  296
                  98
% identity
NCBI Description Arabidopsis thaliana S-adenosylmethionine decarboxylase
                  (SAMdc) mRNA, complete cds
Seq. No.
                  166833
                  LIB3234-015-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1903034
BLAST score
                  250
E value
                  2.0e-21
Match length
                  106
% identity
                  46
                 (X94625) amp-binding protein [Brassica napus]
NCBI Description
Seq. No.
                  166834
                  LIB3234-015-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3482964
BLAST score
                  319
E value
                  1.0e-179
```

```
97
% identity
                  Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
NCBI Description
                  (ESSAII project)
Seq. No.
                  166835
Seq. ID
                  LIB3234-015-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  q3482964
BLAST score
                  193
E value
                  1.0e-104
Match length
                  310
                  92
% identity
                  Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
NCBI Description
                  (ESSAII project)
Seq. No.
                  166836
                  LIB3234-015-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  g2245070
NCBI GI
BLAST score
                  166
E value
                  1.0e-11
Match length
                  102
                  32
% identity
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  166837
Seq. No.
                  LIB3234-015-P1-K1-B6
Seq. ID
                  BLASTX
Method
                  g3377815
NCBI GI
                  562
BLAST score
E value
                  4.0e-58
Match length
                  123
                  91
% identity
                  (AF076275) similar to protein kinases (Pfam: pkinase.hmm,
NCBI Description
                  score: 255.71) [Arabidopsis thaliana]
                  166838
Seq. No.
Seq. ID
                  LIB3234-015-P1-K1-B7
                  BLASTN
Method
                  g395203
NCBI GI
BLAST score
                  52
                  7.0e-21
E value
Match length
                  68
                  69
% identity
NCBI Description A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's
                  166839
Seq. No.
Seq. ID
                  LIB3234-015-P1-K1-B8
                  BLASTX
Method
                  g225280
NCBI GI
BLAST score
                  357
E value
                  5.0e-34
Match length
                  71
                  97
% identity
NCBI Description rpoC-like ORF 548 [Nicotiana tabacum]
```

166840

Seq. No.

Method

BLASTN

```
Seq. ID
                   LIB3234-015-P1-K1-B9
 Method
                   BLASTN
 NCBI GI
                   q4220635
 BLAST score
                   161
 E value
                   2.0e-85
 Match length
                   327 .
                   97
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                   MDB19, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   166841
 Seq. ID
                   LIB3234-015-P1-K1-C1
 Method
                   BLASTX
 NCBI GI
                   q2879800
 BLAST score
                   259
 E value
                   2.0e-22
Match length
                   123
 % identity
                   41
                   (AL021813) phenylalanyl-trna synthetase alpha chain
 NCBI Description
                   [Schizosaccharomyces pombe]
 Seq. No.
                   166842
 Seq. ID
                   LIB3234-015-P1-K1-C10
 Method
                   BLASTX
 NCBI GI
                   q4586249
                   339
 BLAST score
                   7.0e-32
 E value
 Match length
                   102
 % identity
                   63
                   (AL049640) putative pollen surface protein-{Arabidopsis
 NCBI Description
                   thaliana]
 Seq. No.
                   166843
 Seq. ID
                   LIB3234-015-P1-K1-C4
 Method
                   BLASTN
 NCBI GI
                  g2342673
 BLAST score
                   359
 E value
                   0.0e + 00
Match length
                   .367
                   99
 % identity
 NCBI Description
                   Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   166844
 Seq. ID
                   LIB3234-015-P1-K1-C7
 Method
                   BLASTX
 NCBI GI
                   q4582468
 BLAST score
                   549
E value
                   2.0e-56
Match length
                   112
                   99
 % identity
                   (AC007071) putative 40S ribosomal protein; contains
 NCBI Description
                   C-terminal domain [Arabidopsis thaliana]
 Seq. No.
                   166845
 Seq. ID
                   LIB3234-015-P1-K1-C8
```

```
NCBI GI
                  q4140256
BLAST score
                  358
E value
                  0.0e + 00
Match length
                  374
% identity
                  79
NCBI Description Arabidopsis thaliana mRNA for LEA-like protein
Seq. No.
                  166846
Seq. ID
                  LIB3234-015-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3808062
BLAST score
                  159
E value
                  8.0e-11
Match length
                  66
% identity
                  4.5
NCBI Description (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  166847
Seq. ID
                  LIB3234-015-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                  656
E value
                  4.0e-69
Match length.
                  124
                  100
% identity
NCBI Description
                  (AC003027) lcl_prt_seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  166848
Seq. ID
                  LIB3234-015-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2982437
BLAST score
                  453
E value
                 .3.0e-45
                . : 123
Match length
                 ÷68
% identity
NCBI Description (AL022224) terpene cyclase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  166849
Seq. ID
                  LIB3234-015-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2982437
BLAST score
                  355
E value
                  8.0e-34
Match length
                  102
% identity
                  65
                  (AL022224) terpene cyclase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166850
Seq. ID
                  LIB3234-015-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  g4757414
BLAST score
                  356
E value
                  0.0e + 00
Match length
                  372
```

```
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
Seq. No.
                  166851
Seq. ID
                  LIB3234-015-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1708464
                  Ž25
BLAST score
E value
                  1.0e-18
Match length
                  62
% identity
                  66
NCBI Description
                  PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD)
                  (2,3-DIHYDROXY ACID HYDROLYASE) >gi 1213255 emb CAA93689
                  (Z69795) unknown [Schizosaccharomyces pombe]
Seq. No.
                  166852
Seq. ID
                  LIB3234-015-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  486
E value .
                  4.0e-49
Match length
                  112
% identity
                  85
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  166853
Seq. No.
Seq. ID
                  LIB3234-015-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g3980417
BLAST score
                  656
E value
                  4.0e-69
Match length
                  123
% identity - ....-.99
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.
                  166854
Seq. ID
                  LIB3234-015-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g2564049
BLAST score
                  63
E value
                  7.0e-27
Match length
                  131
% identity
                  87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166855
Seq. ID
                  LIB3234-015-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g3149952
BLAST score
                  259
```

2.0e-22

E value

Method

BLASTX

```
Match length
                    44
% identity
                    100
NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]
Seq. No.
                    166856
Seq. ID
                    LIB3234-015-P1-K1-D7
Method
                    BLASTN
NCBI GI
                    g2618604
BLAST score
                    264
E value
                    1.0e-147
Match length
                    362
% identity
                    99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MTG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                    166857
Seq. ID
                    LIB3234-015-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g2160137
BLAST score
                    211
E value
                    7.0e-17
Match length
                    93
% identity
                    56
NCBI Description (AC000375) Similar to Arabidopsis light repressible
                    receptor protein kinase (gb X97774). [Arabidopsis thaliana]
Seq. No.
                    166858
Seq. ID
                    LIB3234-015-P1-K1-E11
Method
                    BLASTX
NCBI GI
                    g2462931
BLAST score
                    634
E value
                    2.0e-66
Match length
                    122
% identity
                    97
                   (Z83833) UDP-glucose:sterol glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   166859
Seq. No.
Seq. ID
                    LIB3234-015-P1-K1-E12
Method
                    BLASTX
NCBI GI
                    g266839
BLAST score
                    271
                    6.0e-24
E value
                    57
Match length
% identity
                    98
                    PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                    COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi_478764_pir_529240 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha
                    chain - Arabidopsis thaliana >gi_16445_emb_CAA47298_
(X66825) proteosome alpha subunit [Arabidopsis thaliana]
                    >gi_3421080 (AF043522) 20S proteasome subunit PAD1
[Arabidopsis thaliana] >gi_742351_prf__2009376B
                    proteasome:SUBUNIT=alpha [Arabidopsis thaliana]
Seq. No.
                    166860
Seq. ID
                    LIB3234-015-P1-K1-E3
```

```
NCBI GI
                   q4204298
BLAST score
                   517
E value
                   9.0e-53
Match length
                   118
% identity
                   85
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   166861
Seq. ID
                   LIB3234-015-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g4261517
BLAST score
                   194
E value
                   6.0e-15
Match length
                   77
% identity
                   58
NCBI Description
                  (AF117334) cysteine proteinase inhibitor [Ipomoea batatas]
Seq. No.
                  166862
Seq. ID
                  LIB3234-015-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q3985934
                   329
BLAST score
E value
                  0.0e + 00
Match length
                  367
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166863
Seq. ID
                  LIB3234-015-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g585744
BLAST score 🕜
                  138
                  7.0e-09
E value
Match length
                  29
                  97
% identity
NCBI Description PHOTOSYSTEM II REACTION CENTRE T PROTEIN
Seq. No.
                  166864
Seq. ID
                  LIB3234-015-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g2275194
BLAST score
                  47
E value
                  2.0e-17
Match length
                  103
% identity
                  86
                  Arabidopsis thaliana chromosome II BAC T08I13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166865
Seq. ID
                  LIB3234-015-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3451071
BLAST score
                  488
E value
                  2.0e-49
Match length
                  104
```

```
% identity
                   95
NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  166866
Seq. ID
                  LIB3234-015-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3763925
BLAST score
                  231
E value
                  3.0e-19
Match length
                  44
% identity
                  100
NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]
                  166867
Seq. No.
Seq. ID
                  LIB3234-015-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  q4468801
BLAST score
                  293
E value
                  1.0e-164
Match length
                  367
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
                  (ESSA project)
Seq. No.
                  166868
Seq. ID
                  LIB3234-015-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q1864017
BLAST score
                  548
E value
                  2.0e-56
Match length
                  104
% identity
                  100
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  166869
Seq. ID
                  LIB3234-015-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  q2264321
BLAST score
                  223
E value
                  1.0e-122
Match length
                  372
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166870
Seq. ID
                  LIB3234-015-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q1107501
BLAST score
                  462
E value
                  2.0e-46
Match length
                  112
% identity
                  84
NCBI Description
                  (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
                  Match to gb_X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
```

% identity

45

```
this gene. [Arabidopsis thaliana]
Seq. No.
                   166871
Seq. ID
                   LIB3234-015-P1-K1-G1
Method
                   BLASTN
NCBI GI
                   g2760165
BLAST score
                   82
E value
                   3.0e-38
Match length
                   360
% identity
                   84
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166872
Seq. ID
                   LIB3234-015-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   g3873174
BLAST score
                   317
                   1.0e-178
E value
Match length
                   353
% identity
                   97
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F14N23,
                   complete sequence [Arabidopsis thaliana]
                   166873
Seq. No.
Seq. ID
                   LIB3234-015-P1-K1-G2
Method
                BLASTX
NCBI GI
                   g131336
BLAST score
                   339
                   6.0e-32
E value
Match length
                   73
% identity
                   93
                  PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi 72715 pir F2NT0P
NCBI Description
                  photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD
                   phosphoprotein [Nicotiana tabacum]
                   >gi_225225 prf 1211235BG photosystem II 10kD
                   phosphoprotein [Nicotiana tabacum]
Seq. No.
                   166874
Seq. ID
                   LIB3234-015-P1-K1-G4
                   BLASTX
Method
                   g3702331
NCBI GI
BLAST score
                   390
E value
                   6.0e-38
                   118
Match length
% identity
                   69
NCBI Description
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  166875
Seq. ID
                  LIB3234-015-P1-K1-G6
Method
                  BLASTX
                  g1669668
NCBI GI
BLAST score
                  215
E value
                  1.0e-17
```

```
NCBI Description (X97131) EF1-alpha [Forsythia x intermedia]
 Seq. No.
                   166876
 Seq. ID
                   LIB3234-015-P1-K1-G7
 Method
                   BLASTN
 NCBI GI
                   g4531433
 BLAST score
                    332
 E value
                   0.0e+00
 Match length
                   364
 % identity
 NCBI Description
                   Arabidopsis thaliana chromosome II P1 MFL8 genomic
                   sequence, complete sequence
 Seq. No.
                   166877
 Seq. ID
                   LIB3234-015-P1-K1-G8
Method
                   BLASTN
NCBI GI
                   g2262155
BLAST score
                   366
E value
                   0.0e + 00
Match length
                   370
% identity
                   100
NCBI Description DNA sequence of Arabidopsis thaliana BAC F5J6 from
                   chromosome IV, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166878
Seq. ID
                   LIB3234-015-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g125576
BLAST score
                   401
E value
                   3.0e-39
Match length
                   96
% identity
                   84
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana
                   >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate
                   kinase [Arabidopsis thaliana]
Seq. No.
                   166879
Seq. ID
                   LIB3234-015-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g3395432
BLAST score
                   513
E value
                   3.0e-52
Match length
                   100
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   166880
Seq. ID
                  LIB3234-015-P1-K1-H11
Method
                   BLASTN
NCBI GI
                  g3334860
BLAST score
                   66
E value
                  1.0e-28
Match length
                  220
% identity
NCBI Description Solanum tuberosum chloroplast tRNA-Asn, tRNA-Arg genes
```

Seq. No.

```
Seq. No.
                    166881
 Seq. ID
                    LIB3234-015-P1-K1-H12
 Method
                    BLASTX
 NCBI GI
                    g3033386
 BLAST score
                    242
                                         \mathcal{F}^{-1}
 E value
                    1.0e-20
Match length
                    82
 % identity
                    66
NCBI Description (AC004238) RING3-like protein [Arabidopsis thaliana]
Seq. No.
                    166882
Seq. ID
                    LIB3234-015-P1-K1-H3
Method
                    BLASTX
NCBI GI
                    g2827699
BLAST score
                    409
E value
                    4.0e-40
Match length
                    96
% identity
                    83
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                    166883
Seq. ID
                    LIB3234-015-P1-K1-H4
Method
                    BLASTX
NCBI GI
                    g4335749
BLAST score
                    533
                    1.0e-54
E value
Match length
                   103
% identity
                    99
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.
                   166884
Seq. ID
                   LIB3234-015-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q1350783
BLAST score
                    324
E value
                    2.0e-30
Match length
                   76
% identity
                   86
NCBI Description
                   RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
                   >gi_282883_pir__S27756 receptor-like protein kinase
precursor - Arabidopsis thaliana >gi_166850 (M84660)
                   receptor-like protein kinase [Arabidopsis thaliana]
                   >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein
                   kinase 5 precursor (RLK5) [Arabidopsis thaliana]
Seq. No.
                   166885
Seq. ID
                   LIB3234-015-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g3033386
BLAST score
                   391
E value
                   5.0e-38
Match length
                   124
% identity
                   (AC004238) RING3-like protein [Arabidopsis thaliana]
NCBI Description
```

```
Seq. ID
                   LIB3234-015-P1-K1-H7
Method
                   BLASTN
NCBI GI
                   g12279
BLAST score
                   89
E value
                   2.0e-42
Match length
                   165
% identity
                   94
                   Spinach chloroplast genes for the D2 and 44 kd reaction
NCBI Description
                   centre, chlorophyll a-binding protein and for tRNA-Ser
                   (UGA)
Seq. No.
                   166887
Seq. ID
                  LIB3234-015-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q1345973
BLAST score
                   421
                   2.0e-41
E value
Match length
                   95
% identity
                  81
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsi\bar{s} thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  166888
Seq. ID
                  LIB3234-015-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q2781354
BLAST score
                  254
E value
                  5.0e-22
Match length
                  49
                  100
% identity
NCBI Description
                 (AC003113) F2401.10 [Arabidopsis thaliana]
Seq. No.
                  166889
Seq. ID
                  LIB3234-016-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3096910
                  535
BLAST score
E value
                  6.0e-55
Match length
                  114
                  88
% identity
                  (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  166890
Seq. ID
                  LIB3234-016-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g4510338
BLAST score
                  339
E value
                  0.0e+00
```

```
% identity
                   100
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F2H17 genomic
                   sequence, complete sequence
 Seq. No.
                   166891
 Seq. ID
                   LIB3234-016-P1-K1-A12
 Method
                   BLASTN
 NCBI GI
                   g3046852
 BLAST score
                   196
 E value
                   1.0e-106
 Match length
                   336
 % identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MQJ16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166892
Seq. ID
                   LIB3234-016-P1-K1-A2
Method
                   BLASTN
NCBI GI
                   g2864607
BLAST score
                   350
E value
                   0.0e+00
Match length
                   357
% identity
                   99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                   (ESSAII project)
Seq. No.
                   166893
Seq. ID
                   LIB3234-016-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   502
E value
                   5.0e-51
Match length
                   95
% identity
                  100
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  166894
Seq. ID
                  LIB3234-016-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g1669668
BLAST score
                  370
E value
                  1.0e-35
Match length
                  80
% identity
                  91
NCBI Description (X97131) EF1-alpha [Forsythia x intermedia]
Seq. No.
                  166895
Seq. ID
                  LIB3234-016-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g4455342
BLAST score
                  143
E value
                  6.0e-09
Match length
                  29
% identity
                  100
                  (AL035522) O-methyltransferase-like protein [Arabidopsis
NCBI Description
                  thaliana]
```

Method

BLASTX

```
Seq. No.
                   166896
 Seq. ID
                   LIB3234-016-P1-K1-A6
 Method
                   BLASTN
 NCBI GI
                   q4455339
 BLAST score
                   242
 E value
                   1.0e-134
 Match length
                   331
 % identity
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
                   (ESSAII project)
 Seq. No.
                   166897
 Seq. ID
                   LIB3234-016-P1-K1-A7
 Method
                   BLASTX
 NCBI GI
                   q3249107
BLAST score
                   434
E value
                   4.0e-43
Match length
                   90
% identity
                   91
NCBI Description
                   (AC003114) Contains similarity to phloem-specific lectin
                   PP2 gb_Z17331 from Cucubita maxima. [Arabidopsis thaliana]
Seq. No.
                   166898
Seq. ID
                   LIB3234-016-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q2662343
BLAST score
                   247
E value
                   4.0e-21
Match length
                   85
% identity
                   58
NCBI Description
                 (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   166899
Seq. ID
                  LIB3234-016-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g99688
BLAST score
                   603
E value
                   6.0e-63
Match length
                  116
% identity
                  99
NCBI Description
                  translation elongation factor eEF-1 alpha chain (gene A4) -
                  Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
Seq. No.
                  166900
Seq. ID
                  LIB3234-016-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  166
E value
                  2.0e-88
Match length
                  355
% identity
                  94
NCBI Description
                  Arabidopsis thaliana BAC IG002N01
Seq. No.
                  166901
Seq. ID
                  LIB3234-016-P1-K1-B10
```

```
NCBI GI
                   q4056485
 BLAST score
                   133
 E value
                   8.0e-08
 Match length
                   89
 % identity
                   10
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   166902
Seq. ID
                   LIB3234-016-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2894574
BLAST score
                   513
E value
                   2.0e-52
                   97
Match length
% identity
                   100
NCBI Description
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
                   >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
Seq. No.
                   166903
Seq. ID
                   LIB3234-016-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q4585966
BLAST score,
                   553
E value
                   5.0e-57
Match length
                   114
% identity
                   94
NCBI Description
                   (AC005287) Putative dihyrdolipoamide acetyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                   166904
Seq. ID
                  LIB3234-016-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                   668
E value
                  2.0e-70
Match length
                  117
% identity
NCBI Description
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  166905
                  LIB3234-016-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935151
BLAST score
                  547
E value
                  2.0e-56
Match length
                  103
% identity
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  166906
Seq. ID
                  LIB3234-016-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  q4006815
BLAST score
                  262
E value
                  1.0e-145
```

```
% identity
 NCBI Description Arabidopsis thaliana chromosome II BAC T6P5 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   166907
 Seq. ID
                   LIB3234-016-P1-K1-B8
 Method
                   BLASTX
 NCBI GI
                   g1619602
 BLAST score
                   388
 E value
                   1.0e-37
 Match length
                   112
 % identity
                   39
 NCBI Description (Y08726) MtN3 [Medicago truncatula]
 Seq. No.
                   166908
 Seq. ID
                   LIB3234-016-P1-K1-B9
 Method
                   BLASTX
 NCBI GI
                   g3582328
 BLAST score
                   256
 E value
                   3.0e-22
 Match length
                   111.
 % identity
                   12
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   166909
Seq. ID
                   LIB3234-016-P1-K1-C1
Method
                   BLASTX
NCBI GI
                  q1711513
BLAST score
                   408
E value
                   5.0e-40
Match length
                   85
% identity
                   99
NCBI Description
                  SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 3 (SRP54)
                  >gi_515681 (U12127) signal recognition particle 54 kDa
                  subunit [Arabidopsis thaliana]
Seq. No.
                  166910
Seq. ID
                  LIB3234-016-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g11837
BLAST score
                  223
E value
                  2.0e-18
Match length
                  70
% identity
                  61
NCBI Description
                  (Z00044) NADH dehydrogenase 27kD subunit [Nicotiana
                  tabacum] >gi_225205_prf__1211235AK bhpB gene [Nicotiana
                  tabacum]
Seq. No.
                  166911
                  LIB3234-016-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2583125
BLAST score
                  524
E value
                  1.0e-53
Match length
                  118
% identity
                  85
NCBI Description (AC002387) putative transketolase precursor [Arabidopsis
```

thaliana] Seq. No. 166912 Seq. ID LIB3234-016-P1-K1-C4 Method BLASTX NCBI GI g2583125 BLAST score 425 E value 5.0e-42 Match length 114 % identity 75 NCBI Description (AC002387) putative transketolase precursor [Arabidopsis thaliana] Seq. No. 166913 Seq. ID LIB3234-016-P1-K1-C5 Method BLASTX NCBI GI g4773885 BLAST score 523 E value 2.0e-53 Match length 99 % identity 98 (AF076243) putative aspartic protease [Arabidopsis NCBI Description thaliana] Seq. No. 166914 Seq. ID LIB3234-016-P1-K1-C7 Method BLASTX NCBI GI g1170503 BLAST score 561 E value 5.0e-58 Match length 113 % identity 98 NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi 322503 pir JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188 (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana] Seq. No. 166915 Seq. ID LIB3234-016-P1-K1-C8 Method BLASTN NCBI GI g4567300

NCBI GI g4567300
BLAST score 219
E value 1.0e-120
Match length 352
% identity 100
NCBI Description Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No. 166916 Seq. ID LIB3234-016-P1-K1-D1 Method BLASTX NCBI GI g119143 BLAST score 470 E value 3.0e-47 Match length 92 % identity 98



```
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                    >gi_81606_pir__S06724 translation elongation factor eEF-1
                   alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453
                    (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1369927_emb_CAA34454_ (X16431) elongation factor
                   1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                    (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                   >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                   >gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
 Seq. No.
                   166917
 Seq. ID
                   LIB3234-016-P1-K1-D7
 Method
                   BLASTX
 NCBI GI
                   g1864017
 BLAST score
                   549
 E value
                   1.0e-56
 Match length
                   105
 % identity
                   99
 NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
 Seq. No.
                   166918
 Seq. ID
                   LIB3234-016-P1-K1-D8
 Method
                   BLASTX
 NCBI GI
                   g4263704
 BLAST score
                   .221
 E value
                   4.0e-18
Match length
                   76
 % identity
                   54
NCBI Description (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
Seq. No.
                   166919
Seq. ID
                  LIB3234-016-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g3402671
BLAST score
                  34.1
E value
                  0.0e+00
Match length
                  345
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T16B24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166920
Seq. ID
                  LIB3234-016-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4581146
BLAST score
                  441
E value
                  6.0e-44
Match length
                  98
% identity
                  91
NCBI Description
                 (AC006919) putative fructose-bisphosphate aldolase,
                  cytoplasmic [Arabidopsis thaliana]
Seq. No.
                  166921
Seq. ID
                  LIB3234-016-P1-K1-E11
Method
                  BLASTN
```

```
NCBI GI
                    q4220643
 BLAST score
                    310
 E value
                    1.0e-174
 Match length
                    342
 % identity
                    98
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                    MWD22, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    166922
 Seq. ID
                    LIB3234-016-P1-K1-E12
 Method
                    BLASTN
 NCBI GI
                    q4159712
 BLAST score
                    334
 E value
                    0.0e + 00
 Match length
                    338
 % identity
                    100
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                   MWI23, complete sequence
 Seq. No.
                   166923
 Seq. ID
                   LIB3234-016-P1-K1-E5
 Method
                   BLASTX
 NCBI GI
                   g3395435
BLAST score
                   407
E value
                   6.0e-40
Match length
                   98
 % identity
                   89
NCBI Description
                   (AC004683) myosin heavy chain-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   166924
                   LIB3234-016-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q166570
BLAST score
                   174
E value
                   1.0e-12
Match length
                   31
% identity
                   100
NCBI Description
                   (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                   166925
Seq. ID
                   LIB3234-016-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g2738248
BLAST score
                   514
E value
                   2.0e-52
Match length
                   98
% identity
                   100
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                  166926
Seq. ID
                  LIB3234-016-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q2880051
BLAST score
                  233
E value
```

2.0e-19

```
Match length
                    56
 % identity
 NCBI Description
                    (AC002340) putative protein kinase [Arabidopsis thaliana]
 Seq. No.
                    166927
 Seq. ID
                    LIB3234-016-P1-K1-F1
 Method
                   BLASTN
 NCBI GI
                    g4589435
 BLAST score
                    316
 E value
                    1.0e-178
 Match length
                    348
 % identity
                    98
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MOE17, complete sequence
 Seq. No.
                   166928
 Seq. ID
                   LIB3234-016-P1-K1-F10
Method
                   BLASTX
 NCBI GI
                   g2244749
 BLAST score
                   609
E value
                   1.0e-63
Match length
                   115
 % identity
                   100
NCBI Description
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                   166929
Seq. ID
                   LIB3234-016-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g633890
BLAST score
                   370
                   1.0e-35
E value
Match length
                   115
% identity
                   66
NCBI Description
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                   vulgare]
Seq. No.
                   166930
Seq. ID
                   LIB3234-016-P1-K1-F5
Method
                   BLASTN
NCBI GI
                   g2618601
BLAST score
                   164
E value
                   3.0e-87
Match length
                   343
% identity
                   97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166931
Seq. ID
                  LIB3234-016-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1929056
BLAST score
                  417
E value
                  4.0e-41
Match length
                  116
% identity
                  73
NCBI Description
                  (Y12090) putative 3,4-dihydroxy-2-butanone kinase
                  [Lycopersicon esculentum]
```

```
Seq. No.
                    166932
Seq. ID
                    LIB3234-016-P1-K1-F7
Method
                    BLASTN
NCBI GI
                    g2642152
BLAST score
                    264
E value
                    1.0e-147
Match length
                    349
% identity
                    100
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T517 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    166933
Seq. ID
                    LIB3234-016-P1-K1-F8
Method
                    BLASTX
NCBI GI
                    g135858
BLAST score
                    204
E value
                    4.0e-16
Match length
                    41
% identity
                    TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                    >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
                    thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                    [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast
                    intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.
                    166934
Seq. ID
                   LIB3234-016-P1-K1-F9
Method
                   BLASTN
NCBI GI
                   g4589410
BLAST score
                   340
E value
                   0.0e + 00
Match length
                   344
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   F2015, complete sequence
Seq. No.
                   166935
Seq. ID
                   LIB3234-016-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   g2351069
BLAST score
                   235
E value
                   1.0e-129
Match length
                   349
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166936
Seq. ID
                   LIB3234-016-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g4454032
BLAST score
                   592
E value
                   1.0e-61
```

Method

BLASTX

```
% identity
                    100
 NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
 Seq. No.
                   166937
 Seq. ID
                   LIB3234-016-P1-K1-G3
 Method
                   BLASTX
 NCBI GI
                   g3334123
 BLAST score
                   377
 E value
                   2.0e-36
 Match length
                   97
 % identity
                   82
 NCBI Description
                   ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of
                   mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787
                   (AC002334) mitochondrial F1-ATPase, gamma subunit
                   [Arabidopsis thaliana]
 Seq. No.
                   166938
 Seq. ID
                   LIB3234-016-P1-K1-G5
 Method
                   BLASTX
 NCBI GI
                   q3157930
 BLAST score
                   548
 E value
                   2.0e-56
 Match length
                   103·
 % identity
                   99
NCBI Description (AC002131) Strong similarity to
                   amino-cyclopropane-carboxylic acid oxidase gb_L27664 from
                   Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                  166939
Seq. ID
                  LIB3234-016-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1363488
BLAST score
                  524
E value
                  1.0e-53
Match length
                  103
% identity
                  99
NCBI Description IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410)
                  IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_
                  (AC006340) auxin-induced IAA8 protein [Arabidopsis
                  thaliana]
Seq. No.
                  166940
Seq. ID
                  LIB3234-016-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g4589969
BLAST score
                  325
E value
                  0.0e+00
Match length
                  346
% identity
                  98
NCBI Description
                 Arabidopsis thaliana chromosome II BAC F1P15 genomic
                  sequence, complete sequence
Seq. No.
                  166941
Seq. ID
                  LIB3234-016-P1-K1-G8
```

```
NCBI GI
                    q3915847
 BLAST score
                    314
 E value
                    5.0e-29
 Match length
                    71
% identity
                    87
NCBI Description
                   40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
                    40S ribosomal protein S2 [Arabidopsis thaliana]
 Seq. No.
                    166942
 Seq. ID
                   LIB3234-016-P1-K1-G9
 Method
                   BLASTX
 NCBI GI
                   g1550740
 BLAST score
                   461
 E value
                   3.0e-46
 Match length
                   88
 % identity
                   100
 NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
 Seq. No.
                   166943
 Seq. ID
                   LIB3234-016-P1-K1-H10
 Method
                   BLASTN
 NCBI GI
                   g4006885
 BLAST score
                   232
 E value
                   1.0e-128
 Match length
                   346
 % identity
 NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                   fragment No
 Seq. No.
                   166944
 Seq. ID
                   LIB3234-016-P1-K1-H2
 Method
                   BLASTX
 NCBI GI
                   q2944446
 BLAST score
                   336
E value
                   1.0e-31
Match length
                   105
 % identity
                   57
NCBI Description (AF050756) cysteine endopeptidase precursor [Ricinus
                   communis]
Seq. No.
                   166945
Seq. ID
                   LIB3234-016-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g2944446
BLAST score
                  272
E value
                   4.0e-24
Match length
                  92
% identity
                  52
                  (AF050756) cysteine endopeptidase precursor [Ricinus
NCBI Description
                  communis]
Seq. No.
                  166946
Seq. ID
                  LIB3234-016-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1531762
BLAST score
                  155
E value
                  2.0e-10
```

```
Match length
                    44
 % identity
                    70
                    (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    166947
 Seq. ID
                   LIB3234-016-P1-K1-H6
 Method
                   BLASTX
 NCBI GI
                   g881615
 BLAST score
                   513
 E value
                   2.0e-52
 Match length
                   108
 % identity
                   93
 NCBI Description
                   (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
                   >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase
                   1 [Arabidopsis thaliana]
 Seq. No.
                   166948
 Seq. ID
                   LIB3234-016-P1-K1-H7
 Method
                   BLASTX
 NCBI GI
                   g3122724
 BLAST score
                   351
 E value
                   2.0e-33
Match length
                   69
 % identity
                   100
NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal
                   protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                   166949
Seq. ID
                   LIB3234-016-P1-K1-H8
Method
                   BLASTN
NCBI GI
                   g3449331
BLAST score
                   346
E value
                   0.0e + 00
Match length
                   346
% identity
                   29
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MNC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166950
Seq. ID
                   LIB3234-016-P1-K1-H9
Method
                   BLASTN
NCBI GI
                  q4733952
BLAST score
                   176
E value
                  2.0e-94
Match length
                  349
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F23H11 genomic
                  sequence, complete sequence
Seq. No.
                  166951
Seq. ID
                  LIB3234-017-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g3935151
BLAST score
                  505
E value
                  2.0e-51
Match length
                  101
```

```
% identity
                    92
 NCBI Description (AC005106) T25N20.15 [Arabidopsis thaliana]
 Seq. No.
                    166952
 Seq. ID
                    LIB3234-017-P1-K1-A10
 Method
                    BLASTX
 NCBI GI
                    g1531758
 BLAST score
                    275
 E value
                    2.0e-24
 Match length
                    67
 % identity
                    79
 NCBI Description
                    (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
                    unknown protein [Arabidopsis thaliana]
 Seq. No.
                    166953
 Seq. ID
                   LIB3234-017-P1-K1-A2
 Method
                   BLASTN
 NCBI GI
                   g4519193
 BLAST score
                   162
 E value
                   6.0e-86
 Match length
                   366
 % identity
                   96
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                   MDC11, complete sequence
 Seq. No.
                   166954
 Seq. ID
                   LIB3234-017-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   g4519193
BLAST score
                   127
E value
                   5.0e~65
Match length
                   353
 % identity
                   92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MDC11, complete sequence
Seq. No.
                   166955
Seq. ID
                   LIB3234-017-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   q602076
BLAST score
                   493
E value
                   5.0e-50
Match length
                   102
% identity
                   22
                  (X77456) pentameric polyubiquitin [Nicotiana tabacum]
NCBI Description
Seq. No.
                  166956
Seq. ID
                  LIB3234-017-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g3449331
BLAST score
                  109
E value
                  2.0e-54
Match length
                  263
% identity
                  49
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MNC17, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                    166957
 Seq. ID
                    LIB3234-017-P1-K1-A8
 Method
                    BLASTX
 NCBI GI
                    q4056502
 BLAST score
                    552
 E value
                    6.0e-57
 Match length
                    117
 % identity
 NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
 Seq. No.
                    166958
 Seq. ID
                    LIB3234-017-P1-K1-A9
 Method
                    BLASTX
 NCBI GI
                    g113595
 BLAST score
                    416
 E value
                    6.0e-41
 Match length
                    118
 % identity
                    65
 NCBI Description ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE)
                    >gi_100562_pir__S15024 aldose reductase-related protein -
barley >gi_18891_emb_CAA40747_ (X57526) aldose
                    reductase-related protein [Hordeum vulgare]
 Seq. No.
                    166959
 Seq. ID
                    LIB3234-017-P1-K1-B1
Method
                    BLASTX
NCBI GI
                    g2801442
 BLAST score
                    561
E value
                    6.0e-58
Match length
                    111
% identity
                    89
NCBI Description
                   (AF028338) ubiquitin-conjugating enzyme 15 [Arabidopsis
                    thalianal
Seq. No.
                   166960
Seq. ID
                   LIB3234-017-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g4503755
BLAST score
                   163
E value
                   3.0e-11
Match length
                   97
% identity
                   45
NCBI Description
                   flavin containing monooxygenase 1
                   >gi_399505_sp_Q01740_fMO1 HUMAN DIMETHYLANILINE
                   MONOOXYGENASE (N-OXIDE FORMING) 1 (FETAL HEPATIC
                   FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE
                   OXIDASE 1) >gi_105847_pir__A40876 dimethylaniline
                   monooxygenase (N-oxide-forming) (EC 1.14.13.8), hepatic 1 -
                   human >gi_182671 (M64082) flavin-containing monooxygenase
                   [Homo sapiens]
Seq. No.
                   166961
Seq. ID
                   LIB3234-017-P1-K1-B11
Method
                   BLASTN
NCBI GI
                   g4757414
BLAST score
                  343
E value
                   0.0e+00
```

```
Match length
                      351
 % identity
                     Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                     MYF24, complete sequence
 Seq. No.
                     166962
 Seq. ID
                     LIB3234-017-P1-K1-B12
 Method
                     BLASTX
 NCBI GI
                     q3169287
 BLAST score
                     596
 E value
                     4.0e-62
 Match length
                     117
 % identity
                     100
                     (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium
 NCBI Description
                     hirsutum)
 Seq. No.
                     166963
 Seq. ID
                     LIB3234-017-P1-K1-B2
 Method
                     BLASTX
 NCBI GI
                     g1345973
 BLAST score
                     400
 E value
                     4.0e-39
 Match length
                     92
 % identity
                     80
                    OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
 NCBI Description
                    >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                    omega-3 fatty acid desaturase [Arabidopsis thaliana]
                    >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                    [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis
                    thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                    desaturase [Arabidopsis thaliana]
Seq. No.
                    166964
Seq. ID
                    LIB3234-017-P1-K1-B3
Method
                    BLASTN
NCBI GI
                    g4531433
BLAST score
                    359
E value
                    0.0e+00
Match length
                    367
% identity
                    99
NCBI Description Arabidopsis thaliana chromosome II P1 MFL8 genomic
                    sequence, complete sequence
Seq. No.
                    166965
Seq. ID
                    LIB3234-017-P1-K1-B4
Method
                    BLASTX
NCBI GI
                    g3075399
BLAST score
                    207
E value
                    2.0e-16
Match length
                    83
% identity
                    49
NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]
Seq. No.
                    166966
Seq. ID
```

LIB3234-017-P1-K1-B5

Method

BLASTX

```
Method
                     BLASTX
 NCBI GI
                     q2809246
 BLAST score
                     200
 E value
                     1.0e-15
 Match length
                     120
 % identity
 NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]
 Seq. No.
                    166967
 Seq. ID
                    LIB3234-017-P1-K1-B6
 Method
                    BLASTX
 NCBI GI
                    g1931655
 BLAST score
                    351
 E value
                    2.0e-33
 Match length
                    70
 % identity
                    100
 NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana]
 Seq. No.
                    166968
 Seq. ID
                    LIB3234-017-P1-K1-C12
 Method
                    BLASTX
 NCBI GI
                    g115767
 BLAST score
                    614
 E value
                    3.0e-64
 Match length
                    118
 % identity
 NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana
                    >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                    protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   166969
                                                                            ٠.
Seq. ID
                   LIB3234-017-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3924597
BLAST score
                   335
E value
                   2.0e-31
Match length
                   122
% identity
                  (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   166970
Seq. ID
                   LIB3234-017-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   g4325340
BLAST score
                   339
E value
                   0.0e+00
Match length
                   363
% identity
                   98
NCBI Description Arabidopsis thaliana BAC T1J1
Seq. No.
                   166971
Seq. ID
                   LIB3234-017-P1-K1-C9
```

Seq. No.

```
NCBF GI
                   g1616787
 BLAST score
                   503
 E value
                   4.0e-51
 Match length
                   94
 % identity
                   100
 NCBI Description (U71122) pyruvate decarboxylase [Arabidopsis thaliana]
 Seq. No.
                   166972
 Seq. ID
                   LIB3234-017-P1-K1-D11
 Method
                   BLASTN
 NCBI GI
                   q2924257
 BLAST score
                   35
 E value
                   3.0e-10
 Match length
                   55
 % identity
                   91
 NCBI Description Tobacco chloroplast genome DNA
 Seq. No.
                   166973
 Seq. ID
                   LIB3234-017-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  g2864607
BLAST score
                  216
E value
                  1.0e-118
Match length
                  299
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                  (ESSAII project)
Seq. No.
                  166974
                  LIB3234-017-P1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3510337
BLAST score
                  235
E value
                  1.0e-129
Match length
                  353
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19E20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166975
Seq. ID
                  LIB3234-017-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2498329
BLAST score
                  137
E value
                  9.0e-16
Match length
                  86
% identity
                  53
NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__$65571
                  pattern-formation protein GNOM - Arabidopsis thaliana
                 >gi_1209633 (U36433) GNOM gene product [Arabidopsis
                 thaliana] >gi_1335997 (U56140) similar to the Saccharomyces
                 cerevisiae Sec7 protein, GenBank Accession Number J03918
                  [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the
                 Saccharomyces cerevisiae Sec7 protein, GenBank Accession
                 Number J03918 [Arabidopsis thaliana]
```

```
Seq. ID
                    LIB3234-017-P1-K1-D4
 Method
                   BLASTX
 NCBI GI
                    q1592677
 BLAST score
                    183
 E value
                    1.0e-13
 Match length
                    38
 % identity
                    95
 NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
 Seq. No.
 Seq. ID
                   LIB3234-017-P1-K1-D7
 Method
                   BLASTX
 NCBI GI
                   g140551
 BLAST score
                   284
 E value
                   2.0e-25
 Match length
                   79
 % identity
                   69
 NCBI Description
                   HYPOTHETICAL 250 KD PROTEIN (ORF 2131)
                   >gi_81505_pir__S01446 hypothetical protein 2131 - spinach
                   chloroplast >gi_12246_emb_CAA30743_ (X07908) ORF 2131 (AA
                   1-2131) [Spinacia oleracea]
 Seq. No.
                   166978
Seq. ID
                   LIB3234-017-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g3152562
BLAST score
                   408
E value
                   5.0e-40
Match length
                   82
% identity
                   100
NCBI Description
                   (AC002986) Similar to proteosome component, micropain
                   (multi-catalytic endopeptidase complex) subunit Y7,
                   gb_X56731 from S. cerevisiae. EST gb_Z25719 comes from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   166979
Seq. ID
                  LIB3234-017-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2052379
BLAST score
                  614
E value
                  3.0e-64
Match length
                  116
% identity
NCBI Description (U66343) calreticulin [Arabidopsis thaliana]
Seq. No.
                  166980
Seq. ID
                  LIB3234-017-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3024434
BLAST score
                  300
E value
                  2.0e-27
Match length
                  80
% identity
                  79
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
                  PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_
```

(D88663) Tat binding protein 1 [Brassica rapa]

```
Seq. No.
                    166981
 Seq. ID
                    LIB3234-017-P1-K1-E12
 Method
                    BLASTX
 NCBI GI
                    g2262164
 BLAST score
                    287
 E value
                    7.0e-26
 Match length
                    84
 % identity
                    70
 NCBI Description
                    (AC002329) putative obtusifoliol 14-alpha demethylase
                    [Arabidopsis thaliana]
 Seq. No.
                   166982
 Seq. ID
                   LIB3234-017-P1-K1-E2
 Method
                   BLASTN
 NCBI GI
                   g4589414
 BLAST score
                   282
 E value
                   1.0e-157
 Match length
                   367
 % identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
 NCBI Description
                   K14B15, complete sequence
Seq. No.
                   166983
Seq. ID
                   LIB3234-017-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   g4432793
BLAST score
                   248
E value
                   1.0e-137
Match length
                   292
% identity
                   96
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T19K21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166984
Seq. ID
                   LIB3234-017-P1-K1-E4
Method
                   BLASTN
NCBI GI
                   g2656026
BLAST score
                   361
E value
                   0.0e+00
Match length
                   365
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDF20
Seq. No.
                  166985
Seq. ID
                  LIB3234-017-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2598461
BLAST score
                  183
E value
                  1.0e-13
Match length
                  104
% identity
                  38
NCBI Description
                  (Z98048) HIP (HSC70-INTERACTING PROTEIN (PROGESTERONE
                  RECEPTOR-ASSOCIATED P48 PROTEIN) [Homo sapiens] >gi_4049268
                  (U17714) putative tumor suppressor ST13 [Homo sapiens]
Seq. No.
                  166986
```

```
Seq. ID
                     LIB3234-017-P1-K1-E6
  Method
                     BLASTX
  NCBI GI
                     q135858
  BLAST score
                     252
                                                           ∹.
 E value
                     1.0e-21
 Match length
                     51
  % identity
                     100
                     TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
 NCBI Description
                     >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
                     Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
                     thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                     [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast
                     intrinsic protein alpha [Arabidopsis thaliana]
 Seq. No.
                    166987
 Seq. ID
                    LIB3234-017-P1-K1-E7
 Method
                    BLASTX
 NCBI GI
                    g2224911
 BLAST score
                    218
 E value
                    9.0e-18
 Match length
                    110
 % identity
                    44
 NCBI Description
                    (U93048) somatic embryogenesis receptor-like kinase [Daucus
                    carota]
 Seq. No.
                    166988
 Seq. ID
                    LIB3234-017-P1-K1-E8
Method
                    BLASTX
NCBI GI
                    g3367520
 BLAST score
                    209
E value
                    1.0e-16
Match length
                    110
% identity
                    41
NCBI Description
                    (AC004392) Similar to protein kinase APK1A,
                    tyrosine-serine-threonine kinase gb_D12522 from A.
                    thaliana. [Arabidopsis thaliana]
Seq. No.
                    166989
Seq. ID
                    LIB3234-017-P1-K1-E9
Method
                    BLASTX
NCBI GI
                    g2129767
BLAST score
                    643
E value
                   1.0e-67
Match length
                   124
% identity
NCBI Description
                   vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
                   precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615
                   (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
                   166990
Seq. ID
                   LIB3234-017-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g1526424
BLAST score
                   433
E value
                   6.0e-43
Match length
                   100
```

```
% identity
                   86
 NCBI Description (D64140) LEA protein in group 3 [Arabidopsis thaliana]
 Seq. No.
                   166991
 Seq. ID
                   LIB3234-017-P1-K1-F11
 Method
                   BLASTN
 NCBI GI
                   g1469227
 BLAST score
                   60
 E value
                   4.0e-25
 Match length
                   116
 % identity
                   88
 NCBI Description B.oleracea mRNA for hypothetical protein
 Seq. No.
                   166992
 Seq. ID
                   LIB3234-017-P1-K1-F12
 Method
                   BLASTN
 NCBI GI
                   g3985955
 BLAST score
                   285
 E value
                   1.0e-159
 Match length
                   360
 % identity
                   93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                   MTH16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   166993
Seq. ID
                   LIB3234-017-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   g2062153
BLAST score
                   257
E value
                   1.0e-142
Match length
                   306
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  166994
Seq. ID
                  LIB3234-017-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  g4467131
BLAST score
                   347
E value
                  0.0e+00
Match length
                  363
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
                  (ESSA project)
Seq. No.
                  166995
Seq. ID
                  LIB3234-017-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  g4582411
BLAST score
                  292
E value
                  1.0e-163
Match length
                  359
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,
```

complete sequence

```
Seq. No.
                   166996
 Seq. ID
                   LIB3234-017-P1-K1-F5
 Method
                   BLASTX
 NCBI GI
                   g118927
 BLAST score
                   145
 E value
                   4.0e-09
 Match length
                   117
 % identity
                   35
 NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC3-06
                   >gi_320603_pir__C45509 desiccation-related protein (clone
                   PCC3-06) - Craterostigma plantagineum >gi_167475 (M62989)
                   dessication-related protein [Craterostigma plantagineum]
                   >gi_227779_prf__1710351C abscisic acid responsive protein C
                   [Craterostigma plantagineum]
 Seq. No.
                   166997
 Seq. ID
                   LIB3234-017-P1-K1-F6
 Method
                  BLASTX
 NCBI GI
                  g421836
BLAST score
                   370
E value
                   1.0e-35
Match length
                  76
% identity
                  100
NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040
                  (M96855) GF14 [Arabidopsis thaliana]
Seq. No.
                  166998
Seq. ID
                  LIB3234-017-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3785989
BLAST score
                  312
E value
                  9.0e-29
Match length
                  117
% identity
                  57
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                  166999
Seq. ID
                  LIB3234-017-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g2459406
BLAST score
                  350
E value
                  0.0e+00
Match length
                  354
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F4P9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167000
Seq. ID
                  LIB3234-017-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1255951
BLAST score
                  387
E value
                  1.0e-37
Match length
                  91
% identity
                  79
NCBI Description (X96932) PS60 [Nicotiana tabacum]
```

```
Seq. No.
                    167001
 Seq. ID
                    LIB3234-017-P1-K1-G1
 Method
                    BLASTN
 NCBI GI
                    q1296310
 BLAST score
                    63
 E value
                    7.0e-27
 Match length
                    135
 % identity
 NCBI Description Arabidopsis thaliana chromosome I cosmid g17311 DNA
 Seq. No.
                    167002
 Seq. ID
                    LIB3234-017-P1-K1-G12
 Method
                    BLASTX
 NCBI GI
                    q1531762
 BLAST score
                    179
 E value
                    4.0e-13
 Match length
                    48
 % identity
                   73
 NCBI Description
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                   thalianal
Seq. No.
                   167003
Seq. ID
                   LIB3234-017-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g1009234
BLAST score
                   471
E value
                   2.0e-47
Match length
                   114
% identity
NCBI Description (L38829) SUP2 gene product [Nicotiana tabacum]
Seq. No.
                   167004
Seq. ID
                   LIB3234-017-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g1531760
BLAST score
                   452
E value
                   3.0e-45
Match length
                 .. 88
% identity
                   100
NCBI Description (X97075) proline oxidase [Arabidopsis thaliana]
Seq. No.
                  167005
Seq. ID
                  LIB3234-017-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1170505
BLAST score
                  494
E value
                  4.0e-50
Match length
                  94
% identity
                  100
NCBI Description
                  EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2)
                  >gi_322504_pir__JC1453 translation initiation factor
                  eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189
                  (X65053) eukaryotic translation in \overline{i} tiation factor 4A-\overline{2}
                  [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7
                  (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis
                  thaliana]
```

```
Seq. No.
                    167006
 Seq. ID
                    LIB3234-017-P1-K1-G6
 Method
                    BLASTX
 NCBI GI
                   q99688
 BLAST score
                    594
 E value
                    7.0e-62
 Match length
                    114
 % identity
                    100
 NCBI Description
                   translation elongation factor eEF-1 alpha chain (gene A4) -
                   Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)
                   elongation factor 1-alpha [Arabidopsis thaliana]
 Seq. No.
                   167007
 Seq. ID
                   LIB3234-017-P1-K1-G8
 Method
                   BLASTX
 NCBI GI
                   g2435395
 BLAST score
                   274
 E value
                   2.0e-24
 Match length
                   63
 % identity
                   73
NCBI Description (U63550) pectate lyase [Fragaria x ananassa]
 Seq. No.
                   167008
 Seq. ID
                   LIB3234-017-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g4585882
BLAST score
                   466
E value
                   8.0e-47
Match length
                   89
% identity
NCBI Description
                   (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   167009
Seq. ID
                  LIB3234-017-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   q4587519
BLAST score
                   548
E value
                   2.0e-56
Match length
                  108
% identity
                   100
                  (AC007060) Strong similarity to F19I3.7 gi_3033380 putative
NCBI Description
                  coatomer epsilon subunit from Arabidopsis Thaliana BAC
                  gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555,
                  gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g
Seq. No.
                  167010
Seq. ID
                  LIB3234-017-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  169
E value
                  4.0e-90
Match length
                  364
% identity
                  90
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
```

sequence, complete sequence

```
Seq. No.
                    167011
  Seq. ID
                    LIB3234-017-P1-K1-H2
 Method
                    BLASTX
 NCBI GI
                    q4490330
 BLAST score
                    609
 E value
                    1.0e-63
 Match length
                    120
 % identity
                    94
 NCBI Description
                    (AL035656) splicing factor-like protein [Arabidopsis
                    thalianal
 Seq. No.
                    167012
 Seq. ID
                    LIB3234-017-P1-K1-H3
 Method
                    BLASTX
 NCBI GI
                    g4115386
 BLAST score
                    497
 E value
                    2.0e-50
 Match length
                    105
 % identity
                    88
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    167013
 Seq. ID
                   LIB3234-017-P1-K1-H6
 Method
                   BLASTN
 NCBI GI
                   q3985952
 BLAST score
                   202
 E value
                   1.0e-110
 Match length
                   318
 % identity
                   99
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                   MRC8, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   167014
Seq. ID
                   LIB3234-017-P1-K1-H7
Method
                   BLASTN
NCBI GI
                   g3241917
BLAST score
                   351
E value
                   0.0e+00
Match length
                   355
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K19B1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167015
Seq. ID
                  LIB3234-017-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g22564
BLAST score
                  160
E value
                  9.0e-85
Match length
                  225
% identity
                  99
NCBI Description A.thaliana tufA gene for elongation factor Tu
Seq. No.
                  167016
Seq. ID
                  LIB3234-018-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2924282
```

```
BLAST score
                    406
 E value
                    9.0e-40
 Match length
                    81
  % identity
                    93
 NCBI Description
                    (Z00044) NADH dehydrogenase ND1 subunit [Nicotiana tabacum]
 Seq. No.
                    167017
 Seq. ID
                    LIB3234-018-P1-K1-A10
 Method
                    BLASTN
 NCBI GI
                    g2281081
 BLAST score
                    345
 E value
                    0.0e+00
 Match length
                    357
 % identity
                    99
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F18019 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    167018
 Seq. ID
                    LIB3234-018-P1-K1-A11
 Method
                    BLASTX
 NCBI GI
                    q881615
 BLAST score
                    471
 E value
                    2.0e-47
 Match length
                    106
 % identity
                    90.
 NCBI Description
                   (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
                   >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase
                    1 [Arabidopsis thaliana]
 Seq. No.
                   167019
 Seq. ID
                   LIB3234-018-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g2160151
BLAST score
                   480
E value
                   2.0e-48
Match length
                   113
% identity
                   85
NCBI Description
                   (AC000375) Strong similarity to Brassica aspartic protease
                   (gb_X77260). [Arabidopsis thaliana]
Seq. No.
                   167020
Seq. ID
                   LIB3234-018-P1-K1-B10
Method
                   BLASTN
NCBI GI
                   g4512656
BLAST score
                   37
E value
                   2.0e-11
Match length
                   268
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                   sequence, complete sequence
Seq. No.
                  167021
Seq. ID
                  LIB3234-018-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2506139
BLAST score
                  286
E value
                  1.0e-25
```

BLAST score

```
Match length
                   80
 % identity
                   75
 NCBI Description
                   COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                   (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
                   archain/delta-COP [Oryza sativa]
 Seq. No.
                   167022
 Seq. ID
                   LIB3234-018-P1-K1-B2
Method
                   BLASTX -
NCBI GI
                   q3869088
BLAST score
                   537
E value
                   4.0e-55
Match length
                   104
% identity
                   99
NCBI Description
                  (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
Seq. No.
                   167023
Seq. ID
                   LIB3234-018-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   g4335744
BLAST score
                   102
E value
                   4.0e-50
Match length
                   240
% identity
                   95
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T4M8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167024
Seq. ID
                   LIB3234-018-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   573
E value
                   2.0e-59
Match length
                   114
% identity
                   96
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                  167025
Seq. ID
                  LIB3234-018-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  g2645198
BLAST score
                  45
E value
                  4.0e-16
Match length
                  162
% identity
                  83
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T26J12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167026
Seq. ID
                  LIB3234-018-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g3047060
```

```
E value
                    1.0e-116
 Match length
                    359
 % identity
                    47
 NCBI Description Arabidopsis thaliana BAC F7N22
 Seq. No.
                    167027
 Seq. ID
                    LIB3234-018-P1-K1-D1
 Method
                    BLASTX
 NCBI GI
                    g1628583
 BLAST score
                    79
 E value
                    2.0e~55
 Match length
                    117
 % identity
                    89
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
 NCBI Description
                    thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
 Seq. No.
                   167028
                   LIB3234-018-P1-K1-D10
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g3985955
 BLAST score
                   268
 E value
                   1.0e-149
Match length
                   351
 % identity
                   93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                   MTH16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167029
Seq. ID
                   LIB3234-018-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g1531762
BLAST score
                   179
E value
                   3.0e-13
Match length
                   48
% identity
                   73
NCBI Description
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   167030
Seq. ID
                   LIB3234-018-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   g3292807
BLAST score
                   138
E value
                   1.0e-71
Match length
                   303
% identity
                   92
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
                   (ESSAII project)
Seq. No.
                   167031
Seq. ID
                  LIB3234-018-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g4757414
BLAST score
                  187
E value
                  1.0e-101
Match length
                  313
```

```
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 NCBI Description
                    MYF24, complete sequence
 Seq. No.
                    167032
 Seq. ID
                    LIB3234-018-P1-K1-E10
 Method
                    BLASTX
 NCBI GI
                    q3928086
 BLAST score
                    379
 E value
                    1.0e-36
 Match length
                    76
 % identity
                    99
 NCBI Description
                   (AC005770) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   167033
 Seq. ID
                   LIB3234-018-P1-K1-E2
 Method
                   BLASTN
 NCBI GI
                   g2281081
 BLAST score
                   42
 E value
                   2.0e-14
Match length
                   96
 % identity
                   84
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F18019 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167034
Seq. ID
                   LIB3234-018-P1-K1-E4
Method
                   BLASTN
NCBI GI
                   g4314374
BLAST score
                   47
                   3.0e-17
E value
Match length
                   166
% identity
                   58
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167035
Seq. ID
                   LIB3234-018-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   g3449331
BLAST score
                   271
E value
                   1.0e-151
Match length
                   343
% identity
                   49
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167036
Seq. ID
                  LIB3234-018-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q3834307
BLAST score
                  632
E value
                  3.0e-66
Match length
                  118
% identity
                  100
NCBI Description
                  (AC005679) Strong similarity to gene T10I14.120 gi 2832679
                  putative protein from Arabidopsis thaliana BAC gb_AL021712.
```

```
ESTs gb\_N65887 and gb\_N65627 come from this gene.
                    [Arabidopsis thaliana]
 Seq. No.
                    167037
 Seq. ID
                    LIB3234-018-P1-K1-E8
 Method
                    BLASTX
 NCBI GI
                    g1490554
 BLAST score
                    181
 E value
                    2.0e-13
 Match length
                    91
 % identity
                    47
 NCBI Description
                    (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
                   thalianal
 Seq. No.
                   167038
 Seq. ID
                   LIB3234-018-P1-K1-F10
 Method
                   BLASTX
 NCBI GI
                   g2887500
 BLAST score
                   192
 E value
                   1.0e-14
 Match length
                   39
 % identity
                   (AC002339) putative AP2 domain-containing protein
 NCBI Description
                   [Arabidopsis thaliana]
 Seq. No.
                   167039
 Seq. ID
                   LIB3234-018-P1-K1-F4
Method
                   BLASTN
NCBI GI
                   g4206788
BLAST score
                   178
E value
                   1.0e-95
Match length
                   182
% identity
                   99
NCBI Description
                   Arabidopsis thaliana syntaxin-related protein At-SYR1
                   (At-Syr1) mRNA, complete cds
Seq. No.
                   167040
Seq. ID
                   LIB3234-018-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   q543815
BLAST score
                   470
E value
                   3.0e-47
Match length
                   92
% identity
                   95
                  FLORAL HOMEOTIC PROTEIN APETALA3 >gi_282855_pir__A42095
NCBI Description
                  homeotic protein AP3 - Arabidopsis thaliana >gi 166608
                   (M86357) APETELA3 [Arabidopsis thaliana]
Seq. No.
                  167041
Seq. ID
                  LIB3234-018-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2501812
BLAST score
                  475
E value
                  7.0e-48
Match length
                  118
% identity
NCBI Description
                  (U91509) glycolate oxidase [Arabidopsis thaliana]
```

% identity

```
Seq. No.
                     167042
 Seq. ID
                     LIB3234-018-P1-K1-G1
 Method
                     BLASTN
 NCBI GI
                     g1030693
 BLAST score
                     71
 E value
                     8.0e-32
 Match length
                     123
 % identity
                     87
 NCBI Description
                    Arabidopsis thaliana mRNA for fatty acid desaturase in
                     endoplasmic reticulum, complete cds
 Seq. No.
                     167043
 Seq. ID
                    LIB3234-018-P1-K1-G2
 Method
                    BLASTX
 NCBI GI
                    g131336
 BLAST score
                    339
 E value
                    6.0e-32
 Match length
                    73
 % identity
                    PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P
 NCBI Description
                    photosystem II phosphoprotein psbH - common tobacco
                    chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD phosphoprotein [Nicotiana tabacum]
                    >gi_225225_prf__1211235BG photosystem II 10kD
phosphoprotein [Nicotiana tabacum]
 Seq. No.
                    167044
 Seq. ID
                    LIB3234-018-P1-K1-G3
Method
                    BLASTN
NCBI GI
                    g3046855
BLAST score
                    323
E value
                    0.0e+00
Match length
                    359
% identity
                    98
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                    MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                    167045
Seq. ID
                    LIB3234-018-P1-K1-G7
Method
                    BLASTN
NCBI GI
                    q3172156
BLAST score
                    99
E value
                    2.0e-48
Match length
                   183
% identity
                   88
NCBI Description
                   Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   167046
Seq. ID
                   LIB3234-018-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g141631
BLAST score
                   63
E value
                   3.0e-26
Match length
                   87
```

Seq. ID

Method

```
NCBI Description ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
                   BETA >gi_82218_pir_ A05196 hypothetical protein 512 -
                   common tobacco chloroplast >gi_11842 emb_CAA77362 (Z00044)
                   acetyl-CoA carboxylase beta subunit [Nicotiana tabacum]
                   Seq. No.
                   167047
 Seq. ID
                   LIB3234-018-P1-K1-H1
 Method
                   BLASTN
 NCBI GI
                   g3269280
 BLAST score
                   342
E value
                   0.0e + 00
Match length
                   354
 % identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, Pl clone M4I22
                   (ESSAII project)
Seq. No.
                   167048
Seq. ID
                   LIB3234-018-P1-K1-H2
Method
                   BLASTX
NCBI GI ·
                   g399013
BLAST score
                   411
E value
                   2.0e-40
Match length
                   79
% identity
                  100
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana]
                  >gi_445607_prf__1909354A adenylate translocator
                   [Arabidopsis thaliana]
Seq. No.
                  167049
Seq. ID
                  LIB3234-018-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3135270
BLAST score
                  400
E value
                  4.0e-39
Match length
                  80
% identity
                  100
NCBI Description
                  (AC003058) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  167050
Seq. ID
                  LIB3234-018-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g3273742
BLAST score
                  184
E value
                  3.0e-99
Match length
                  269
                  96
% identity
NCBI Description
                  Arabidopsis thaliana lipid transfer protein 2 precursor
                  (LTP2) gene, complete cds
Seq. No.
                  167051
```

LIB3234-019-P1-K1-A1

BLASTX

BLAST score

```
NCBI GI
                    q112682
 BLAST score
                    477
 E value
                    4.0e-48
 Match length
                   114
 % identity
                   80
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__$08510
 NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
 Seq. No.
                   167052
 Seq. ID
                   LIB3234-019-P1-K1-A12
 Method
                   BLASTN
 NCBI GI
                   g16450
 BLAST score
                   33
 E value
                   7.0e-10
 Match length
                   62
 % identity
                   85
 NCBI Description A.thaliana rab18 gene
 Seq. No.
                   167053
Seq. ID
                   LIB3234-019-P1-K1-A8
Method
                   BLASTN
NCBI GI
                   g16450
BLAST score
                   78
E value
                   3.0e-36
Match length
                   138
% identity
                   92
NCBI Description A.thaliana rab18 gene
Seq. No.
                   167054
Seq. ID
                   LIB3234-019-P1-K1-A9
Method
                   BLASTN
NCBI GI
                   g4159703
BLAST score
                   37
E value
                  1.0e-11
Match length
                  129
% identity
                  89
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K5F14, complete sequence
Seq. No.
                  167055
Seq. ID
                  LIB3234-019-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g21911
BLAST score
                  196
E value
                  4.0e-15
Match length
                  79
% identity
                  46
NCBI Description (X62625) vicilin [Theobroma cacao]
Seq. No.
                  167056
Seq. ID
                  LIB3234-019-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  g4757414
```

```
E value
                     0.0e + 00
 Match length
                     362
 % identity
                     98.
 NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                    MYF24, complete sequence
 Seq. No.
                    167057
 Seq. ID
                    LIB3234-019-P1-K1-B5
 Method
                    BLASTN
 NCBI GI
                    g3449313
 BLAST score
                    285
 E value
                    1.0e-159
 Match length
                    317
 % identity
                    97
 NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                    K21P3, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    167058
 Seq. ID
                    LIB3234-019-P1-K1-B9
 Method
                    BLASTX
NCBI GI
                    q131336
BLAST score
                    335
E value
                    2.0e-31
Match length
                    73
% identity
                    92
                   PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P
NCBI Description
                   photosystem II phosphoprotein psbH - common tobacco
                   chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD
                   phosphoprotein [Nicotiana tabacum]
                   >gi_225225_prf__1211235BG photosystem II 10kD
                   phosphoprotein [Nicotiana tabacum]
Seq. No.
                   167059
Seq. ID
                   LIB3234-019-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   g4589445
BLAST score
                   85
E value
                   5.0e-40
Match length
                   225
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
NCBI Description
                   MWL2, complete sequence
Seq. No.
                   167060
Seq. ID
                   LIB3234-019-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q1345973
BLAST score
                   418
E value
                   3.0e-41
Match length
                   92
% identity
                   84
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Árabidopsīs thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
```

```
thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                    desaturase [Arabidopsis thaliana]
 Seq. No.
                    167061
 Seq. ID
                   LIB3234-019-P1-K1-C2
 Method
                   BLASTN
 NCBI GI
                   g3449331
 BLAST score
                   370
 E value
                   0.0e + 00
 Match length
                   382
 % identity
                   25
                   Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
 NCBI Description
                   MNC17, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   167062
 Seq. ID
                   LIB3234-019-P1-K1-C5
 Method
                   BLASTN
 NCBI GI
                   g2924728
 BLAST score
                   378
 E value
                   0.0e + 00
Match length
                   378
 % identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                   MXH1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167063
Seq. ID
                   LIB3234-019-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   539
E value
                   2.0e-55
Match length
                   102
% identity
                   100
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   167064
Seq. ID
                   LIB3234-019-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   g2351069
BLAST score
                   314
E value
                   1.0e-176
Match length
                   378
% identity
                   95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167065
Seq. ID
                  LIB3234-019-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  509
E value
                  8.0e-52
Match length
                  101
% identity
                  99
NCBI Description
                  (AC003027) lcl_prt_seq No definition line found
                  [Arabidopsis thaliana]
```

microsomal omega-3 fatty acid desaturase [Arabidopsis

```
Seq. No.
                     167066
 Seq. ID
                     LIB3234-019-P1-K1-D1
 Method
                     BLASTN
 NCBI GI
                     q2358139
 BLAST score
                     122
 E value
                     4.0e-62
 Match length
                     277
 % identity
                     87
 NCBI Description Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete
                     sequence [Arabidopsis thaliana]
 Seq. No.
                     167067
 Seq. ID
                     LIB3234-019-P1-K1-D2
 Method
                     BLASTX
 NCBI GI
                     g1617274
 BLAST score
                     289
 E value
                     5.0e-26
Match length
                     78
 % identity
                     74
NCBI Description (Z72152) AMP-binding protein [Brassica napus]
 Seq. No.
                     167068
 Seq. ID
                     LIB3234-019-P1-K1-D4
Method
                     BLASTX
NCBI GI
                     g464707
BLAST score
                     533
E value
                   _1.0e-54
Match length
                    105
% identity
                    100
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
                    protein S18.A - Arabidopsis thaliana
                    >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                     [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                     S18 ribosomal protein [Arabidopsis thaliana]
                     >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                    [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                    S18 ribosomal protein [Arabidopsis thaliana]
                    >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                    gb_R30430 come from this gene. [Arabidopsis thaliana]
                    >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
                    protein [Arabidopsis thaliana]
Seq. No.
                    167069
Seq. ID
                    LIB3234-019-P1-K1-D5
Method
                    BLASTN
NCBI GI
                    g3150396
BLAST score
                    349
                    0.0e+00
E value
Match length
                    381
% identity
                    98
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T27E13 genomic
```

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                    167070
 Seq. ID
                    LIB3234-019-P1-K1-E1
 Method
                    BLASTX
 NCBI GI
                    q114591
 BLAST score
                    358
 E value
                    2.0e-34
 Match length
                    75
 % identity
                    99
                    ATP SYNTHASE EPSILON CHAIN >gi_81663_pir__S01903
 NCBI Description
                    H+-transporting ATP synthase (\overline{EC}\ 3.6.1.34) epsilon chain -
                    Arabidopsis thaliana chloroplast >gi_11334_emb_CAA31381_
                    (X12889) Cf1 ATPase epsilon subunit \overline{(AA 1 - 13\overline{2})}
                    [Arabidopsis thaliana]
 Seq. No.
                    167071
 Seq. ID
                    LIB3234-019-P1-K1-E11
 Method
                    BLASTX
 NCBI GI
                    g3738338
 BLAST score
                    214
 E value
                    3.0e-17
 Match length
                    75
 % identity
                    59
                   (AC005170) putative polygalacturonase [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    167072
Seq. ID
                    LIB3234-019-P1-K1-E12
Method
                    BLASTN
NCBI GI
                    q2182289
BLAST score
                    314
E value
                    1.0e-176
Match length
                    373
% identity
                   98
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F11P17 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167073
Seq. ID
                   LIB3234-019-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g4432856
BLAST score
                   198
E value
                   4.0e-19
Match length
                   87
% identity
NCBI Description
                  (AC006300) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                   167074
Seq. ID
                   LIB3234-019-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g1350634
BLAST score
                   419
E value
                   2.0e-41
Match length
                   93
% identity
                   89
NCBI Description
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L23
                  >gi_12213_emb_CAA46567_ (X65615) ribosomal protein L23
                   [Sinapis alba]
```

```
Seq. No.
                   167075
 Seq. ID
                   LIB3234-019-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   g3702315
BLAST score
                   250
E value
                   1.0e-138
Match length
                   382
 % identity
                   Arabidopsis thaliana chromosome II BAC T3F17 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167076
Seq. ID
                   LIB3234-019-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g113595
BLAST score
                   413
E value
                   1.0e-40
Match length
                   123
% identity
NCBI Description
                   ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE)
                   >gi_100562_pir__S15024 aldose reductase-related protein -
                   barley >gi_18891_emb_CAA40747 (X57526) aldose
                   reductase-related protein [Hordeum vulgare]
Seq. No.
                   167077
Seq. ID
                   LIB3234-019-P1-K1-F9
Method
                   BLASTN
NCBI GI
                   g3702729
BLAST score
                   365
E value
                   0.0e+00
Match length
                   365
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167078
Seq. ID
                  LIB3234-019-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  g2924733
BLAST score
                  371
E value
                  0.0e + 00
Match length
                  375
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167079
                  LIB3234-019-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  401
E value
                  3.0e-39
Match length
                  93
% identity
                  80
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir_JQ2335 omega-3 fatty acid desaturase (EC
```

BLAST score

E value

105

6.0e-52

1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

```
Seq. No.
                    167080
 Seq. ID
                    LIB3234-019-P1-K1-G3
 Method
                   BLASTX
 NCBI GI
                   g1885356
 BLAST score
                   302
 E value
                   1.0e-27
 Match length
                   104
 % identity
                   54
 NCBI Description (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]
 Seq. No.
                   167081
 Seq. ID
                   LIB3234-019-P1-K1-G7
 Method
                   BLASTN
 NCBI GI
                   g2864607
 BLAST score
                   363
 E value
                   0.0e+00
 Match length
                   367
 % identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                   (ESSAII project)
Seq. No.
                   167082
Seq. ID
                   LIB3234-019-P1-K1-G8
Method
                   BLASTN
NCBI GI
                   g2264314
BLAST score
                   264
E value
                   1.0e-147
Match length
                   360
% identity
                   93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167083
Seq. ID
                  LIB3234-019-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  g2642152
BLAST score
                  368
E value
                  0.0e+00
Match length
                  376
% identity
                  Arabidopsis thaliana chromosome II BAC T517 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3234-019-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  g2477521
```

```
Match length
                     264
 % identity
                    Arabidopsis thaliana chromosome I BAC F22K20 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    167085
 Seq. ID
                    LIB3234-019-P1-K1-H12
 Method
                    BLASTX
 NCBI GI
                    g133960
 BLAST score
                    205
E value
                    3.0e-16
Match length
                    49
 % identity
                    86
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_70876_pir__R3NT4
NCBI Description
                    ribosomal protein S4 - common tobacco chloroplast
                    >gi_11834_emb_CAA77354_ (Z00044) ribosomal protein S4
[Nicotiana tabacum] >gi_225202_prf__1211235AG ribosomal
                    protein S4 [Nicotiana tabacum]
Seq. No.
                    167086
Seq. ID
                    LIB3234-019-P1-K1-H2
Method
                    BLASTX
NCBI ĢI
                    g112682
BLAST score
                    676
E value
                    2.0e-71
Match length
                    127
% identity
                    100
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                    cruciferin precursor (CRB) - Arabidopsis thaliana
                    >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                    storage protein [Arabidopsis thaliana]
Seq. No.
                    167087
                    LIB3234-019-P1-K1-H4
Seq. ID
Method
                    BLASTN
NCBI GI
                    q563624
BLAST score
                    72
E value
                    3.0e-32
Match length
                    99
% identity
                    95
NCBI Description S.tuberosum (PU141) mRNA for U14 small nucleolar RNA
Seq. No.
                   167088
Seq. ID
                   LIB3234-019-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g1170503
BLAST score
                   438
E value
                   2.0e-43
Match length
                   84
% identity
                   100
NCBI Description
                   EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
                   >gi_322503_pir__JC1452 translation initiation factor
                   eIF-4Al - Arabidopsis thaliana >gi_16554_emb_CAA46188
                   (X65052) eukaryotic translation initiation factor 4A-\overline{1}
                   [Arabidopsis thaliana]
```

Seq. ID

Method

```
Seq. No.
                   167089
 Seq. ID
                   LIB3234-019-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q4539348
BLAST score
                   487
E value
                   3.0e-49
Match length
                   116
% identity
                   82
NCBI Description
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.
                   167090
Seq. ID
                   LIB3234-020-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   q4096078
BLAST score
                   113
E value
                   7.0e-57
Match length
                   222
% identity
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167091
Seq. ID
                   LIB3234-020-P1-K1-A2
Method
                   BLASTN
NCBI GI
                   g4096078
BLAST score
                   145
E value
                   9.0e-76
Match length
                  348
% identity
                  94
NCBI Description Arabidopsis thaliana chromosome I BAC T5A14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167092
Seq. ID
                  LIB3234-020-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g4455223
BLAST score
                  355
E value
                  1.0e-33
Match length
                  132
% identity
                  41
                  (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167093
Seq. ID
                  LIB3234-020-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q4049401
BLAST score
                  587
E value
                  5.0e-61
Match length
                  121
% identity
                  94
NCBI Description
                  (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
                  thaliana]
Seq. No.
                  167094
```

LIB3234-020-P1-K1-A6

BLASTN

```
NCBI GI
                    g2894591
 BLAST score
                    298
                    1.0e-167
 E value
 Match length
                    374
 % identity
                    95
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
                   (ESSAII project)
 Seq. No.
                    167095
 Seq. ID
                    LIB3234-020-P1-K1-A7
Method
                   BLASTX
NCBI GI
                    q4204263
BLAST score
                    321
E value
                    9.0e-30
Match length
                   102
% identity
                    65
NCBI Description (AC005223) 40409 [Arabidopsis thaliana]
Seq. No.
                   167096
Seq. ID
                   LIB3234-020-P1-K1-A8
Method
                   BLASTN
NCBI GI
                   g4756963
BLAST score
                   314
E value
                   1.0e-176
Match length
                   358
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                   167097
Seq. ID
                   LIB3234-020-P1-K1-A9
Method
                   BLASTN
NCBI GI
                   g4756963
BLAST score
                   147
E value
                   5.0e-77
Match length
                   315
% identity
                   87
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                   167098
Seq. ID
                   LIB3234-020-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q543712
BLAST score
                   634
E value
                   2.0e-66
Match length
                   122
% identity
                   97
NCBI Description
                   1-AMINOCYCLOPROPANE-2-CARBOXYLATE SYNTHASE 2 (ACC SYNTHASE
                   2) (S-ADENOSYL-L-METHIONINE METHYLTHIOADENOSINE-LYASE 2)
                   >gi_476924_pir__A47199 1-aminocyclopropane-1-carboxylate
                   synthase (EC 4.4.1.14) - Arabidopsis thaliana

>gi_16148_emb_CAA78260_ (Z12614) 1-aminocyclopropane

1-carboxylate synthase [Arabidopsis thaliana] >gi_166580
                   (M95595) 1-aminocyclopropane-1-carboxylate synthase
                   [Arabidopsis thaliana] >gi_2505881_emb_CAA73310 (Y12776)
                   ACC-synthase [Arabidopsis thaliana]
```

Seq. No.

```
Seq. No.
                   167099
                   LIB3234-020-P1-K1-B5
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g3420042
 BLAST score
                   163
 E value
                   1.0e-86
Match length
                   351
 % identity
                   98
NCBI Description Arabidopsis thaliana chromosome II BAC T13E15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167100
Seq. ID
                   LIB3234-020-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g4678358
BLAST score
                   176
E value
                   9.0e-52
Match length
                   127
% identity
                   85
                   (AL049659) cytochrome p450 like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   167101
Seq. ID
                   LIB3234-020-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g3121825
BLAST score
                   161
E value
                   9.0e-17
Match length
                   107
% identity
                   51
NCBI Description
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
                  ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                  bas1 protein [Spinacia oleracea]
Seq. No.
                   167102
Seq. ID
                  LIB3234-020-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g3808062
BLAST score
                  143
E value
                   6.0e-09
Match length
                  61
% identity
                  44
NCBI Description (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  167103
Seq. ID
                  LIB3234-020-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2832707
BLAST score
                  213
E value
                  1.0e-17
Match length
                  45
% identity
                  96
NCBI Description
                  (AL021713) translation initiation factor eIF-2 gamma
                  chain-like protein [Arabidopsis thaliana]
```

```
Seq. ID
                   LIB3234-020-P1-K1-C4
 Method
                   BLASTX
 NCBI GI
                   q1169598
 BLAST score
                   346
 E value
                   1.0e-32
 Match length
                   77
 % identity
                   84
 NCBI Description
                   OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                   (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12
                   desaturase [Arabidopsis thaliana]
 Seq. No.
                   167105
 Seq. ID
                   LIB3234-020-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   q3335169
BLAST score
                   581
E value
                   3.0e-60
Match length
                   112
% identity
                   98
NCBI Description
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                   >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                   protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                   167106
Seq. ID
                   LIB3234-020-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   g2760166
BLAST score
                   304
E value
                   1.0e-171
Match length
                   312
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MBK20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167107
                  LIB3234-020-P1-K1-C7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4159712
BLAST score
                   218
E value
                   1.0e-119
Match length
                   380
% identity
                   96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
Seq. No.
                  167108
Seq. ID
                  LIB3234-020-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g1346760
BLAST score
                  337
E value
                  1.0e-31
Match length
                  68
% identity
                  96
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 6
NCBI Description
                  >gi_829255_emb_CAA86339_ (Z46253) protein phosphatase type
                  1 [Arabidopsis thaliana] >gi 3153203 (U80921)
                 \circserine/threonine protein phosphatase type one [Arabidopsis
```

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thaliana]
```

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167109
Seq. No.
Seq. ID
                   LIB3234-020-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g4204299
BLAST score
                   72
                   6.0e-31
E value
Match length
                   104
                   70
% identity
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   167110
Seq. ID
                   LIB3234-020-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   g4580745
BLAST score
                   104
E value
                   2.0e-51
Match length
                   381
% identity
                   96
                  Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
NCBI Description
                   complete sequence
Seq. No.
                   167111
Seq. ID
                   LIB3234-020-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g631291
BLAST score
                   393
E value
                   3.0e-38
Match length
                   89
% identity
                   91
                  MAP kinase-activated protein kinase 2 - human
NCBI Description
                   >gi_407075 emb CAA53094 (X75346) MAP kinase activated
                   protein kinase-2 [Homo sapiens]
Seq. No.
                   167112
Seq. ID
                   LIB3234-020-P1-K1-D4
Method
                   BLASTN
NCBI GI
                   g3859590
BLAST score
                   135
E value
                   8.0e-70
Match length
                   319
% identity
                   96
NCBI Description
                  Arabidopsis thaliana BAC T15B16
Seq. No.
                  167113
Seq. ID
                  LIB3234-020-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2961542
BLAST score
                  412
E value
                  2.0e-40
Match length
                  94
% identity
                  84
                  (AF050463) zinc finger transcription factor [Arabidopsis
NCBI Description
                  thaliana]
```

```
Seq. No.
                   167114
 Seq. ID
                   LIB3234-020-P1-K1-D9
Method
                   BLASTX
                   g4455223
NCBI GI
BLAST score
                   323
E value
                   5.0e-30
Match length
                   124
% identity
                   37
NCBI Description
                   (AL035440) putative DNA binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   167115
Seq. ID
                   LIB3234-020-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g112681
BLAST score
                   575
E value
                   1.0e-59
Match length
                   125
                   90
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana) >gi_808936_emb_CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   167116
Seq. ID
                  LIB3234-020-P1-K1-E10
Method
                  BLASTX
NCBI GI
                   g2961542
BLAST score
                   513
E value
                   3.0e-52
Match length
                   93
% identity
                  100
NCBI Description
                   (AF050463) zinc finger transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  167117
Seq. ID
                  LIB3234-020-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g627537
BLAST score
                  425
E value
                  6.0e-42
Match length
                  91
% identity
                  90
NCBI Description
                  mitogen activated protein kinase activated protein kinase
                  (EC 2.7.1.-) 2 - human >gi_530090 (U12779) MAP kinase
                  activated protein kinase 2 [Homo sapiens]
Seq. No.
                  167118
Seq. ID
                  LIB3234-020-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3413718
BLAST score
                  603
E value
                  7.0e-63
Match length
                  117
% identity
                  98
NCBI Description
                  (AC004747) alpha-vacuolar processing enzyme [Arabidopsis
```

Method

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enzyme [Arabidopsis thaliana]
 Seq. No.
                     167119
 Seq. ID
                     LIB3234-020-P1-K1-E7
Method
                     BLASTX
NCBI GI
                     g114654
BLAST score
                     282
E value
                     3.0e-25
Match length
                     81
% identity
                    78
NCBI Description
                    ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
                    >gi_67898_pir__LWNTA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - common tobacco
                    chloroplast >gi_11812_emb_CAA77343 (Z00044) ATPase III
                    subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase subunit III [Nicotiana tabacum] >gi_224347_prf__1102209A
                    ATPase III, H translocating [Nicotiana sp.]
                    >gi_225272_prf__1211235G ATPase III [Nicotiana tabacum]
Seq. No.
                    167120
Seq. ID
                    LIB3234-020-P1-K1-F1
Method
                    BLASTX
NCBI GI
                    q3834322
BLAST score
                    378
E value
                    2.0e-36
Match length
                    91
% identity
                    78
NCBI Description
                    (AC005679) EST gb R30300 comes from this gene. [Arabidopsis
                    thaliana]
Seq. No.
                    167121
                    LIB3234-020-P1-K1-F12
Seq. ID
Method
                    BLASTN
NCBI GI
                    q3859840
BLAST score
                    356
E value
                    0.0e+00
Match length
                    376
                    79
% identity
NCBI Description
                    Plastid transformation vector pGS31A 16S ribosomal RNA
                    gene, partial sequence; aminoglycoside 3'-adenyltransferase
                    (aadA) gene, complete cds
Seq. No.
                    167122
Seq. ID
                    LIB3234-020-P1-K1-F2
Method
                    BLASTX
NCBI GI
                    g494550
BLAST score
                    255
E value
                    2.0e-22
Match length
                    80
% identity
                    66
NCBI Description
                    Homo sapiens >gi_494551_pdb 1RHG B Homo sapiens
                    >gi_494552_pdb_1RHG_C Homo sapiens
Seq. No.
                    167123
Seq. ID
```

thaliana] >gi_3643591 (AC005395) alpha-vacuolar processing

LIB3234-020-P1-K1-F6

BLASTX

E value

```
NCBI GI
                   q1769905
BLAST score
                   356
E value
                   7.0e-34
Match length
                   110
% identity
                   66
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   167124
Seq. ID
                   LIB3234-020-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g2194125
BLAST score
                   230
E value
                   4.0e-19
Match length
                   59
% identity
                   80
                   (AC002062) ESTs gb_R30459, gb_N38441 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   167125
Seq. ID
                   LIB3234-020-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g4584528
BLAST score
                   332
E value
                   3.0e-31
Match length
                   78
% identity
                   83
                  (AL049607) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167126
Seq. ID
                  LIB3234-020-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g4584519
BLAST score
                  133
E value
                  8.0e-69
Match length
                  237
% identity
                  89
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18
                   (ESSA project)
Seq. No.
                  167127
                  LIB3234-020-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4454447
BLAST score
                  89
E value
                  2.0e-42
Match length
                  269
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167128
Seq. ID
                  LIB3234-020-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  q12218
BLAST score
                  211
```

1.0e-115

```
321
Match length
% identity
                   92
NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly
Seq. No.
                  167129
                  LIB3234-020-P1-K1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4455290
BLAST score
                  32
                  8.0e-09
E value
Match length
                  60
% identity
                  88
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5
                  (ESSAII project)
Seq. No.
                  167130
Seq. ID
                  LIB3234-020-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g4584528
BLAST score
                  482
E value
                  1.0e-48
Match length
                  104
% identity
                  91
NCBI Description (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                  167131
Seq. ID
                  LIB3234-020-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  524
E value
                  1.0e-53
Match length
                  121
                  83
% identity
                  (AC003027) lcl prt seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  167132
Seq. ID
                  LIB3234-020-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g541546
BLAST score
                  499
E value
                  1.0e-50
Match length
                  128
% identity
                  18
NCBI Description
                  ubiquitin precursor - Volvox carteri
                  >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox
                  carteri]
Seq. No.
                  167133
Seq. ID
                  LIB3234-020-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g4455290
BLAST score
                  255
E value
                  1.0e-141
Match length
                  347
% identity
                  94
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5
```

```
(ESSAII project)
 Seq. No.
                   167134
 Seq. ID
                   LIB3234-020-P1-K1-H6
 Method
                   BLASTN
 NCBI GI
                   g3702733
 BLAST score
                   333
 E value
                   0.0e + 00
 Match length
                   373
 % identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MJP23, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   167135
 Seq. ID
                   LIB3234-020-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g1531762
BLAST score
                   195
 E value
                   5.0e-15
                   51
Match length
% identity
                   75
NCBI Description
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   167136
Seq. ID
                   LIB3234-021-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g1592677
BLAST score
                   193
                   9.0e-15
E value
Match length
                   38
% identity
                   100
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   167137
Seq. ID
                   LIB3234-021-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g4115386
BLAST score
                   513
E value
                   2.0e-52
Match length
                   114
% identity
                   83
NCBI Description
                   (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                   167138
Seq. ID
                  LIB3234-021-P1-K1-A9
Method
                  BLASTX
NCBI GI
                   g1531762
BLAST score
                  162
E value
                   4.0e-11
Match length
                  39
% identity
                  82
NCBI Description
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  167139
Seq. ID
                  LIB3234-021-P1-K1-B1
```

Seq. ID

```
BLASTX
Method
NCBI GI
                  g1490554
BLAST score
                  438
                  2.0e-43
E value
Match length
                  107
% identity
                  86
                  (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  167140
Seq. No.
Seq. ID
                  LIB3234-021-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q4006897
BLAST score
                  468
                  4.0e-47 ·
E value
Match length
                  115
% identity
                  78
NCBI Description (Z99708) globulin-like protein [Arabidopsis thaliana]
Seq. No.
                  167141
Seq. ID
                  LIB3234-021-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g585382
BLAST score
                  578
                  6.0e-60
E value
Match length
                  118
% identity
                  93
                  40S RIBOSOMAL PROTEIN SA (P40) (LAMININ RECEPTOR HOMOLOG)
NCBI Description
                  >gi 322536 pir S30570 laminin receptor homolog -
                  Arabidopsis thaliana >gi_16380_emb_CAA48794_ (X69056)
                  laminin receptor homologue [Arabidopsis thaliana]
Seq. No.
                  167142
Seq. ID
                  LIB3234-021-P1-K1-B3
                  BLASTX
Method
NCBI GI
                  g2129767
                  659
BLAST score
E value
                  2.0e-69
                  123
Match length
                  100
% identity
                  vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
NCBI Description
                  precursor - Arabidopsis thaliana >gi 1805364 dbj BAA09615
                  (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
                  167143
Seq. ID
                  LIB3234-021-P1-K1-C1
                  BLASTX
Method
                  g2738248
NCBI GI
BLAST score
                  282
E value
                  2.0e-25
                  65
Match length
% identity
NCBI Description
                  (U97200) cobalamin-independent methionine synthase
                  [Arabidopsis thaliana]
Seq. No.
                  167144
```

LIB3234-021-P1-K1-C11

Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g4678347
BLAST score
                  211
                  6.0e-17
E value
Match length
                  71
% identity
                  52
                  (AL049659) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167145
Seq. ID
                  LIB3234-021-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q1490554
BLAST score
                  424
                  7.0e-42
E value
                  103
Match length
% identity
                  85
                  (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  167146
Seq. No.
Seq. ID
                  LIB3234-021-P1-K1-C3
Method
                  BLASTX
                  q136739
NCBI GI
BLAST score
                  380
E value
                  1.0e-36
                  122
Match length
% identity
                  63
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  167147
Seq. ID
                  LIB3234-021-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  q3702739
BLAST score
                  336
E value
                  0.0e+00
                  340
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MXE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167148
Seq. ID
                  LIB3234-021-P1-K1-D10
                  BLASTN
Method
NCBI GI
                  g3108208
BLAST score
                  285
E value
                  1.0e-159
                  350
Match length
% identity
                  Arabidopsis thaliana eukaryotic cap-binding protein (eIF4E)
NCBI Description
                  mRNA, complete cds
                  167149
Seq. No.
```

LIB3234-021-P1-K1-D12

NCBI GI

g166765

```
Method
                   BLASTX
NCBI GI
                   q3341679
BLAST score
                   142
E value
                   2.0e-12
Match length
                    63
% identity
                   70
                    (AC003672) dynamin-like protein phragmoplastin 12
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   167150
Seq. ID
                   LIB3234-021-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q4704766
BLAST score
                   367
E value
                   3.0e - 35
Match length
                   102
% identity
                   43
NCBI Description
                    (AF131223) protein disulfide isomerase homolog; PDI
                    [Datisca glomerata]
Seq. No.
                   167151
Seq. ID
                   LIB3234-021-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q464775
BLAST score
                   357
E value
                   5.0e - 34
Match length
                   89
% identity
                   74
                   SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707)
NCBI Description
                   superoxide dismutase (manganese) [Hevea brasiliensis]
                   167152
Seq. No.
Seq. ID
                   LIB3234-021-P1-K1-D8
Method
                   BLASTX
                   g2244749
NCBI GI
BLAST score
                   481
E value
                   1.0e-48
                   104
Match length
% identity
                   88
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   167153
                   LIB3234-021-P1-K1-E10
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3298532
BLAST score
                   281
                   1.0e-157
E value
                   317
Match length
                   97
% identity
                   Arabidopsis thaliana chromosome II BAC T26B15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167154
Seq. ID
                   LIB3234-021-P1-K1-E11
                   BLASTX
Method
```

```
416
BLAST score
                  6.0e-41
E value
Match length
                  81
% identity
                  98
NCBI Description (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]
Seq. No.
                  167155
                  LIB3234-021-P1-K1-E12
Seq. ID
Method
                  BLASTN
                  g2244991
NCBI GI
BLAST score
                  224
E value
                  1.0e-123
Match length
                  310
% identity
                  95
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  167156
Seq. ID
                  LIB3234-021-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q4388728
BLAST score
                  260
E value
                  1.0e-22
Match length
                  62
                  87
% identity
                  (AC006413) putative qrrl-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167157
                  LIB3234-021-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  148
E value
                  1.0e-77
Match length
                  240
% identity
                  90
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  167158
Seq. ID
                  LIB3234-021-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2160158
BLAST score
                  508
                  1.0e-51
E value
Match length
                  100
% identity
                  100
                  (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb EF1G XENLA). ESTs gb T20564, gb T45940, gb T04527 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  167159
Seq. ID
                  LIB3234-021-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g1946354
BLAST score
                  86
```

7.0e-41

E value

```
166
Match length
                  88
% identity
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
NCBI Description
                   sequence, complete sequence
                  167160
Seq. No.
                  LIB3234-021-P1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4580745
BLAST score
                  236
                  1.0e-130
E value
                  336
Match length
% identity
                  94
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
                  complete sequence
Seq. No.
                  167161
Seq. ID
                  LIB3234-021-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q4704766
BLAST score
                  289
                  3.0e - 34
E value
                  99
Match length
                  38
% identity
                   (AF131223) protein disulfide isomerase homolog; PDI
NCBI Description
                   [Datisca glomerata]
Seq. No.
                  167162
Seq. ID
                  LIB3234-021-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  g4159703
BLAST score
                  181
E value
                  2.0e-97
Match length
                  201
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5F14, complete sequence
Seq. No.
                  167163
Seq. ID
                  LIB3234-021-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  110
E value
                  2.0e-10
                  76
Match length
                  67
% identity
NCBI Description
                  (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  167164
Seq. ID
                  LIB3234-021-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g527636
BLAST score
                  43
                  2.0e-15
E value
Match length
                  75
% identity
                  89
NCBI Description Arabidopsis thaliana clone HAT7 homeobox protein mRNA,
```

complete cds

Seq. No. 167165 Seq. ID LIB3234-021-P1-K1-H4

Method BLASTN
NCBI GI 94159712
BLAST score 197
E value 1.0e-107
Match length 351
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 167166

Seq. ID LIB3234-021-P1-K1-H6

Method BLASTX
NCBI GI g2129659
BLAST score 276
E value 1.0e-24
Match length 92
% identity 62

NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi 725260

(L40954) oleosin [Arabidopsis thaliana]

Seq. No. 167167

Seq. ID LIB3234-021-P1-K1-H7

Method BLASTX
NCBI GI g633890
BLAST score 253
E value 7.0e-22
Match length 78
% identity 65

NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum

÷

vulgare]

Seq. No. 167168

Seq. ID LIB3234-021-P1-K1-H8

Method BLASTX
NCBI GI g1946369
BLAST score 241

E value 8.0e-29 Match length 98 % identity 72

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 167169

Seq. ID LIB3234-021-P1-K1-H9

Method BLASTN
NCBI GI 94757392
BLAST score 271
E value 1.0e-151
Match length 302
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No. 167170

Seq. ID

```
Seq. ID
                  LIB3234-022-P1-K1-A3
                  BLASTX
Method
NCBI GI
                  g3219938
BLAST score
                  179
                  4.0e-13
E value
Match length
                  107
                  37
% identity
                  HYPOTHETICAL 34.9 KD PROTEIN C57A10.11C IN CHROMOSOME I
NCBI Description
                  >qi 2058378 emb CAB08174 (Z94864) hypothetical protein
                  [Schizosaccharomyces pombe]
Seq. No.
                  167171
Seq. ID
                  LIB3234-022-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q267073
BLAST score
                  618
                  1.0e-64
E value
Match length
                  118
                  97
% identity
                  TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir_ JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  167172
                  LIB3234-022-P1-K1-A6
Seq. ID
Method
                  BLASTX
                  g115767
NCBI GI
                  629
BLAST score
                  7.0e-66
E value
                  123
Match length
% identity
                  97
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >qi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  167173
Seq. No.
                  LIB3234-022-P1-K1-A7
Seq. ID
                  BLASTX
Method
                  g118926
NCBI GI
                  208
BLAST score
                  2.0e-18
E value
                  102
Match length
                  51
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi 167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi 227781_prf __1710351E abscisic acid responsive protein E
                  [Craterostigma plantagineum]
                  167174
Seq. No.
                  LIB3234-022-P1-K1-A9
```

```
Method
                  BLASTX
NCBI GI
                  q1708025
BLAST score
                  395
                  1.0e-38
E value
Match length
                  97
% identity
                  81
                  GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+]
NCBI Description
                  >gi 840731 emb CAA56125 (X79677) glycerol-3-phosphate
                  dehydrogenase (NAD+) [Cuphea lanceolata]
Seq. No.
                  167175
                  LIB3234-022-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4587680
BLAST score
                  416
E value
                  7.0e-41
Match length
                  107
% identity
                  71
                  (AC007197) putative cytochrome p450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167176
Seq. ID
                  LIB3234-022-P1-K1-B11
Method ...
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  551 ***
E value
                  1.0e-56
Match length
                  131
% identity
                  80
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsīs thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  167177
Seq. ID
                  LIB3234-022-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q544285
                  202
BLAST score
                  8.0e-16
E value
                  43
Match length
                  86
% identity
                  FIBRILLARIN >gi 422056 pir S33690 fibrillarin - fission
NCBI Description
                  yeast (Schizosaccharomyces pombe) >gi 296704_emb_CAA49550_
                  (X69930) fibrillarin [Schizosaccharomyces pombe]
                  >qi 3687500 emb CAA21168 (AL031788) fibrillarin
                  [Schizosaccharomyces pombe]
                  167178
Seq. No.
Seq. ID
                  LIB3234-022-P1-K1-B3
                  BLASTX
Method
                  g629500
NCBI GI
BLAST score
                  485
                  5.0e-49
E value
                  105
Match length
                  92
% identity
NCBI Description 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) -
```

E value

0.0e + 00

```
1-aminocyclopropane-1-carboxylate synthase [Arabidopsis
                    thalianal
                    167179
Seq. No.
                    LIB3234-022-P1-K1-B5
Seq. ID
Method
                    BLASTN
NCBI GI
                    g12216
BLAST score
                    37
E value
                    3.0e-11
Match length
                    115
% identity
                    88
NCBI Description Sinapis alba chloroplast rps16 gene
Seq. No.
                    167180
                    LIB3234-022-P1-K1-B6
Seq. ID
Method
                    BLASTX
                    q1170373
NCBI GI
BLAST score
                    628
E value
                    1.0e-65
Match length
                    138
                    91
% identity
NCBI Description
                    HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302
                    heat shock cognate protein 70-1 - Arabidopsis thaliana
                    >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70
                    cognate [Arabidopsis thaliana]
Seq. No.
                    167181
                    LIB3234-022-P1-K1-B7
Seq. ID
                    BLASTX
Method
                    q2605714
NCBI GI
BLAST score
                    520
E value
                    4.0e-53
                    122
Match length
% identity
NCBI Description
                    (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                    thaliana
Seq. No.
                    167182
Seq. ID
                    LIB3234-022-P1-K1-B9
Method
                    BLASTX
NCBI GI
                    g267073
BLAST score
                    578
                    7.0e-60
E value
Match length
                    106
                    99
% identity
                    TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir_ JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
NCBI Description
                    beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                    167183
Seq. ID
                    LIB3234-022-P1-K1-C11
Method
                    BLASTN
NCBI GI
                    g4589434
BLAST score
                    362
```

Arabidopsis thaliana >gi_166578 (M95594)

```
Match length
                   410
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ7, complete sequence
Seq. No.
                  167184
                  LIB3234-022-P1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2088638
BLAST score
                  38
E value
                  1.0e-12
Match length
                   42
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167185
                  LIB3234-022-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2182289
BLAST score
                  278
E value
                   1.0e-155
Match length
                  278
                  100
% identity
                  Arabidopsis thaliana chromosome I BAC F11P17 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167186
                  LIB3234-022-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1592677
BLAST score
                  250
                  9.0e-22
E value
Match length
                  65
% identity
                  83
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167187
                  LIB3234-022-P1-K1-D2
Seq. ID
                  BLASTX
Method
                  g2275211
NCBI GI
BLAST score
                   664
                   6.0e-70
E value
                  134
Match length
                  99
% identity
                  (ACO02337) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
                  167188
Seq. No.
                  LIB3234-022-P1-K1-D3
Seq. ID
                  BLASTX
Method
                  q1707364
NCBI GI
BLAST score
                  248
                   4.0e-21
E value
Match length
                  106
% identity
                  39
```

NCBI Description (X94626) AATP2 [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                  167189
Seq. ID
                  LIB3234-022-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q1592677
BLAST score
                  214
E value
                  3.0e-17
Match length
                  113
% identity
                  43
NCBI Description
                 (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.
                  167190
Seq. ID
                  LIB3234-022-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  q3869064
BLAST score
                  55
E value
                  5.0e-22
Match length
                  163
% identity
                  88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K1013, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167191
Seq. ID
                  LIB3234-022-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  328
E value
                  1.0e-30
Match length
                  104
% identity
                  62
                  oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
NCBI Description
                  (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  167192
Seq. ID
                  LIB3234-022-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q4589435
BLAST score
                  118
E value
                  8.0e-60
Match length
                  222
% identity
                  88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOE17, complete sequence
Seq. No.
                  167193
Seq. ID
                  LIB3234-022-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g21911
BLAST score
                  155
E value
                  3.0e-10
Match length
                  64
% identity
                  45
NCBI Description (X62625) vicilin [Theobroma cacao]
Seq. No.
                  167194
Seq. ID
                  LIB3234-022-P1-K1-F11
Method
                  BLASTX
```

g1619602

Method

BLASTN

```
BLAST score
                    384
                    4.0e-37
E value
Match length
                    96
                    75
% identity
NCBI Description
                   (Y08726) MtN3 [Medicago truncatula]
                    167195
Seq. No.
Seq. ID
                    LIB3234-022-P1-K1-F5
Method
                    BLASTN
NCBI GI
                    q4512656
BLAST score
                    64
E value
                    1.0e-27
Match length
                    184
                    87
% identity
                   Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                    sequence, complete sequence
Seq. No.
                    167196
Seq. ID
                    LIB3234-022-P1-K1-F6
Method
                    BLASTX
NCBI GI
                    g133788
BLAST score
                    476
E value
                    7.0e-48
Match length
                    100
% identity
                    89
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S14 >gi_70987_pir__R3NT14
NCBI Description
                    ribosomal protein S14 - common tobacco chloroplast >gi_11828_emb_CAA77350_ (Z00044) ribosomal protein S14 [Nicotiana tabacum] >gi_225196_prf__1211235AA ribosomal
                    protein S14 [Nicotiana tabacum]
Seq. No.
                    167197
Seq. ID
                    LIB3234-022-P1-K1-F7
Method
                    BLASTX
NCBI GI
                    g2129570
                    277
BLAST score
                    6.0e-25
E value
Match length
                    71
                    82
% identity
                    DAD-1 homolog - Arabidopsis thaliana
NCBI Description
                    >gi_1184193_emb_CAA64837_ (X95585) DAD-1 homologue
                    [Arabidopsis thaliana]
                    167198
Seq. No.
Seq. ID
                    LIB3234-022-P1-K1-G1
                    BLASTN
Method
                    g2262155
NCBI GI
BLAST score
                    86
                    1.0e-40
E value
                    240
Match length
                    91
% identity
                    DNA sequence of Arabidopsis thaliana BAC F5J6 from
NCBI Description
                    chromosome IV, complete sequence [Arabidopsis thaliana]
                    167199
Seq. No.
Seq. ID
                    LIB3234-022-P1-K1-G10
```

```
NCBI GI
                  a3522932
                  323
BLAST score
                  0.0e + 00
E value
                  407
Match length
                  98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  167200
Seq. No.
Seq. ID
                  LIB3234-022-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q2062163
BLAST score
                  95
E value
                  3.0e-03
Match length
                  132
% identity
                  16
NCBI Description
                  (ACO01645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
                  167201
Seq. No.
Seq. ID
                  LIB3234-022-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  q4220644
BLAST score
                  38
E value
                  4.0e-12
                  106
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXL8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167202
Seq. ID
                  LIB3234-022-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  q4220638
BLAST score
                  58
E value
                  4.0e-24
Match length
                  162
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167203
Seq. ID
                  LIB3234-022-P1-K1-H1
Method
                  BLASTN
                  g4760411
NCBI GI
BLAST score
                  305
E value
                  1.0e-171
Match length
                  333
% identity
                  98
                  Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
NCBI Description
                  complete sequence
                  167204
Seq. No.
Seq. ID
                  LIB3234-022-P1-K1-H5
Method
                  BLASTX
                  g112682
NCBI GI
```

449

BLAST score

```
E value
                  6.0e-45
Match length
                  91
                  92
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana) >gi_808937_emb_CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  167205
Seq. ID
                  LIB3234-022-P1-K1-H6
Method
                  BLASTN
NCBI GI
                  q1865682
BLAST score
                  81
E value
                  7.0e-38
Match length
                  148
% identity
                  89
NCBI Description A.thaliana 16 kb chromosome 1 DNA fragment
                  167206
Seq. No.
Seq. ID
                  LIB3234-022-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  q2618604
BLAST score
                  259
E value
                  1.0e-144
Match length
                  263
                  65
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167207
Seq. ID
                  LIB3234-025-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3746809
                  309
BLAST score
                  9.0e-29
E value
Match length
                  65
% identity
                  92
                  (AF082882) adenylate kinase [Arabidopsis thaliana]
NCBI Description
                  167208
Seq. No.
Seq. ID
                  LIB3234-025-P1-K1-A12
Method
                  BLASTN
                  g2262097
NCBI GI
                  40
BLAST score
E value
                  4.0e-13
Match length
                  152
% identity
                  91
                  Arabidopsis thaliana chromosome IV BAC T19F6 genomic
NCBI Description
                  sequence, complete sequence
                  167209
Seq. No.
Seq. ID
                  LIB3234-025-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  q4510392
BLAST score
                  40
                  1.0e-13
E value
```

```
Match length
                   64
 % identity
                   91
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC T17D12 genomic
                   sequence, complete sequence
 Seq. No.
Seq. ID
                   167210
                   LIB3234-025-P1-K1-A4
 Method
                   BLASTX
 NCBI GI
                   g4468813
 BLAST score
                   268
 E value
                   1.0e-23
Match length
                   111
 % identity
                   49
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                   167211
Seq. ID
                   LIB3234-025-P1-K1-A6
Method
                   BLASTN
NCBI GI
                   g4165340
BLAST score
                   37
E value
                   2.0e-11
Match length
                   53
% identity
                   92
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F11M15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167212
Seq. ID
                   LIB3234-025-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g2522534
BLAST score
                   154
                   2.0e-13
E value
Match length
                   113
% identity
                   45
NCBI Description
                  (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]
Seq. No.
                   167213
Seq. ID
                  LIB3234-025-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2342674
BLAST score
                   370
E value
                   1.0e-35
Match length
                   104
% identity
                   76
NCBI Description
                   (AC000106) Similar to ATP-dependent Clp protease
                   (gb_D90915). EST gb_N65461 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  167214
Seq. ID
                  LIB3234-025-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q3880026
BLAST score
                  141
E value
                  1.0e-08
Match length
                  72
% identity
NCBI Description
                  (275550) Similarity with Schizosaccharomyces hypothetical
```

Match length

386

```
this gene [Caenorhabditis elegans]
Seq. No.
                   167215
Seq. ID
                   LIB3234-025-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g3874214
BLAST score
                   310
E value
                   2.0e-28
Match length
                   122
% identity
                   53
NCBI Description
                  (Z83217) Similarity to Yeast E1-E2 ATPase YELO31W
                   (SW:YED1_YEAST); cDNA EST EMBL:D27574 comes from this gene;
                   cDNA EST EMBL: D33757 comes from this gene; cDNA EST
                   EMBL: D34256 comes from this gene; cDNA EST EMBL: D37288
                   comes from
Seq. No.
                   167216
Seq. ID
                   LIB3234-025-P1-K1-B6
Method
                   BLASTN
NCBI GI
                   g2584827
BLAST score
                   272
E value
                   1.0e-151
Match length
                   336
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                   167217
Seq. ID
                  LIB3234-025-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1255448
BLAST score
                  638
E value
                  6.0e-67
Match length
                  130
% identity
                  96
NCBI Description
                  (D50468) mitogen-activated protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  167218
Seq. ID
                  LIB3234-025-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  224
                  1.0e-123
E value
Match length
                  364
% identity
                  90
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167219
Seq. ID
                  LIB3234-025-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g4589438
BLAST score
                  251
E value
                  1.0e-139
```

gene (TREMBL ID G847708); cDNA EST EMBL:M89418 comes from

```
99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQJ2, complete sequence
Seq. No.
                  167220
Seq. ID
                  LIB3234-025-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g3241920
BLAST score
                  193
                  1.0e-104
E value
Match length
                  221
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167221
Seq. ID
                  LIB3234-025-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g4757401
BLAST score
                  286
E value
                  1.0e-160
Match length
                  341
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGH6, complete sequence
Seq. No.
                  167222
Seq. ID
                  LIB3234-025-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g3510247
BLAST score
                  152
E value
                  3.0e-80
                  172
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F19D11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167223
Seq. No.
Seq. ID
                  LIB3234-025-P1-K1-C7
                  BLASTX
Method
NCBI GI
                  g4115362
BLAST score
                  211
E value
                  3.0e-39
                  116
Match length
% identity
                  69
NCBI Description (AC005957) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  167224
Seq. ID
                  LIB3234-025-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g120675
BLAST score
                  480
                  2.0e-48
E value
                  110
Match length
                  83
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
```

```
alba]
                  167225
Seq. No.
                  LIB3234-025-P1-K1-D10
Seq. ID
Method
                  BLASTN
                  g1050427
NCBI GI
                  344
BLAST score
                  0.0e + 00
E value
                  348
Match length
                  100
% identity
NCBI Description A.thaliana mRNA for an exon from SNAP25A protein
                  167226
Seq. No.
                  LIB3234-025-P1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4490732
                  482
BLAST score
                  1.0e-48
E value
                  114
Match length
                  82
% identity
                  (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                protein [Arabidopsis thaliana]
                                                                 ж.
                  167227
Seq. No.
                  LIB3234-025-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1168410
BLAST score
                  414
                  1.0e-40
E value
Match length
                  118
% identity
                  71
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2
NCBI Description
                  >gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi_927505_emb_CAA61947_ (X89829)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
Seq. No.
                  167228
                  LIB3234-025-P1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  138
E value
                  1.0e-71
Match length
                  281
                  83
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  167229
                  LIB3234-025-P1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2196463
BLAST score
                  287
                  1.0e-160
E value
Match length
                  323
% identity
                  97
```

dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >qi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis

...

Seq. No.

```
NCBI Description Arabidopsis thaliana chloroplast trnC, rpoB & rpoCl genes
Seq. No.
                  167230
                  LIB3234-025-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129641
BLAST score
                  552
                  7.0e-57
E value
Match length
                  101
% identity
                  100
                 major latex protein type 1 - Arabidopsis thaliana
NCBI Description
                  >gi 1107493 emb CAA63026 (X91960) major latex protein
                  typel [Arabidopsis thaliana]
Seq. No.
                  167231
Seq. ID
                  LIB3234-025-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g2342727
BLAST score
                  410
E value
                  3.0e-40
Match length
                  106
% identity
NCBI Description (AC002341) hypothetical protein [Arabidopsis thaliana]
                 167232
Seq. No.
                  LIB3234-025-P1-K1-D7
Seq. ID
Method
                 BLASTN
NCBI GI
                  g4159712
BLAST score
                  170
E value
                  1.0e-90
Match length
                  282
                  91
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
Seq. No.
                  167233
                  LIB3234-025-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1592677
                  220
BLAST score
                  6.0e-18
E value
Match length
                  103
% identity
                  48
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.
                  167234
Seq. ID
                  LIB3234-025-P1-K1-E1
Method
                  BLASTN
NCBI GI
                  q4159712
BLAST score
                  146
                  2.0e-76
E value
Match length
                  202
% identity
                  96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                 MWI23, complete sequence
```

Match length

```
Seq. ID
                  LIB3234-025-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q4056500 ·
                  217
BLAST score
                  1.0e-17
E value
Match length
                  43
                  100
% identity
                  (AC005896) putative acetyltransferase [Arabidopsis
NCBI Description
Seq. No.
                  167236
Seq. ID
                  LIB3234-025-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q1345973
BLAST score
                  274
E value
                  2.0e-24
Match length
                  81
% identity
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.1\overline{4.99.-} CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  167237
Seq. ID
                  LIB3234-025-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g2623294
BLAST score
                  169
E value
                  4.0e-90
Match length
                  257
% identity
                  92
                  Arabidopsis thaliana chromosome II BAC T20B5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167238
Seq. No.
Seq. ID
                  LIB3234-025-P1-K1-E3
                  BLASTX
Method
NCBI GI
                  g2494131
BLAST score
                  591
E value
                  2.0e-61
Match length
                  121
% identity
                  98
                  (AC002376) Strong similarity to Lycopersicon aldehyde
NCBI Description
                  oxidase (gb U82559). [Arabidopsis thaliana]
                  167239
Seq. No.
                  LIB3234-025-P1-K1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4263704
BLAST score
                  267
                  2.0e-23
E value
```

Match length

```
55
% identity
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
                   167240
Seq. No.
Seq. ID
                   LIB3234-025-P1-K1-E6
Method
                   BLASTN
                   q16171
NCBI GI
BLAST score
                   33
E value
                   6.0e-09
Match length
                   381
% identity
                   36
NCBI Description Arabodopsis thaliana tandemly repeated sequence AR3
                   167241
Seq. No.
                   LIB3234-025-P1-K1-E8
Seq. ID
Method
                   BLASTN
                   g2351071
NCBI GI
                   147
BLAST score
                   5.0e-77
E value
Match length
                   368
                   95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MVA3, complete sequence [Arabidopsis thaliana]
                   167242
Seq. No.
Seq. ID
                   LIB3234-025-P1-K1-F1
Method
                   BLASTX
                   g2129641
NCBI GI
                   338
BLAST score
                   5.0e-45
E value
                   90
Match length
% identity
                   99
                   major latex protein type 1 - Arabidopsis thaliana
NCBI Description
                   >gi_1107493_emb_CAA63026_ (X91960) major latex protein
                   typel [Arabidopsis thaliana]
                   167243
Seq. No.
Seq. ID
                   LIB3234-025-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g1362026
BLAST score
                   501
E value
                   7.0e-51
Match length
                   97
                   98
% identity
                   probable serine/threonine-specific protein kinase (EC
NCBI Description
                   2.7.1.-) BSK1 - rape >gi_289372 (L12393) serine/threonine protein kinase [Brassica napus] >gi_1097353_prf__2113401A
                   protein kinase [Brassica napus]
                   167244
Seq. No.
Seq. ID
                   LIB3234-025-P1-K1-F11
Method
                   BLASTN
NCBI GI
                   q12216
BLAST score
                   84
E value
                   2.0e-39
```

```
% identity
NCBI Description Sinapis alba chloroplast rps16 gene
                  167245
Seq. No.
                  LIB3234-025-P1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4159708
                  49
BLAST score
                  1.0e-18
E value
Match length
                  156
% identity
                  88
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MKP6, complete sequence
                  167246
Seq. No.
                  LIB3234-025-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  q902584
NCBI GI
                  478
BLAST score
                  3.0e-48
E value
                  99
Match length
% identity
                  14
NCBI Description
                  (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea
                  mays]
                  167247
Seq. No.
                  LIB3234-025-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3252816
BLAST score
                  345
E value
                  1.0e-32
Match length
                  107
% identity
                   66
                   (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3810589 (AC005398) hypothetical protein [Arabidopsis
                  thaliana]
Seq. No.
                  167248
                  LIB3234-025-P1-K1-F6
Seq. ID
Method
                  BLASTX
                  g3318617
NCBI GI
BLAST score
                  362
E value
                  1.0e-34
Match length
                  80
% identity
                  86
                   (AB016066) mitochondrial phosphate transporter [Arabidopsis
NCBI Description
                  thaliana]
                  167249
Seq. No.
                  LIB3234-025-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618604
BLAST score
                  167
E value
                   6.0e-89
Match length
                  182
% identity
                  98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
```

Method

BLASTN

```
MTG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167250
                  LIB3234-025-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244772
BLAST score
                  578
                  6.0e-60
E value
Match length
                  104
% identity
                  99
NCBI Description (297335) transport protein [Arabidopsis thaliana]
Seq. No.
                  167251
                  LIB3234-025-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006934
BLAST score
                  546
E value
                  4.0e-56
Match length
                  109
% identity
                  95
NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                  167252
Seq. ID
                  LIB3234-025-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  q4757395
BLAST score
                  235
                  î.0e-129
E value
Match length
                  310
% identity
                  94
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21L13, complete sequence
Seq. No.
                  167253
Seq. ID
                  LIB3234-025-P1-K1-G2
                  BLASTN
Method
NCBI GI
                  g4662637
BLAST score
                  95
                  6.0e-46
E value
Match length
                  222
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC T25M19 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  167254
Seq. ID
                  LIB3234-025-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q166570
BLAST score
                  165
                  1.0e-11
E value
Match length
                  31
                  97
% identity
NCBI Description (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                  167255
Seq. ID
                  LIB3234-025-P1-K1-G7
```

E value

2.0e-28

```
NCBI GI
                  g2735774
                   39
BLAST score
                  8.0e-13
E value
Match length
                  115
% identity
                  83
NCBI Description
                  Corallocarpus bainesii 18S ribosomal RNA gene, complete
                  sequence
Seq. No.
                  167256
Seq. ID
                  LIB3234-025-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  q3063438
BLAST score
                  333
                  0.0e + 00
E value
                  369
Match length
% identity
NCBI Description
                  Complete sequence of Arabidopsis F22013, complete sequence
                   [Arabidopsis thaliana]
                  167257
Seq. No.
Seq. ID
                  LIB3234-025-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  g4262221
BLAST score
                  39
                  1.0e-12
E value
Match length
                  63
                  90
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F10A8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167258
Seq. ID
                  LIB3234-025-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2262113
BLAST score
                  437
E value
                  2.0e-43
Match length
                  129
% identity
                  68
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167259
                  LIB3234-025-P1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449331
BLAST score
                  47
E value
                  2.0e-17
Match length
                  154
% identity
                  83
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167260
Seq. ID
                  LIB3234-025-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q2160158
BLAST score
                  309
```

BLAST score

```
62
Match length
                     98
% identity
                     (ACO00132) Similar to elongation factor 1-gamma
NCBI Description
                     (gb_EF1G_XENLA). ESTs gb_T20564, gb T45940, gb T04527 come
                     from this gene. [Arabidopsis thaliana]
Seq. No.
                    167261
Seq. ID
                    LIB3234-025-P1-K1-H3
                    BLASTX
Method
NCBI GI
                    g1542941
BLAST score
                    207
                    2.0e-16
E value
                    106
Match length
% identity
                     41
NCBI Description
                    (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
                    167262
Seq. No.
Seq. ID
                    LIB3234-025-P1-K1-H5
Method
                    BLASTX
NCBI GI
                    g135535
BLAST score
                    350
                    2.0e-33
E value
                     91
Match length
                    76
% identity
                    T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
NCBI Description
                    (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide
Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_
(D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                    alpha/TCP-1 [Arabidopsis thaliana]
                    167263
Seq. No.
Seq. ID
                    LIB3234-026-Q1-K1-A1
                    BLASTX
Method
NCBI GI
                    g1419090
BLAST score
                    210
                    6.0e-17
E value
                    93
Match length
                    47
% identity
                    (X94968) 37kDa chloroplast inner envelope membrane
NCBI Description
                    polypeptide precursor [Nicotiana tabacum]
                    167264
Seq. No.
Seq. ID
                    LIB3234-026-Q1-K1-A10
                    BLASTX
Method
NCBI GI
                    g541847
BLAST score
                    539
                    2.0e-55
E value
                    103
Match length
                    97
% identity
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
Seq. No.
                    167265
Seq. ID
                    LIB3234-026-Q1-K1-A11
Method
                    BLASTX
NCBI GI
                    g1429213
```

BLAST score

```
E value
                  6.0e-63
                  118
Match length
                  99
% identity
                  (X98773) peroxidase ATP4a [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167266
Seq. ID
                  LIB3234-026-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q136739
BLAST score
                  308
E value
                  3.0e-28
Match length
                  97
                  64
% identity
NCBI Description
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir_ XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
                  167267
Seq. No.
Seq. ID
                  LIB3234-026-Q1-K1-A2
Method
                  BLASTN
NCBI GI
                  q3510341
BLAST score
                  319
E value
                  1.0e-179
Match length
                  363
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC16, complete sequence [Arabidopsis thaliana]
                  167268
Seq. No.
Seq. ID
                  LIB3234-026-Q1-K1-A8
Method
                  BLASTN
NCBI GI
                  g4587582
                  53
BLAST score
                  4.0e-21
E value
Match length
                  188
% identity
                  Arabidopsis thaliana chromosome II BAC T16B14 genomic
NCBI Description
                  sequence, complete sequence
                  167269
Seq. No.
Seq. ID
                  LIB3234-026-Q1-K1-B10
                  BLASTN
Method
NCBI GI
                  g4519190
BLAST score
                  232
E value
                  1.0e-128
                  345
Match length
% identity
                  92
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K6A12, complete sequence
                  167270
Seq. No.
Seq. ID
                  LIB3234-026-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2980787
```

```
E value
                       1.0e-52
   Match length
                       268
... % identity
                       91
                       Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
   NCBI Description
                       (ESSAII project)
   Seq. No.
                       167271
   Seq. ID
                       LIB3234-026-Q1-K1-B6
   Method
                       BLASTN
   NCBI GI
                       q3738275
   BLAST score
                       237
   E value
                       1.0e-130
   Match length
                       348
   % identity
   NCBI Description
                      Arabidopsis thaliana chromosome II BAC F17A22 genomic
                       sequence, complete sequence [Arabidopsis thaliana]
   Seq. No.
                       167272
   Seq. ID
                       LIB3234-026-Q1-K1-C1
  Method
                       BLASTN
   NCBI GI
                       q4567290
   BLAST score
                       54
   E value
                       2.0e-21
                    .- 102
  Match length
                       64
   % identity
  NCBI Description Arabidopsis thaliana chromosome II BAC F18P14 genomic
                       sequence, complete sequence
  Seq. No.
                       167273
  Seq. ID
                       LIB3234-026-Q1-K1-C11
  Method
                      BLASTX
  NCBI GI
                       g1170839
  BLAST score
                       567
  E value
                       1.0e-58
  Match length
                      120
  % identity
                       93
                      LOW-TEMPERATURE-INDUCED 65 KD PROTEIN
  NCBI Description
                      >gi_419758 pir__S30153 low-temperature-induced protein 65 -
                      Arabidopsis thaliana >gi_16388_emb_CAA47902_ (X67670) lti65
                       [Arabidopsis thaliana]
  Seq. No.
                      167274
  Seq. ID
                      LIB3234-026-Q1-K1-C3
  Method
                      BLASTX
  NCBI GI
                      g418473
  BLAST score
                      385
  E value
                      3.0e-37
  Match length
                      119
  % identity
                      60
  NCBI Description
                      GTP-BINDING PROTEIN TYPA/BIPA (TYROSINE PHOSPHORYLATED
                      PROTEIN A) >gi_628735_pir__S40816 hypothetical protein o591 - Escherichia coli >gi_304976 (L19201) matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar to elongation
                      factor G, TetM/TetO tetracycline-resistance proteins
                      [Escherichia coli] >gi_1790302 (AE000462) putative
```

GTP-binding factor [Escherichia coli]

BLAST score

```
Seq. No.
                  167275
Seq. ID
                  LIB3234-026-Q1-K1-C7
Method
                  BLASTN
                                                             3.
NCBI GI
                  g2584827
BLAST score
                   266
E value
                  1.0e-148
Match length
                   336
% identity
                   97
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167276
Seq. ID
                  LIB3234-026-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q4584528
BLAST score
                   418
E value
                  3.0e-41
Match length
                  120
% identity
                  72
NCBI Description (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                  167277
Seq. ID
                  LIB3234-026-Q1-K1-C9
Method
                  BLASTN
NCBI GI
                  g16450
BLAST score
                  50
E value
                  4.0e-19
Match length
                  204
                  89
% identity
NCBI Description A.thaliana rab18 gene
Seq. No.
                  167278
Seq. ID
                  LIB3234-026-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4678205
BLAST score
                  99
E value
                  4.0e-43
Match length
                  116
% identity
NCBI Description
                 (AC007134) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  167279
Seq. ID
                  LIB3234-026-Q1-K1-D10
Method
                  BLASTN
NCBI GI
                  g511598
BLAST score
                  89
E value
                  2.0e-42
Match length
                  263
% identity
NCBI Description
                  Arabidopsis thaliana cell wall protein (APTR-1) gene,
                  complete cds
Seq. No.
                  167280
Seq. ID
                  LIB3234-026-Q1-K1-D11
Method
                  BLASTN
NCBI GI
                  g4199934
```

Method

NCBI GI

BLASTN

g4757417

```
E value
                   1.0e-172
Match length
                   362
% identity
                   89
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC T3P18,
                   complete sequence [Arabidopsis thaliana]
                   167281
Seq. No.
Seq. ID
                   LIB3234-026-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   g462147
BLAST score
                   99
E value
                   2.0e-53
Match length
                   120
% identity
                   GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                   (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase (EC 5.3.1.9) - Arabidopsis thaliana
                   >gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate
                   isomerase [Arabidopsis thaliana]
Seq. No.
                   167282
Seq. ID
                   LIB3234-026-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   q2117612
BLAST score
                   483
E value
                   8.0e-49
Match length
                   108
% identity
                   88
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
Seq. No.
                   167283
Seq. ID
                   LIB3234-026-Q1-K1-D3
Method
                   BLASTN
NCBI GI
                   g4220468
BLAST score
                   185
E value
                   1.0e-99
Match length
                   339
% identity
                   94
                  Arabidopsis thaliana chromosome II BAC T8011 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167284
Seq. ID
                   LIB3234-026-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g2435522
BLAST score
                   178
E value
                   4.0e-13
Match length
                   77
% identity
                   44
NCBI Description
                   (AF024504) contains similarity to other AMP-binding enzymes
                   [Arabidopsis thaliana]
Seq. No.
                   167285
Seq. ID
                   LIB3234-026-Q1-K1-D7
```

NCBI GI

```
BLAST score
                   39
E value
                   9.0e-13
Match length
                   94
                   94
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  T30G6, complete sequence
Seq. No.
                  167286
Seq. ID
                  LIB3234-026-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g133750
BLAST score
                   477
                  4.0e-48
E value
Match length
                  95
                  97
% identity
NCBI Description
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
                  >gi_320170_pir__A26574 ribosomal protein S12 - soybean
                  chloroplast >gi_11572_emb_CAA28661_ (X05013) rps12 [Glycine
Seq. No.
                  167287
Seq. ID
                  LIB3234-026-Q1-K1-E10
Method
                  BLASTN
                  g2264306
NCBI GI
BLAST score
                   34
                  1.0e-09
E value
Match length
                  159
% identity
                  84
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167288
Seq. ID
                  LIB3234-026-Q1-K1-E12
Method
                  BLASTN
NCBI GI
                  q4159708
BLAST score
                  150
E value
                  5.0e-79
Match length
                  182
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MKP6, complete sequence
Seq. No.
                  167289
Seq. ID
                  LIB3234-026-Q1-K1-E2
Method
                  BLASTN
NCBI GI
                  g4220640
BLAST score
                  108
E value
                  1.0e-53
                  308
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPE11, complete sequence [Arabidopsis thaliana]
                  167290
Seq. No.
Seq. ID
                  LIB3234-026-Q1-K1-E4
Method
                  BLASTX
```

g3193222

Seq. No.

```
BLAST score
                   171
E value
                   3.0e-12
Match length
                   65
                   72
% identity
NCBI Description
                   (AF068687) malate dehydrogenase [Glycine max]
                   167291
Seq. No.
Seq. ID
                   LIB3234-026-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   q4138179
BLAST score
                   452
E value
                   4.0e-45
Match length
                   92
                   93
% identity
NCBI Description
                   (AJ223969) elongation factor 1 alpha subunit [Malus
                   domestica]
Seq. No.
                   167292
Seq. ID
                   LIB3234-026-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   g119350
BLAST score
                   276
E value
                   1.0e-24
Match length
                   72
                   78
% identity
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                   thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                   [Arabidopsis thaliana]
                   >gi_4581151_gb_AAD24635.1 AC006919 13 (AC006919) enolase
                   (2-phospho-D-glycerate hydroylase); identical to P25696
                   [Arabidopsis thaliana]
                   167293
Seq. No.
Seq. ID
                   LIB3234-026-Q1-K1-F10
Method
                   BLASTN
NCBI GI
                   g2275194
BLAST score
                   242
E value
                   1.0e-134
                   307
Match length
                   98
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T08I13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167294
Seq. ID
                   LIB3234-026-Q1-K1-F3
Method
                   BLASTN
NCBI GI
                   q4159705
BLAST score
                   73
E value
                   5.0e-33
                   244
Match length
                   83
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MGD8, complete sequence
```

NCBI GI

```
Seq. ID
                   LIB3234-026-Q1-K1-F6
Method
                   BLASTX
                   g3327204
NCBI GI
BLAST score
                   271
E value
                   5.0e-24
Match length
                  - 106
% identity
                   57
NCBI Description (AB014595) KIAA0695 protein [Homo sapiens]
Seq. No.
                   167296
Seq. ID
                   LIB3234-026-Q1-K1-F7
Method
                   BLASTN
NCBI GI
                   g1800278
BLAST score
                   55
                   3.0e-22
E value
Match length
                   184
% identity
                   86
NCBI Description
                  Arabidopsis thaliana putative Cys3His zinc finger protein
                   (ATCTH) mRNA, complete cds
Seq. No.
                   167297
Seq. ID
                  LIB3234-026-Q1-K1-G11
Method
                   BLASTN
NCBI GI
                   q4096078
BLAST score
                   86
E value
                   9.0e-41
Match length
                   224
% identity
                  84
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167298
Seq. ID
                  LIB3234-026-Q1-K1-G6
Method
                  BLASTX
                  q1170149
NCBI GI
BLAST score
                  200
E value
                  1.0e-15
Match length
                  104
% identity
                  64
NCBI Description HEAT SHOCK PROTEIN 101 >gi 537446 (U13949) AtHSP101
                  [Arabidopsis thaliana]
Seq. No.
                  167299
Seq. ID
                  LIB3234-026-Q1-K1-H10
Method
                  BLASTN
NCBI GI
                  g4757395
BLAST score
                  .183
E value
                  2.0e-98
Match length
                  369
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21L13, complete sequence
Seq. No.
                  167300
Seq. ID
                  LIB3234-026-Q1-K1-H11
Method
                  BLASTX
```

g4510349

NCBI Description

```
BLAST score
                   167
                   1.0e-11
E value
Match length
                   74
% identity
                   62
NCBI Description
                  (AC006921) putative bZIP transcription factor [Arabidopsis
                   thaliana]
                   167301
Seq. No.
Seq. ID
                   LIB3234-026-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                   567
E value
                  1.0e-58
Match length
                  109
% identity
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  167302
Seq. ID
                  LIB3234-026-Q1-K1-H2
Method
                  BLASTN
NCBI GI
                  q3386593
BLAST score
                  133
E value
                  1.0e-68
Match length
                  326
% identity
                  87
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167303
Seq. ID
                  LIB3234-026-Q1-K1-H7
Method
                  BLASTX
                  q4371279
NCBI GI
BLAST score
                  136
                  1.0e-08
E value
Match length
                  46
% identity
                  61
NCBI Description
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  167304
Seq. ID
                  LIB3234-030-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  g2262097
BLAST score
                  190
E value
                  1.0e-102
Match length
                  357
% identity
                  89
```

sequence, complete sequence

Arabidopsis thaliana chromosome IV BAC T19F6 genomic

```
Seq. No.
                   167305
Seq. ID
                   LIB3234-030-P1-K1-A10
Method
                   BLASTX
NCBI GI
                    g4406787
BLAST score
                    525
                    1.0e-53
E value
Match length
                    103
% identity
                    99
NCBI Description (AC006532) NADH dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   167306
Seq. ID
                   LIB3234-030-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2947060
BLAST score
                   477
E value
                    4.0e-48
Match length
                   102
% identity
                    81
NCBI Description (AC002521) putative membrane protein [Arabidopsis thaliana]
Seq. No.
                   167307
Seq. ID
                   LIB3234-030-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q3281868
BLAST score
                   645
                   8.0e-68
E value
Match length
                  - 124
% identity
                   98
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
                   167308
Seq. No.
Seq. ID
                   LIB3234-030-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g114532
BLAST score
                   561
                   6.0e-58
E value
Match length
                   125
% identity
                   90
NCBI Description ATP SYNTHASE ALPHA CHAIN >gi_67824_pir__PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain -
                   common tobacco chloroplast >gi 11769 emb CAA23471 (V00162)
                   alpha subunit of ATPase [Nicot\overline{i}ana tabacum]
                   >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit
[Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha
                    [Nicotiana tabacum]
Seq. No.
                   167309
Seq. ID
                   LIB3234-030-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g131164
BLAST score
                   163
E value
                   3.0e-11
Match length
                   48
                   67
% identity
NCBI Description PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT
                   VII) (9 KD POLYPEPTIDE) (PSI-C) >gi_65727_pir__FERZA
```

photosystem I iron-sulfur protein psaC - rice chloroplast

```
>gi_65728_pir__FEWT1 photosystem I iron-sulfur protein psaC
- wheat chloroplast >gi_12051_emb_CAA33954_ (X15901) PSI
9kDa protein [Oryza sativa] >gi_12350_emb_CAA31555_
(X13158) photosystem I 8 kDa subunit [Triticum aestivum]
>gi_167038 (L06607) photosystem I subunit C [Hordeum
vulgare] >gi_4150873_emb_CAA09816_ (AJ011848) PSI 9 kDa
protein [Hordeum vulgare] >gi_226558_prf__1601522B
photosystem I 8kD protein [Triticum aestivum]
>gi_226671_prf__1603356CY photosystem I 9kD protein [Oryza
sativa]
```

```
Seq. No.
                   167310
Seq. ID
                   LIB3234-030-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   q2781345
BLAST score
                   507
E value
                   2.0e-51
Match length
                   133
% identity
                   75
NCBI Description
                  (AC003113) F2401.2 [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3234-030-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2213607
BLAST score
                   273
E value
                   4.0e-24
```

NCBI Description (AC000103) F21J9.1 [Arabidopsis thaliana]

 Seq. No.
 167312

 Seq. ID
 LIB3234-030-P1-K1-B4

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 102

 F makes
 102

108

60

BLAST score 102 E value 1.0e-28 Match length 92 % identity 80

Match length

% identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 167313

Seq. ID LIB3234-030-P1-K1-B6

Method BLASTN
NCBI GI g4415905
BLAST score 60
E value 4.0e-25

Match length 290 % identity 79

NCBI Description Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167314

Seq. ID LIB3234-030-P1-K1-C12

Method BLASTX

Method

BLASTX

```
NCBI GI
                   q82232
BLAST score
                   530
E value
                   3.0e-54
Match length
                   125
% identity
                   83
NCBI Description
                  rpoC protein homolog - common tobacco chloroplast
Seq. No.
                   167315
Seq. ID
                  LIB3234-030-P1-K1-C2
Method
                  BLASTN
NCBI GI
                   q4757401
BLAST score
                   174
                   4.0e-93
E value
Match length
                   218
% identity
                   95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGH6, complete sequence
Seq. No.
                  167316
Seq. ID
                  LIB3234-030-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  q4220635
                   52
BLAST score
                   3.0e-20
E value
Match length
                  254
% identity
                  81
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167317
Seq. ID
                  LIB3234-030-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  72
                  5.0e-57
E value
Match length
                  125
                  94
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  167318
Seq. ID
                  LIB3234-030-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  q3985958
BLAST score
                  151
                  1.0e-79
E value
                  203
Match length
                  94
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
                  167319
Seq. No.
                  LIB3234-030-P1-K1-D3
Seq. ID
```

Match length

```
NCBI GI
                   q3043536
BLAST score
                   175
E value
                   1.0e-12
Match length
                   79
% identity
                   53
NCBI Description
                  (AB000708) SAUR [Raphanus sativus]
Seq. No.
                   167320
Seq. ID
                   LIB3234-030-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g4104058
BLAST score
                   238
E value
                   5.0e-20
Match length
                   89
% identity
                   51
NCBI Description
                   (AF031195) blue copper-binding protein homolog [Triticum
                   aestivum]
                   167321
Seq. No.
Seq. ID
                  LIB3234-030-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g2342717
BLAST score
                   95
E value
                   6.0e-46
Match length.
                   350
% identity
                   93
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T14G11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167322
Seq. ID
                  LIB3234-030-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2342724
BLAST score
                  617
                  2.0e-64
E value
Match length
                  126
% identity
                  96
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167323
Seq. ID
                  LIB3234-030-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g2618602
BLAST score
                  49
                  2.0e-18
E value
Match length
                  182
                  87
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167324
Seq. ID
                  LIB3234-030-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g1169598
BLAST score
                  378
E value
                  2.0e-36
```

BLAST score

```
% identity
NCBI Description
                   OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                   (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                   desaturase [Arabidopsis thaliana]
Seq. No.
                   167325
                   LIB3234-030-P1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112682
BLAST score
                   349
E value
                   3.0e-33
Match length
                   81
% identity
                   84
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidops\overline{i}s thalian\overline{a}
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   167326
Seq. ID
                   LIB3234-030-P1-K1-F12
Method
                   BLASTN
NCBI GI
                   g4589437
BLAST score
                   257
E value
                   1.0e-142
Match length
                   378
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MPN9, complete sequence
Seq. No.
                   167327
Seq. ID
                   LIB3234-030-P1-K1-F3
Method
                   BLASTX
NCBI GI
                  g3738332
BLAST score
                   619
E value
                   1.0e-64
                   125
Match length
                   96
% identity
NCBI Description
                   (AC005170) putative eukaryotic initiation factor
                   [Arabidopsis thaliana]
Seq. No.
                   167328
                  LIB3234-030-P1-K1-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3282170
BLAST score
                   99
E value
                   2.0e-48
                   215
Match length
                   87
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F8K4 sequence,
                  complete sequence [Arabidopsis thaliana]
                  167329
Seq. No.
Seq. ID
                  LIB3234-030-P1-K1-G2
Method<sup>*</sup>
                  BLASTN
NCBI GI
                  g3510347
```

```
E value
                  8.0e-73
                  292
Match length
                  88
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167330
Seq. ID
                  LIB3234-030-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  517
E value
                  8.0e-53
Match length
                  104
                  95
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  167331
Seq. ID
                  LIB3234-030-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g2656031
BLAST score
                  281
E value
                  1.0e-157
Match length
                  354
                  95
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXC20
Seq. No.
                  167332
Seq. ID
                  LIB3234-033-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g4262250
BLAST score
                  373
                  6.0e-36
E value
Match length
                  74
% identity
                  100
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                  167333
Seq. ID
                  LIB3234-033-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1881585
BLAST score
                  201
E value
                  9.0e-16
Match length
                  104
% identity
                  48
NCBI Description (U72489) remorin [Solanum tuberosum]
Seq. No.
                  167334
Seq. ID
                  LIB3234-033-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  q3869068
BLAST score
                  200
E value
                  1.0e-108
Match length
                  321
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC16, complete sequence [Arabidopsis thaliana]
```

NCBI GI

```
Seq. No.
                   167335
Seq. ID
                  LIB3234-033-P1-K1-D10
Method
                  BLASTN
NCBI GI
                   g3047074
BLAST score
                   81
                   6.0e-38
E value
Match length
                   167
% identity
                   91
NCBI Description Arabidopsis thaliana BAC F21E10
Seq. No.
                   167336
                  LIB3234-033-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539459
BLAST score
                   177
                   6.0e-13
E value
Match length
                   47
% identity
                   60
NCBI Description
                  (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3234-033-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  q3831448
BLAST score
                  230
E value
                   1.0e-126
Match length
                   351
% identity
                   95
                  Arabidopsis thaliana chromosome II BAC T32F6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167338
Seq. ID
                  LIB3234-033-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2252828
BLAST score
                  489
E value
                  2.0e-49
                  106
Match length
% identity
                  91
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167339
Seq. ID
                  LIB3234-033-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  472
                  9.0e-48
E value
Match length
                  93
% identity
                  95
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  167340
Seq. ID
                  LIB3234-033-P1-K1-E4
Method
                  BLASTX
```

22598

q4185505

```
365
BLAST score
                   6.0e-35
E value
                  105
Match length
                  70
% identity
                   (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                   [Brassica napus]
                  167341
Seq. No.
Seq. ID
                  LIB3234-033-P1-K1-E6
                  BLASTN
Method
NCBI GI
                  q510237
BLAST score
                  43
                  2.0e-15
E value
Match length
                  152
                  80
% identity
NCBI Description Arabadopsis thaliana Landsberg NT1 mRNA
Seq. No.
                  167342
Seq. ID
                  LIB3234-033-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g4455262
BLAST score
                  48
                  1.0e-18
E value
Match length
                  76
% identity
                  91
                        .,....
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                   (ESSAII project)
Seq. No.
                  167343
Seq. ID
                  LIB3234-033-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  g3193282
BLAST score
                  63
                  7.0e-27
E value
                  195
Match length
                  84
% identity
NCBI Description Arabidopsis thaliana BAC T14P8
Seq. No.
                  167344
                  LIB3234-033-P1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3785968
                  75
BLAST score
                  4.0e-34
E value
Match length
                  147
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F2I9 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167345
Seq. No.
Seq. ID
                  LIB3234-033-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3335331
BLAST score
                  181
                  1.0e-97
E value
                  193
Match length
                  98
% identity
```





NCBI Description Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 167346

Seq. ID LIB3234-033-P1-K1-F9

Method BLASTX
NCBI GI g1107501
BLAST score 440
E value 8.0e-44
Match length 102
% identity 87

NCBI Description (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)

Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from

this gene. [Arabidopsis thaliana]

Seq. No. 167347

Seq. ID LIB3234-033-P1-K1-G10

Method BLASTN
NCBI GI 94559319
BLAST score 258
E value 1.0e-143
Match length 303
% identity 96

NCBI Description Arabidopsis thaliana chromosome II BAC F14N22 genomic

sequence, complete sequence

Seq. No. 167348

Seq. ID LIB3234-033-P1-K1-G12

Method BLASTX
NCBI GI g1345973
BLAST score 328
E value 2.0e-37
Match length 96
% identity 83

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 167349

Seq. ID LIB3234-033-P1-K1-G4

Method BLASTN
NCBI GI g4159712
BLAST score 60
E value 4.0e-25
Match length 132
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 167350

Method

BLASTX

```
LIB3234-033-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3243274
                  161
BLAST score
                  1.0e-11
E value
                 . 53
Match length
                  64
% identity
                 (AF072134) TCP3 [Arabidopsis thaliana]
NCBI Description
                  167351
Seq. No.
Seq. ID
                  LIB3234-033-P1-K1-H12
                  BLASTN
Method
NCBI GI
                  g4199934
BLAST score
                  265
                  1.0e-147
E value
                  354
Match length
                  91
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  167352
Seq. No.
Seq. ID
                  LIB3234-033-P1-K1-H3
                  BLASTX
Method
NCBI GI
                  g2894574
                              .
BLAST score
                  224
                  9.0e-19
E value
                  51
Match length
                  86
% identity
                  (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
NCBI Description
                  >gi 2961341 emb CAA18099.1 (AL022140) peroxidase prxr1
                  [Arabidopsis thaliana]
                  167353
Seq. No.
                  LIB3234-033-P1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3046853
                  205
BLAST score
                  1.0e-111
E value
                  269
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRA19, complete sequence [Arabidopsis thaliana]
                  167354
Seq. No.
Seg. ID
                  LIB3234-037-P1-K1-A10
Method
                  BLASTN
                  q4519195
NCBI GI
BLAST score
                  356
                  0.0e + 00
E value
                  363
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MQC12, complete sequence
Seq. No.
                  167355
Seq. ID
                  LIB3234-037-P1-K1-A11
```

Method

BLASTN

```
q419760
NCBI GI
                  574
BLAST score
                  2.0e-59
E value
                  121
Match length
% identity
                  52
                  P-glycoprotein atpgpl - Arabidopsis thaliana
NCBI Description
                  >gi 3849833 emb CAA43646 (X61370) P-glycoprotein
                   [Arabidopsis thaliana]
                  167356
Seq. No.
                  LIB3234-037-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  q2708741
NCBI GI
BLAST score
                  629
                  6.0e-66
E value
Match length
                  124
% identity
                  99
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167357
                  LIB3234-037-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q133750
BLAST score
                  209
                  9.0e-17
E value
Match length
                  78
% identity
                  60
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                  >gi 320170 pir A26574 ribosomal protein S12 - soybean
                  chloroplast >gi 11572 emb CAA28661 (X05013) rps12 [Glycine
                  max]
                  167358
Seq. No.
Seq. ID
                  LIB3234-037-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2315140
BLAST score
                  374
                  5.0e-36
E value
                  76
Match length
                  93
% identity
                   (AB006187) S-adenosylmethionine synthase [Nicotiana
NCBI Description
                  tabacum]
                  167359
Seq. No.
                  LIB3234-037-P1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832674
BLAST score
                  210
                  5.0e-17
E value
                  80
Match length
                  64
% identity
                   (AL021712) fibrillin precursor-like protein [Arabidopsis
NCBI Description
                  thaliana)
                  167360
Seq. No.
Seq. ID
                  LIB3234-037-P1-K1-B1
```

```
NCBI GI
                  g4159712
BLAST score
                  60
                  3.0e-25
E value
Match length
                  172
% identity
                  84
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWI23, complete sequence
Seq. No.
                  167361
                  LIB3234-037-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1666171
BLAST score
                  295
                  1.0e-29
E value
Match length
                  91
% identity
                  69
                 (Y09105) unknown [Nicotiana plumbaginifolia]
NCBI Description
Seq. No.
                  167362
Seq. ID
                  LIB3234-037-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g4191771
BLAST score
                  119
E value
                  3.0e-60
Match length
                 . 292
% identity
                  88
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3P11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167363
Seq. ID
                  LIB3234-037-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  g2961335
BLAST score
                  33
E value
                  3.0e-09
Match length
                  41
% identity
                  95
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20
                  (ESSAII project)
Seq. No.
                  167364
Seq. ID
                  LIB3234-037-P1-K1-B6
Method
                  BLASTN
                  g2244950
NCBI GI
                  137
BLAST score
E value
                  4.0e-71
Match length
                  291
                  87
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  167365
Seq. ID
                  LIB3234-037-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g3549651
BLAST score
                  63
```

7.0e-27

E value

Seq. No.

```
177
Match length
                  88
% identity.
NCBI Description Arabidopsis thaliana MAP3K epsilon gene
                  167366
Seq. No.
                  LIB3234-037-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  q4376233
NCBI GI
                  327
BLAST score
                  2.0e-30
E value
Match length
                  65
% identity
                  94
NCBI Description (X00798) L2 protein [Nicotiana debneyi]
                  167367
Seq. No.
                  LIB3234-037-P1-K1-C1
Seq. ID
                  BLASTX
Method
                  g2914703
NCBI GI
                  623
BLAST score
                  4.0e-65
E value
Match length
                  132
% identity
                  64
NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]
                  167368
Seq. No.
                  LIB3234-037-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  g1546694
NCBI GI
                  250
BLAST score
                  2.0e-21
E value
                  57
Match length
% identity
                  88
NCBI Description (X98806) peroxidase ATP20a [Arabidopsis thaliana]
                  167369
Seq. No.
Seq. ID
                  LIB3234-037-P1-K1-C5
                  BLASTX
Method
                  g4582468
NCBI GI
                434
BLAST score
                  5.0e-43
E value
                  95
Match length
                  94
% identity
                  (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
                  167370
Seq. No.
Seq. ID
                  LIB3234-037-P1-K1-C7
Method
                  BLASTN
                  g4559375
NCBI GI
                  133
BLAST score
                  1.0e-68
E value
                  265
Match length
                  98
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic
                  sequence, complete sequence
```

NCBI GI

```
Seq. ID
                  LIB3234-037-P1-K1-D1
Method ·
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  338
E value
                  9.0e-32
                  77
Match length
% identity
                  83
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                  167372
Seq. No.
Seq. ID
                  LIB3234-037-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g3241927
BLAST score
                  341
                  0.0e + 00
E value
Match length
                  365
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167373
Seq. ID
                  LIB3234-037-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g2570223
BLAST score
                  40
                  3.0e-13
E value
Match length
                  86
% identity
                  86
                  Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167374
Seq. ID
                  LIB3234-037-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  q4580745
BLAST score
                  136
                  2.0e-70
E value
                  283
Match length
% identity
                  89
                  Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
NCBI Description
                  complete sequence
Seq. No.
                  167375
Seq. ID
                  LIB3234-037-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  g4589410
BLAST score
                  37
                  2.0e-11
E value
Match length
                  119
% identity
                  88
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F2015, complete sequence
                  167376
Seq. No.
Seq. ID
                  LIB3234-037-P1-K1-D9
Method
                  BLASTN
```

g3128136

Seq. ID

Method

NCBI GI

```
310
BLAST score
                   1.0e-174
E value
Match length
                   366
                   96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K1F13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167377
Seq. ID
                   LIB3234-037-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g2827139
BLAST score
                   244
E value
                   8.0e-21
Match length
                   105
% identity
                   50
NCBI Description
                   (AF027172) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana] >gi 4049343_emb_CAA22568_
                   cellulose synthase catalytic subunit (RSW1) [Arabidopsis
                   thaliana]
Seq. No.
                   167378
Seq. ID
                   LIB3234-037-P1-K1-E2
Method
                   BLASTN
NCBI GI
                   q2924652
BLAST score
                   42
                   2.0e-14
E value
Match length
                   172
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9L2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167379
Seq. ID
                  LIB3234-037-P1-K1-E5
Method
                  BLASTN
NCBI GI
                   q3985957
BLAST score
                   260
                   1.0e-144
E value
Match length
                   352
% identity
                   93
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167380
Seq. ID
                  LIB3234-037-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  q4063756
BLAST score
                  122
E value
                   4.0e-62
Match length
                  214
% identity
                  89
                  Arabidopsis thaliana chromosome II BAC T9F8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167381
```

LIB3234-037-P1-K1-E8

BLASTN

g4580745

E value

5.0e-14

```
52
BLAST score
                   2.0e-20
E value
Match length
                   264
% identity
                   80
NCBI Description
                   Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
                   complete sequence
Seq. No.
                   167382
Seq. ID
                   LIB3234-037-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   g1785673
BLAST score
                   75
E value
                   3.0e - 34
Match length
                   202
% identity
                   81
NCBI Description A.thaliana mitochondrial genome, part A
Seq. No.
                   167383
Seq. ID
                   LIB3234-037-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g2454182
BLAST score
                   559
E value
                   1.0e-57
Match length
                   124
% identity
                   89
                   (U80185) pyruvate dehydrogenase El alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
                   167384
Seq. No.
                   LIB3234-037-P1-K1-F11
Seq. İD
Method
                   BLASTX
NCBI GI
                   q91152
BLAST score
                   198
                   2.0e-15
E value
Match length
                   81
                   23
% identity
NCBI Description nuclear protein, 25K - mouse
                   167385
Seq. No.
                   LIB3234-037-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1710530
BLAST score
                   651
                   2.0e-68
E value
                   120
Match length
% identity.
                   97
                   60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
NCBI Description
                   ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
                   167386
Seq. No.
Seq. ID
                   LIB3234-037-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g231586
BLAST score
                   68
```

```
Match length
                  73
% identity
                  66
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_82027_pir__S20504 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >gi 18831 emb_CAA41401_ (X58498) mitochondrial ATP synthase
                  beta-subunit [Hevea brasiliensis]
                  167387
Seq. No.
                  LIB3234-037-P1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4544435
BLAST score
                  367
E value
                  0.0e + 00
Match length
                  379
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F14M13 genomic
NCBI Description
                  sequence, complete sequence
                  167388
Seq. No.
Seq. ID
                  LIB3234-037-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q4455272
BLAST score
                  377
E value
                  2.0e-36
Match length
                  119
                  61
% identity
                  (AL035527) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167389
                  LIB3234-037-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  g3776005
NCBI GI
BLAST score
                  130
                  3.0e-24
E value
Match length
                  100
% identity
                  61
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  167390
Seq. No.
                  LIB3234-038-P1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1531762
BLAST score
                  161
E value
                  4.0e-11
Match length
                  45
% identity
                  71
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  167391
Seq. No.
                  LIB3234-038-P1-K1-A10
Seq. ID
                  BLASTX
Method
                  g1709379
NCBI GI
                  157
BLAST score
                  1.0e-10
E value
```

Match length

```
% identity
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
NCBI Description
                  >qi 881441 (U27653) NADH-plastoquinone oxidoreductase
                  [Lupinus luteus]
Seq. No.
                  167392
                  LIB3234-038-P1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4586053
BLAST score
                  159
E value
                  1.0e-10
Match length
                  56
                  61
% identity
NCBI Description (AC007020) putative lacasse [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  q4589410
BLAST score
                  310
                  1.0e-174
E value
Match length
                  332
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F2015, complete sequence
                  167394
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2507222
BLAST score
                  496
E value
                  2.0e-50
Match length
                  111
                  .87
% identity
                  KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi 1709236 (U09505)
NCBI Description
                  kinase associated protein phosphatase [Arabidopsis
                  thaliana]
                  167395
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g633890
BLAST score
                  264
                  3.0e-23
E value
Match length
                  82
% identity
                  66
NCBI Description
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                  vulgare]
Seq. No.
                  167396
Seq. ID
                  LIB3234-038-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g4589410
BLAST score
                  196
                  1.0e-106
E value
Match length
                  240
% identity
                  95
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   F2015, complete sequence
                   167397
Seq. No.
Seq. ID
                   LIB3234-038-P1-K1-A9
Method
                   BLASTN
                   g2828182
NCBI GI
BLAST score
                   323
E value
                   0.0e+00
Match length
                   348
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167398
Seq. ID
                  LIB3234-038-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  163
E value
                  1.0e-86
Match length
                  221
% identity
                  96
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                  167399
Seq. ID
                  LIB3234-038-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g633890
BLAST score
                  277
                  1.0e-24
E value
Match length
                  85
% identity
                  66
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                  vulgare]
Seq. No.
                  167400
                  LIB3234-038-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3402745
BLAST score
                  182
E value
                  7.0e-98
Match length
                  342
% identity
                  95
NCBI Description
                 Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
                  (ESSAII project)
Seq. No.
                  167401
Seq. ID
                  LIB3234-038-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q3309082
BLAST score
                  259
E value
                  1.0e-22
Match length
                  54
% identity
                  94
                  (AF076251) calcineurin B-like protein 1 [Arabidopsis
NCBI Description
```

thaliana]

```
167402
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g1742955
BLAST score
                  347
                  7.0e-33
E value
Match length
                  67
% identity
                  100
NCBI Description
                  (271446) CLC-b chloride channel protein [Arabidopsis
                  thaliana]
Seq. No.
                  167403
                  LIB3234-038-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2781394
BLAST score
                  451
E value
                  4.0e-45
Match length
                  93
% identity
                  100
NCBI Description (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
Seq. No.
                  167404
                  LIB3234-038-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2118307
BLAST score
                  494
E value
                  4.0e-50
Match length
                  99
                  100
% identity
                  cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
NCBI Description
                  >gi_804950_emb_CAA58893_ (X84097) cysteine synthase
                  [Arabidopsis thaliana] >gi_1096196_prf__2111276A Ser(Ac)
                  thiol lyase [Arabidopsis thaliana]
                  167405
Seq. No.
                  LIB3234-038-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4581161
BLAST score
                  46
                  7.0e-17
E value
                  46
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
NCBI Description
                  sequence, complete sequence
                  167406
Seq. No.
                  LIB3234-038-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4467094
BLAST score
                  64
                  1.0e-27
E value
Match length
                  64
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
NCBI Description
                  (ESSA project)
```

Seq. No.

```
LIB3234-038-P1-K1-C1
Seq. ID
Method
                  BLASTX
                  g4467114
NCBI GI
BLAST score
                  260
                  1.0e-22
E value
                  104
Match length
% identity
                  59
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  167408
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-C2
Method
                  BLASTX
                  g4467114
NCBI GI
                  239
BLAST score
                  3.0e-20
E value
                  104
Match length
% identity
                  55
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167409
                  LIB3234-038-P1-K1-C5
Seq. ID
Method
                  BLASTX
                  g4262250
NCBI GI
BLAST score
                  241
                  1.0e-20
E value
                  70
Match length
                  73
% identity
NCBI Description
                  (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                  167410
Seq. ID
                  LIB3234-038-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g1279568
BLAST score
                  41
E value
                  9.0e-14
Match length
                  49
% identity
                  96
NCBI Description Nicotiana acuminata chloroplast JLB region, 1-250bp
Seq. No.
                  167411
                  LIB3234-038-P1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832667
BLAST score
                  46
                  9.0e-17
E value
Match length
                  114
% identity
                  85
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14
NCBI Description
                   (ESSAII project)
                  167412
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-D12
                  BLASTX
Method
                  g231586
NCBI GI
                  146
BLAST score
                  3.0e-09
E value
```

Match length

```
% identity
                   46
                   ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_82027_pir__S20504 H+-transporting ATP synthase (EC
                   3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >gi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase
                   beta-subunit [Hevea brasiliensis]
                   167413
Seq. No.
                   LIB3234-038-P1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1448941
BLAST score
                   512
                   3.0e-52
E value
Match length
                   109
% identity
                   91
                  (L48181) ypt-related protein [Brassica campestris]
NCBI Description
Seq. No.
                   167414
Seq. ID
                   LIB3234-038-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   q3377819
BLAST score
                   211
E value
                   6.0e-17
                   67
Match length
                   70
% identity
NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]
Seq. No.
                   167415
Seq. ID
                   LIB3234-038-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g119975
BLAST score
                   468
E value
                   4.0e-47
Match length
                   100
% identity
                   93
                   FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin
NCBI Description
                   [2Fe-2S] precursor - Arabidopsis thaliana
                   >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
Seq. No.
                   167416
Seq. ID
                   LIB3234-038-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g4467132
BLAST score
                   447
E value
                   1.0e-44
Match length
                   116
% identity
                   77
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                   167417
Seq. No.
Seq. ID
                   LIB3234-038-P1-K1-D9
Method
                   BLASTN
                   g12219
NCBI GI
BLAST score
                   168
```

1.0e-89

E value

```
Match length
                  341
% identity
                  86
                  Mustard chloroplast trnk gene for tRNA-Lys(UUU)
NCBI Description
                  167418
Seq. No.
                  LIB3234-038-P1-K1-E1
Seq. ID
Method
                  BLASTN
                  q12219
NCBI GI
                  44
BLAST score
E value
                  8.0e-16
Match length
                  183
% identity
                  86
NCBI Description Mustard chloroplast trnk gene for tRNA-Lys(UUU)
                  167419
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2832620
BLAST score
                  375
E value
                  3.0e-36
Match length
                  106
% identity
                  68
                  (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167420
                  LIB3234-038-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1620986
BLAST score
                  353
                  1.0e-33
E value
                  97
Match length
% identity
                  69
                  (Y08858) 40S ribosomal protein S17 [Nicotiana
NCBI Description
                  plumbaginifolia.
                  167421
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-E3
                  BLASTN
Method
NCBI GI
                  g2245073
                  333
BLAST score
E value
                  0.0e+00
                  349
Match length
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  167422
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-E4
                  BLASTX
Method
NCBI GI
                  g4417271
BLAST score
                  559
E value
                  1.0e-57
                  119
Match length
                  89
% identity
                   (AC007019) putative cellulose synthase catalytic subunit
NCBI Description
```

[Arabidopsis thaliana]

Method

BLASTX

```
Seq. No.
                     167423
                     LIB3234-038-P1-K1-E6
Seq. ID
                     BLASTX
Method
                     q127041
NCBI GI
                     526
BLAST score
                     7.0e-54
E value
                     102
Match length
                     99
% identity
                    S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                     ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                     >gi 81647_pir__JN0131 methionine adenosyltransferase (EC
                     2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077)
                     S-adenosylmethionine synthetase [Arabidopsis thaliana]
                     167424
Seq. No.
                     LIB3234-038-P1-K1-E8
Seq. ID
Method
                     BLASTN
NCBI GI
                     q4512656
                     150
BLAST score
                     8.0e-79
E value
                     259
Match length
                     89
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic
                     sequence, complete sequence
                     167425
Seq. No.
                     LIB3234-038-P1-K1-F10
Seq. ID
Method
                     BLASTX
NCBI GI
                     q119143
                     159
BLAST score
                     3.0e-48
E value
                     103
Match length
% identity
                     85
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                     >gi_81606_pir__S06724 translation elongation factor eEF-1
                     alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                     (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                     >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                     >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                     167426
Seq. ID
                     LIB3234-038-P1-K1-F11
Method
                     BLASTX
NCBI GI
                     g3582329
BLAST score
                     450
E value
                     6.0e-45
Match length
                     119
                     74
% identity
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                     167427
Seq. No.
Seq. ID
                     LIB3234-038-P1-K1-F12
```

```
g3582329
NCBI GI
BLAST score
                   69
                   3.0e-20
E value
                   90
Match length
                   61
 % identity
                   (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                   167428
Seq. No.
                   LIB3234-038-P1-K1-F2
· Seq. ID
Method
                   BLASTX
NCBI GI
                   g2924258
BLAST score
                   475
                   7.0e-48
E value
Match length
                   116
                   80
 % identity
                   (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
NCBI Description
 Seq. No.
                   167429
                   LIB3234-038-P1-K1-F5
 Seq. ID
 Method
                   BLASTN
                   q2980757
NCBI GI
 BLAST score
                   274
 E value
                   1.0e-153
                   313
Match length
                   97
 % identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
 NCBI Description
                   (ESSAII project)
                   167430
 Seq. No.
                   LIB3234-038-P1-K1-F7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g226120
 BLAST score
                   186
 E value
                   5.0e-14
                   83
 Match length
 % identity
                   45
                  vicilin gene B [Saguinus oedipus]
 NCBI Description
                   167431
 Seq. No.
                   LIB3234-038-P1-K1-F8
 Seq. ID
                   BLASTX
 Method
                   g1628583
 NCBI GI
                   567
 BLAST score
                   1.0e-58
 E value
                   111
 Match length
                   99 .
 % identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
 NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   167432
 Seq. No.
                   LIB3234-038-P1-K1-G2
 Seq. ID
                   BLASTN
 Method
                   g2914688
 NCBI GI
                   261
 BLAST score
                   1.0e-145
 E value
```

Match length

```
94
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  167433
Seq. No.
                  LIB3234-038-P1-K1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3047074
BLAST score
                  71
                  1.0e-31
E value
Match length
                  150
% identity
                  87
NCBI Description Arabidopsis thaliana BAC F21E10
                  167434
Seq. No.
                  LIB3234-038-P1-K1-G6
Seq. ID
Method
                  BLASTN
                  g3241920
NCBI GI
BLAST score
                  192
E value
                  1.0e-104
Match length
                  364
                  97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167435
                  LIB3234-038-P1-K1-G7
Seq. ID
Method
                  BLASTX
                  q1864017
NCBI GI
                  528
BLAST score
                  4.0e-54
E value
                  100
Match length
% identity
                  100
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  167436
Seq. ID
                  LIB3234-038-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q140285
BLAST score
                  207
                  2.0e-16
E value
Match length
                  42
                  95
% identity
                  HYPOTHETICAL 19 KD PROTEIN (ORF 168)
NCBI Description
                  >gi 2924263 emb CAA77415 (Z00044) Ycf3 protein [Nicotiana
                  tabacum]
                  167437
Seq. No.
Seq. ID
                  LIB3234-038-P1-K1-H11
Method
                  BLASTN
                  q2618605
NCBI GI
                  306
BLAST score
                  1.0e-172
E value
Match length
                  326
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUK11, complete sequence [Arabidopsis thaliana]
```

```
167438
Seq. No.
                   LIB3234-038-P1-K1-H3
Seq. ID
                    BLASTX
Method
                   g3980412
NCBI GI
BLAST score
                    216
E value
                    2.0e-17
                    58
Match length
                    20
% identity
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.
                    167439
                   LIB3234-038-P1-K1-H5
Seq. ID
Method
                    BLASTN
                   g2570223
NCBI GI
BLAST score
                    42
E value
                   1.0e-14
Match length
                    74
                    89
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                    167440
                    LIB3234-038-P1-K1-H6
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3955041
BLAST score
                    261
E value
                    8.0e-23
Match length
                    98
% identity
                    52
NCBI Description (AJ010068) nhp2+ protein [Schizosaccharomyces pombe]
Seq. No.
                    167441
                    LIB3234-038-P1-K1-H7
Seq. ID
Method
                    BLASTX
NCBI GI
                    q112737
BLAST score
                    350
E value
                    3.0e - 33
Match length
                    81
                    85
% identity
                    2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                    (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                    >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                    precursor [Arabidopsis thaliana]
Seq. No.
                    167442
Seq. ID
                    LIB3234-038-P1-K1-H8
Method
                    BLASTN
NCBI GI
                    q4519187
BLAST score
                    319
E value ·
                  · 1.0e-179
Match length
                    351
                    97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
```

K1G2, complete sequence 167443 Seq. No. LIB3234-038-P1-K1-H9 Seq. ID Method BLASTX . J. . NCBI GI q3258569 105 BLAST score 8.0e-28 E value 70 Match length % identity 93 NCBI Description (U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana] Seq. No. 167444 Seq. ID LIB3234-039-P1-K1-A10 Method BLASTN NCBI GI q1313927 BLAST score 35 3.0e-10 E value 128 Match length 88 % identity NCBI Description B.oleracea mRNA for IFA binding protein (sp10) 167445 Seq. No. Seq. ID LIB3234-039-P1-K1-A11 · Method BLASTX NCBI GI q4678259 BLAST score 212 E value 4.0e-17 Match length 115 15 % identity NCBI Description (AL049657) putative protein [Arabidopsis thaliana] Seq. No. 167446 LIB3234-039-P1-K1-A3 Seq. ID Method BLASTN NCBI GI q2760170 BLAST score . 96 1.0e-46 E value Match length 284 % identity 91 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MIO24, complete sequence [Arabidopsis thaliana] 167447 Seq. No. LIB3234-039-P1-K1-A6 Seq. ID Method BLASTX NCBI GI g2501021 100 BLAST score 7.0e-14 E value 66 Match length

Seq. No. 167448

% identity

NCBI Description

62

[Synechocystis sp.]

LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)

>gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase

```
Seq. ID
                   LIB3234-039-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g3935151
BLAST score
                   562
E value
                   4.0e-58
Match length
                   108
% identity
                   97
NCBI Description
                   (AC005106) T25N20.15 [Arabidopsis thaliana]
Seq. No.
                   167449
Seq. ID
                  LIB3234-039-P1-K1-A9
                   BLASTN
Method
                   q2760170
NCBI GI
BLAST score
                   65
                   4.0e-28
E value
Match length
                   187
% identity
                   88
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MIO24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167450
Seq. ID
                   LIB3234-039-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q1864017
BLAST score
                   525
                   9.0e-54
E value
Match length
                   101
% identity
                   99
                   (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
                   167451
Seq. No.
                   LIB3234-039-P1-K1-B11
Seq. ID
                   BLASTX
Method
                   g625977
NCBI GI
                   456
BLAST score
                   1.0e-45
E value
Match length
                   90
                   99
% identity
                  p40 protein homolog - Arabidopsis thaliana >qi 402904
NCBI Description
                   (U01955) laminin receptor-like protein [Arabidopsis
                   thaliana]
                   167452
Seq. No.
                  LIB3234-039-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g132863
BLAST score
                   45
                   3.0e-52
E value
                   109
Match length
                   91
% identity
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L2
NCBI Description
                   >gi 12214 emb CAA46568 (X65615) ribosomal protein L2
                   [Sinapis alba]
                   167453
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-B2
                  BLASTX
Method
```

```
NCBI GI
                  g3132475
BLAST score
                  472
                  2.0e-47
E value
                  115
Match length
                  82
% identity
                  (AC003096) similar to proline-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                  167454
Seq. No.
                  LIB3234-039-P1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3281868
BLAST score
                  54
                  3.0e-40
E value
Match length
                  112
                  76
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                  167455
Seq. No.
                  LIB3234-039-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3132469
BLAST score
                  57
E value
                  3.0e-23
Match length
                  256 -
                  86
% identity
                  Arabidopsis thaliana chromosome II BAC T29F13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167456
Seq. No.
                  LIB3234-039-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2618683
                  154
BLAST score
E value
                  3.0e-81
Match length
                  359
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167457
                  LIB3234-039-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406780
BLAST score
                  572
E value
                  3.0e-59
Match length
                  115
% identity
                  95
NCBI Description
                   (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                  167458
                  LIB3234-039-P1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159707
                  322
BLAST score
```

0.0e + 00

E value

```
Match length
                  352
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJK13, complete sequence
Seq. No.
                  167459
Seq. ID
                  LIB3234-039-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g399013
BLAST score
                  314
E value
                  4.0e-29
Match length
                  108
                  62
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi 16175 emb CAA46518 (X65549)
                  adenylate translocator [Arabidopsis thaliana]
                  >gi 445607 prf 1909354A adenylate translocator
                  [Arabidopsis thaliana]
Seq. No.
                  167460
                  LIB3234-039-P1-K1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4559375
BLAST score
                  279
E value
                  1.0e-156
Match length
                  358
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F11C10 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  167461
                  LIB3234-039-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1531762
BLAST score
                  191
                  1.0e-14
E value
                  50
Match length
                  74
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167462
Seq. ID
                  LIB3234-039-P1-K1-C6
                  BLASTX
Method
NCBI GI
                  q113171
BLAST score
                  474
                  9.0e-48
E value
                  102
Match length
                  96
% identity
NCBI Description
                  ACYL CARRIER PROTEIN 1 PRECURSOR (ACP)
                  >gi_81596_pir__S03267 acyl carrier protein precursor -
                  Arabidopsis thaliana >gi 16152 emb CAA31991 (X13708) acyl
                  carrier protein [Arabidopsis thaliana]
```

Seq. No.

```
Seq. ID
                  LIB3234-039-P1-K1-C7
                  BLASTN
Method
NCBI GI
                  g4559375 ·
BLAST score
                  276
                  1.0e-154
E value
Match length
                  343
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F11C10 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  167464
Seq. ID
                  LIB3234-039-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  q4559375
BLAST score
                  277
E value
                  1.0e-154
Match length
                  344
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F11C10 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  167465
Seq. ID
                  LIB3234-039-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3335171
BLAST score
                  172
E value
                  2.0e-12
Match length
                  67
% identity
                  55
NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
Seq. No.
                  167466
Seq. ID
                  LIB3234-039-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4586053
BLAST score
                  244
E value
                  8.0e-21
Match length
                  114
                  48
% identity
NCBI Description (AC007020) putative lacasse [Arabidopsis thaliana]
Seq. No.
                  167467
Seq. ID
                  LIB3234-039-P1-K1-D10
                  BLASTX
Method
NCBI GI
                  g4704613
                  356
BLAST score
                  6.0e-34
E value
                  82
Match length
                  88
% identity
                 (AF109695) monodehydroascorbate reductase [Brassica juncea]
NCBI Description
                  167468
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3142294
BLAST score
                  382
```

6.0e-37

E value

```
Match length
                   88
                   89
 % identity
 NCBI Description (AC002411) Strong similarity to initiation factor eIF-2,
                   gb_U37354 from S. pombe. ESTs gb T41979, gb N37284 and
                   gb N37529 come from this gene. [Arabidopsis thaliana]
                   167469
· Seq. No.
 Seq. ID
                   LIB3234-039-P1-K1-D4
 Method
                   BLASTX
 NCBI GI
                   q3075394
 BLAST score
                   559
 E value
                   9.0e-58
 Match length
                   115
                   95
 % identity
                   (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
 NCBI Description
                   thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead
                   protein [Arabidopsis thaliana]
 Seq. No.
                   167470
 Seq. ID
                   LIB3234-039-P1-K1-D6
 Method
                   BLASTN
 NCBI GI
                   g2760172
 BLAST score
                   273
 E value
                   1.0e-152
 Match length
                   273
                   100
 % identity
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUB3, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   167471
 Seq. ID
                   LIB3234-039-P1-K1-D7
 Method
                   BLASTX
                   g3805962
 NCBI GI
                   259
 BLAST score
                   1.0e-22
 E value
                   112
 Match length
                   53
 % identity
                   (Y13772) laccase [Populus balsamifera subsp. trichocarpa]
 NCBI Description
                   167472
 Seq. No.
 Seq. ID
                   LIB3234-039-P1-K1-D8
 Method
                   BLASTX
 NCBI GI
                   g2459446
 BLAST score
                   448
                   9.0e-45
 E value
                   116
 Match length
 % identity
                   78
                    (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
 NCBI Description
                   thaliana]
                   167473
 Seq. No.
 Seq. ID
                   LIB3234-039-P1-K1-D9
 Method
                   BLASTN
 NCBI GI
                   g4757412
 BLAST score
                   286
 E value
                   1.0e-160
```

Match length

BLAST score

```
% identity
                  95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                MXK23, complete sequence
                167474
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-E1
                  BLASTX
Method
NCBI GI
                  q1172599
BLAST score
                  451
E value
                  4.0e-45
                  88
Match length
                  100
% identity
                  PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                  COMPLEX SUBUNIT C5) (TAS-F22/FAFP98)
                  >gi_600387_emb_CAA47753_ (X67338) proteosome subunit
                  [Arabidopsis thaliana]
                  167475
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  g4092472
BLAST score
                  34
E value
                  1.0e-09
                  46 _
Match length
                  96
% identity
NCBI Description Arabidopsis thaliana BAC F1K3 from chromosome IV near 21
                  cM, complete sequence [Arabidopsis thaliana]
                  167476
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2501056
BLAST score
                  450
E value
                  6.0e-45
Match length
                  101
                  92
% identity
NCBI Description
                  SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
                  >gi 2129737 pir S71293 seryl-tRNA synthetase - Arabidopsis
                  thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA
                  Synthetase [Arabidopsis thaliana]
                  167477
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-E12
                  BLASTN
Method
NCBI GI
                  g4512690
BLAST score
                  282
E value
                  1.0e-157
Match length
                  352
                  95
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic
                  sequence, complete sequence
                  167478
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  g3510347
```

```
E value
                  1.0e-110
Match length
                  354
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167479
                  LIB3234-039-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1769905
BLAST score
                  259
                  2.0e-22
E value
Match length
                  79
% identity
                  65
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                  [Arabidopsis thaliana] .
Seq. No.
                  167480
Seq. ID
                  LIB3234-039-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g584998
BLAST score
                  149
                  1.0e-09
E value
Match length
                  64
% identity
                  44
                  FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTOCHROME P450
NCBI Description
                  LXXVA2) (P-450EG1) >gi 629713 pir S43342 flavonoid
                  hydroxylase cytochrome P450 - eggplant
                  >gi 395261 emb CAA50155 (X70824) flavonoid hydroxylase
                  (P450) [Solanum melongena]
Seq. No.
                  167481
Seq. ID
                  LIB3234-039-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  283
                  2.0e-25
E value
                  89
Match length
                  64
% identity
                  oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
NCBI Description
                  (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  167482
Seq. ID
                  LIB3234-039-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g585536
BLAST score
                  534
E value
                  8.0e-55
Match length
                  111
% identity
                  91
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
NCBI Description
                  >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
                  [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)
                  thioglucosidase [Arabidopsis thaliana]
```

Seq. No.

Method

BLASTX

```
LIB3234-039-P1-K1-F11
Seq. ID
Method
                  BLASTX
                   g2642215
NCBI GI
BLAST score
                   191
E value
                   1.0e-14
                   36 .. . .
Match length
                   97
% identity
                  (AF030386) NOI protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   167484
                  LIB3234-039-P1-K1-F12
Seq. ID
                  BLASTX
Method
NCBI GI
                   g485514
BLAST score
                   258
E value
                   2.0e-22
Match length
                   77
% identity
                   64
                  ADR11-2 protein - soybean (fragment)
NCBI Description
                  >gi 296443 emb CAA49341 (X69640) auxin down regulated
                   [Glycine max]
Seq. No.
                   167485
Seq. ID
                  LIB3234-039-P1-K1-F2
Method
                  BLASTX
NCBI GI
                   g2921158
BLAST score
                   526
E value
                   7.0e-54
                  117
Match length
% identity
                   91
                  (AF022909) ClpC [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167486
Seq. ID
                  LIB3234-039-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q1053047
BLAST score
                   460
E value
                  4.0e-46
Match length
                  92
                  100
% identity
                   (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
NCBI Description
                  histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                   [Glycine max]
                  167487
Seq. No.
                  LIB3234-039-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2760164
BLAST score
                  69
                  2.0e-30
E value
                  209
Match length
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18P6, complete sequence [Arabidopsis thaliana]
                  167488
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-G12
```

```
NCBI GI
                  q3273743
BLAST score
                  345
E value
                  1.0e-32
Match length
                  88
                  81
% identity
                  (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi 3786019 (AC005499) unknown protein
                  [Arabidopsis thaliana]
                  167489
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g266989
BLAST score
                  90
                  7.0e-33
E value
Match length
                  118
% identity
                  69
                  GTP-BINDING PROTEIN SAR1B >gi 322517 pir_S28603
NCBI Description
                  GTP-binding protein - Arabidopsis thaliana >gi_166734
                   (M95795) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  167490
                  LIB3234-039-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131336
BLAST score
                  53
E value
                  6.0e-24
Match length
                  72
% identity
                  89
                  PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P
NCBI Description
                  photosystem II phosphoprotein psbH - common tobacco
                  chloroplast >gi 11857 emb_CAA77374_ (Z00044) PSII 10kD
                  phosphoprotein [Nicotiana tabacum]
                  >gi 225225 prf 1211235BG photosystem II 10kD
                  phosphoprotein [Nicotiana tabacum]
                  167491
Seq. No.
                  LIB3234-039-P1-K1-G5
Seq. ID
                  BLASTN
Method
                  g2618599
NCBI GI
                  310
BLAST score
                  1.0e-174
E value
                  362
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBD2, complete sequence [Arabidopsis thaliana]
                  167492
Seq. No.
                  LIB3234-039-P1-K1-G7
Seq. ID
                  BLASTN
Method
                  q2689438
NCBI GI
                  166
BLAST score
                  2.0e-88
E value
Match length
                  301
                  96
% identity
                  Arabidopsis thaliana BAC F2401 chromosome 1, complete
NCBI Description
```

sequence [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                  167493
                  LIB3234-039-P1-K1-H11
Seq. ID
Method
                  BLASTX
                  g3776559
NCBI GI
BLAST score
                  145
E value ear.
                  1.0e-09
                  77
Match length
                  47
% identity
                  (AC005388) Strong similarity to gene F14J9.26 gi 3482933
NCBI Description
                  cdc2 protein kinase homolog from A. thaliana BAC
                  gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                  gene. [Arabidopsis thaliana]
                  167494
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g984307
BLAST score
                  34
E value
                  1.0e-09
Match length
                  34
% identity
                  100
                  Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                  cds, beta-carboxyltransferase (accD), photosystem I
                  component (psaI), ORF 202 protein (ORF 203), ORF 151
                  protein (ORF 151), ORF 103 protein (ORF 103), ORF 229
                  precurso
                  167495
Seq. No.
                  LIB3234-039-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112682
                  94
BLAST score
E value
                  4.0e-25
                  106
Match length
                  59
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  167496
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-H4
                  BLASTN
Method
                  g4079614
NCBI GI
BLAST score
                  102
                  4.0e-50
E value
                  310
Match length
% identity
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167497
Seq. No.
Seq. ID
                  LIB3234-039-P1-K1-H5
Method
                  BLASTX
```

g3776559

BLAST score

```
BLAST score
                   253
E value
                   5.0e-22
Match length
                   98
% identity
                   52
NCBI Description
                   (AC005388) Strong similarity to gene F14J9.26 gi 3482933
                   cdc2 protein kinase homolog from A. thaliana BAC
                   gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   167498
Seq. ID
                   LIB3234-039-P1-K1-H6
Method
                   BLASTN
NCBI GI
                   g3522932
BLAST score
                   319
E value
                   1.0e-179
Match length
                   364
% identity
                   96
                   Arabidopsis thaliana chromosome II BAC F14M4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167499
Seq. ID
                   LIB3234-039-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q1854445
BLAST score
                   376
E value
                   3.0e-36
Match length
                   87
% identity
                   79
NCBI Description
                  (D83971) CPRD14 protein [Vigna unguiculata]
Seq. No.
                   167500
Seq. ID
                   LIB3234-039-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g4204299
BLAST score
                   583
E value
                   1.0e-60
Match length
                   116
% identity
                   99
                   (AC003027) lcl prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   167501
Seq. ID
                  LIB3234-040-P1-K1-A11
Method
                   BLASTX
NCBI GI
                  q4580460
BLAST score
                   600
E value
                   2.0e-62
Match length
                  125
% identity
                   94
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167502
Seq. ID
                  LIB3234-040-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3695023
```

```
1.0e-23
 E value
 Match length
                   98
                   52
 % identity
 NCBI Description (AF055850) unknown [Arabidopsis thaliana]
 Seq. No.
                   167503
 Seq. ID
                   LIB3234-040-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g2894574
BLAST score
                   556
E value
                   2.0e-57
Match length
                   106
% identity
                   100
NCBI Description
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
                   >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
Seq. No.
                   167504
Seq. ID
                   LIB3234-040-P1-K1-A6
Method
                   BLASTN
NCBI GI
                   g3702722
BLAST score
                   37
E value
                   2.0e-11
Match length
                   137
% identity
                   82
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K12B20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167505
Seq. ID
                   LIB3234-040-P1-K1-A7
Method
                   BLASTN
NCBI GI
                   g4589430
BLAST score
                   209
                   1.0e-114
E value
Match length
                   375
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLD14, complete sequence
Seq. No.
                  167506
Seq. ID
                  LIB3234-040-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g4468993
BLAST score
                  597
E value
                  4.0e-62
Match length
                  113
% identity
                  100
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167507
Seq. ID
                  LIB3234-040-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g399298
BLAST score
                  199
E value
                  2.0e-15
Match length
                  66
% identity
```

```
NCBI Description
                   STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN)
                    >gi_1084343_pir__S22529 cold-regulated protein kin2 - .
                    Arabidopsis thaliana >gi_16230_emb_CAA38894_ (X55053) cold
                    regulated [Arabidopsis thaliana]
 Seq. No.
                    167508
 Seq. ID
                    LIB3234-040-P1-K1-B10
 Method
                    BLASTX
 NCBI GI
                    q3334404
 BLAST score
                    616
 E value
                    2.0e-64
 Match length
                    128
 % identity
                    93
 NCBI Description
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
                   SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit
                   A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical
                   to gb_U65638 Arabidopsis thaliana vacuolar type ATPase
                   subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189,
                   gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027,
                   gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472
 Seq. No.
                   167509
 Seq. ID
                   LIB3234-040-P1-K1-B11
 Method
                   BLASTX
 NCBI GI
                   g112682
 BLAST score
                   163
 E value
                   3.0e-11
Match length
                   112
 % identity
                   40
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   167510
Seq. ID
                  LIB3234-040-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g1345132
BLAST score
                   620
E value
                   8.0e-65
Match length
                  128
% identity
                   93
                  (U47029) ERECTA [Arabidopsis thaliana]
NCBI Description
                  >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase
                  [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
                  protein kinase, ERECTA [Arabidopsis thaliana]
Seq. No.
                  167511
Seq. ID
                  LIB3234-040-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g1402904
BLAST score
                  93
E value
                  1.0e-22
Match length
                  113
% identity
                  59
NCBI Description
```

(X98313) peroxidase [Arabidopsis thaliana]

```
Seq. No.
                      167512
    Seq. ID
                      LIB3234-040-P1-K1-B5
   Method
                      BLASTX
   NCBI GI
                     g133812
   BLAST score
                     113
   E value
                     3.0e-16
   Match length
                     61
   % identity
                     84
   NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S16 >gi_71000_pir__R3IS16
                     ribosomal protein S16 - white mustard chloroplast
                     >gi_12217_emb_CAA31944_ (X13609) 16S ribosomal protein
   Seq. No.
                     167513
   Seq. ID
                     LIB3234-040-P1-K1-B6
  Method
                     BLASTX
  NCBI GI
                     g1531762
  BLAST score
                     195
  E value
                    5.0e-15
  Match length
                    51
  % identity
                    75
  NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
  Seq. No.
                    167514
  Seq. ID
                    LIB3234-040-P1-K1-B7
  Method
                    BLASTX
  NCBI GI
                    g4704730
  BLAST score
                    166
  E value
                    1.0e-11
 Match length
                    55
 % identity
                    60
 NCBI Description (AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]
 Seq. No.
                   167515
 Seq. ID
                   LIB3234-040-P1-K1-B8
 Method
                   BLASTN
 NCBI GI
                   g2494110
 BLAST score
                   321
 E value
                   0.0e+00
 Match length
                   351
 % identity
                   98
NCBI Description
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167516
Seq. ID
                  LIB3234-040-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g1429212
BLAST score
                  169
E value
                  4.0e-90
Match length
                  258
% identity
                  94
NCBI Description A.thaliana mRNA for peroxidase ATP4a, EST clone 4G6T7P
Seq. No.
                  167517
```

```
Seq. ID
                     LIB3234-040-P1-K1-C12
  Method
                     BLASTX
   NCBI GI
                     g231660
  BLAST score
                     257
  E value
                     3.0e-22
  Match length
                     132
  % identity
                     48
  NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
  Seq. No.
                    167518
  Seq. ID
                    LIB3234-040-P1-K1-C3
  Method
                    BLASTX
  NCBI GI
                    g3983125
  BLAST score
                    453
  E value
                    3.0e-45
  Match length
                    117
  % identity
                    77
  NCBI Description
                   (AF097648) phosphate/triose-phosphate translocator
                    precursor [Arabidopsis thaliana]
 Seq. No.
                    167519
 Seq. ID
                    LIB3234-040-P1-K1-C4
 Method
                    BLASTN
 NCBI GI
                    q2656029
 BLAST score
                    356
 E value
                   0.0e+00
 Match length
                   372
 % identity
                   99
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
 Seq. No.
                   167520
 Seq. ID
                   LIB3234-040-P1-K1-C5
 Method
                   BLASTN
 NCBI GI
                   g2842474
 BLAST score
                   187
 E value
                   1.0e-101
Match length
                   367
% identity
                   96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                   (ESSAII project)
Seq. No.
                   167521
Seq. ID
                  LIB3234-040-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g4584519
BLAST score
                  294
E value
                  1.0e~165
Match length
                  339
% identity
                  96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18
                  (ESSA project)
Seq. No.
                  167522
Seq. ID
                  LIB3234-040-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g1402933
```

```
BLAST score
                   115
 E value
                   7.0e-58
 Match length
                   204
 % identity
                   86
 NCBI Description
                   A.thaliana genomic DNA fragment (ecotype DIJON-0/LANDSBERG
                   ERECTA/ LEIDEN-0/LLAGOSTERA-0)
 Seq. No.
                   167523
 Seq. ID
                   LIB3234-040-P1-K1-C9
 Method
                   BLASTX
 NCBI GI
                   g2673917
 BLAST score
                   524
 E value
                   1.0e-53
 Match length
                   130
 % identity
                   57
 NCBI Description
                   (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
                   thaliana]
 Seq. No.
                   167524
 Seq. ID
                   LIB3234-040-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   g3047100
BLAST score
                   286
E value
                   1.0e-160
Match length
                   378
% identity
                   93
NCBI Description Arabidopsis thaliana BAC F6N23
Seq. No.
                   167525
Seq. ID
                  LIB3234-040-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                   208
E value
                  7.0e-21
Match length
                  108
% identity
                  56
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  167526
Seq. ID
                  LIB3234-040-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q4406820
BLAST score
                  354
E value
                  1.0e-33
Match length
                  68
% identity
NCBI Description
                  (AC006201) putative ras superfamily member [Arabidopsis
                  thaliana]
Seq. No.
                  167527
Seq. ID
                  LIB3234-040-P1-K1-D2
```

E value

2.0e-44

```
Method
                   BLASTX
 NCBI GI
                   q4262250
 BLAST score
                    404 -...
 E value
                   2.0e-39
 Match length
                   81
 % identity
                   100
                   (AC006200) putative aldolase [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   167528
 Seq. ID
                   LIB3234-040-P1-K1-D3
 Method
                   BLASTN
NCBI GI
                   g2182289
BLAST score
                   81
 E value
                   1.0e-37
Match length
                   247
% identity
                   92
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F11P17 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167529
Seq. ID
                   LIB3234-040-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q3150404
BLAST score
                   229
E value
                   5.0e-19
                   66
Match length
% identity
                   74
NCBI Description
                   (AC004165) putative mitochondrial carrier protein
                   [Arabidopsis thaliana]
Seq. No.
                   167530
                   LIB3234-040-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3850978
BLAST score
                   259
E value
                   2.0e-22
Match length
                   54
% identity
                   91 `
NCBI Description
                  (AF060429) ATP synthase beta subunit [Embothrium coccineum]
Seq. No.
                   167531
Seq. ID
                   LIB3234-040-P1-K1-E1
Method
                   BLASTN
NCBI GI
                   g4490291
BLAST score
                   342
E value
                  0.0e+00
Match length
                   373
% identity
                   98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
                   (ESSA project)
Seq. No.
                  167532
Seq. ID
                  LIB3234-040-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q1498053
BLAST score
                  446
```

. . .

Seq. No.

```
Match length
                   110
 % identity
                   80
 NCBI Description
                   (U64436) ribosomal protein S8 [Zea mays]
 Seq. No.
                   167533
                   LIB3234-040-P1-K1-E11
 Seq. ID
Method
                   BLASTN
 NCBI GI
                   q4199934
 BLAST score
                   257
 E value
                   1.0e-142
 Match length
                   364
 % identity
                   91
 NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC T3P18,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   167534
Seq. ID
                   LIB3234-040-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   q1345973
BLAST score
                   69
E value
                   2.0e-59
Match length
                   122
% identity
                   93
NCBI Description
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                   1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505 (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  167535
Seq. ID
                  LIB3234-040-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  473
E value
                  1.0e-47
Match length
                  122
% identity
                  76
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  167536
Seq. ID
                  LIB3234-040-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  q3869065
BLAST score
                  285
E value
                  1.0e-159
Match length
                  312
% identity
                  99
NCBI Description.
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K24M7, complete sequence [Arabidopsis thaliana]
```

Method

BLASTX

```
Seq. ID
                   LIB3234-040-P1-K1-E9
 Method
                   BLASTX
 NCBI GI
                   q1864017
 BLAST score
                   535
 E value
                   7.0e-55
 Match length
                   106
 % identity
                   96
 NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
 Seq. No.
                   167538
Seq. ID
                   LIB3234-040-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q3236254
BLAST score
                   149
E value
                   1.0e-09
Match length
                   65
% identity
                   48
NCBI Description
                   (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                   167539
Seq. ID
                   LIB3234-040-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q2129767
BLAST score
                   598
E value
                   3.0e-62
Match length
                   121
% identity
                   93
NCBI Description
                   vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
                   precursor - Arabidopsis thaliana >gi_1805364_dbj BAA09615
                   (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
                   167540
Seq. ID
                   LIB3234-040-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2129767
BLAST score
                   469
E value
                   2.0e-47
Match length
                   94
% identity
                   91
NCBI Description
                  vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
                  precursor - Arabidopsis thaliana >gi 1805364 dbj BAA09615
                   (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
                  167541
Seq. ID
                  LIB3234-040-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g4662647
BLAST score
                  56
E value
                  3.0e-23
Match length
                  124
% identity
                  87
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3K12 genomic
                  sequence, complete sequence
Seq. No.
                  167542
Seq. ID
                  LIB3234-040-P1-K1-F6
```

```
NCBI GI
                   g137580
 BLAST score
                    214
 E value
                   3.0e-17
 Match length
                   121
 % identity
                   36
                   VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)
 NCBI Description
                   >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone
                   C72) - upland cotton >gi_167375 (M16891) vicilin precursor
                   [Gossypium hirsutum]
 Seq. No.
                   167543
 Seq. ID
                   LIB3234-040-P1-K1-F8
 Method
                   BLASTN
 NCBI GI
                   q4699904
 BLAST score
                   38
E value
                   3.0e-12
Match length
                   162
% identity
                   81
                   Genomic sequence for Arabidopsis thaliana BAC F1E22,
NCBI Description
                   complete sequence
Seq. No.
                   167544
Seq. ID
                   LIB3234-040-P1-K1-G1
Method
                   BLASTX L
NCBI GI
                   g1113941
BLAST score
                   367
E value
                   3.0e-35
Match length
                   109
                   71
% identity
NCBI Description
                  (U40713) Pv42p [Phaseolus vulgaris]
Seq. No.
                   167545
Seq. ID
                   LIB3234-040-P1-K1-G10
Method
                   BLASTN
NCBI GI
                   g4589434
BLAST score
                   231
E value
                   1.0e-127
Match length
                   302
% identity
                   97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNJ7, complete sequence
Seq. No.
                  167546
Seq. ID
                  LIB3234-040-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  g4581138
BLAST score
                  290
E value
                  1.0e-162
Match length
                  374
% identity
                  84
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F1011 genomic
                  sequence, complete sequence
Seq. No.
                  167547
Seq. ID
                  LIB3234~040-P1-K1-G2
Method
                  BLASTX
NCBI GI
```

g1592677

```
265
BLAST score
                  3.0e-23
E value
                  102
Match length
                  55
% identity
                 (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
                  167548
Seq. No.
                  LIB3234-040-P1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3150396
BLAST score
                  257
                  1.0e-142
E value
                  346
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC T27E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167549
Seq. No.
Seq. ID
                  LIB3234-040-P1-K1-G6
                  BLASTX
Method
NCBI GI
                  q1086249
BLAST score
                  302
                  1.0e-27
E value
                  126
Match length
                  44
% identity
                  subtilisin-like protease - Alnus glutinosa
NCBI Description
                  >gi 75,7522 emb CAA59964 (X85975) subtilisin-like protease
                  [Alnus glutinosa]
                  167550
Seq. No.
Seq. ID
                  LIB3234-040-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g2244991
                  288
BLAST score
                  1.0e-161
E value
                  375
Match length
                  94
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  167551
Seq. ID
                  LIB3234-040-P1-K1-H1
                  BLASTX
Method
NCBI GI
                  g4455329
                  588
BLAST score
                  4.0e-61
E value
                  124
Match length
% identity
                  (AL035525) lysine-ketoglutarate reductase/saccharopine
NCBI Description
                  [Arabidopsis thaliana]
                  167552
Seq. No.
Seq. ID
                  LIB3234-040-P1-K1-H10
                  BLASTX
Method
NCBI GI
                  g3885334
BLAST score
                  593
E value
                  1.0e-61
```

```
Match length
                  123
                  93
% identity
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  167553
Seq. No.
Seq. ID
                  LIB3234-040-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3885334
                  270
BLAST score
                  5.0e-24
E value
Match length
                  60
% identity
                  90
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  167554
Seq. No.
                  LIB3234-040-P1-K1-H12
Seq. ID
Method
                  BLASTX
                  g1703375
NCBI GI
BLAST score
                  410
E value
                  2.0e-40
                  88
Match length
% identity
                  91
                  ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
NCBI Description
                  DcARF1 [Daucus carota]
                  167555
Seq. No.
Seq. ID
                  LIB3234-040-P1-K1-H2
                  BLASTX
Method
                  g2924262
NCBI GI
BLAST score
                  617
                  2.0e-64
E value
Match length
                  122
                  92
% identity
NCBI Description (Z00044) PSII 44kd protein [Nicotiana tabacum]
Seq. No.
                  167556
                  LIB3234-040-P1-K1-H3
Seq. ID
                  BLASTX
Method
                  g120675
NCBI GI
BLAST score
                  452
                  4.0e-45
E value
                  88
Match length
                  95
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                  >gi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                  alba]
                  167557
Seq. No.
Seq. ID
                  LIB3234-040-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g3135751
                  228
BLAST score
```

6.0e-19

E value

```
Match length
                   44
% identity
                   95
                   (AJ006095) 26S protease regulatory subunit 6 [Cicer
NCBI Description
                   arietinum]
                   167558
Seq. No.
                  LIB3234-040-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g543841
BLAST score
                   481
E value
                   2.0e-48
                   96
Match length
                   97
% identity
                  ADP-RIBOSYLATION FACTOR 1 >qi 322518 pir S28875
NCBI Description
                  ADP-ribosylation factor 1 - Arabidopsis thaliana >qi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi 4630747 gb AAD26597.1 AC007236 2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                   167559
Seq. ID
                  LIB3234-040-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                   431
E value
                   1.0e-42
Match length
                   97
% identity
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  167560
Seq. No.
                  LIB3234-040-P1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3169172
                   403
BLAST score
                  2.0e-39
E value
                  89
Match length
% identity
                  82
                   (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                  thaliana] >qi 3445214 (AC004786) putative serine
                  carboxypeptidase I [Arabidopsis thaliana]
                  167561
Seq. No.
                  LIB3234-040-P1-K1-H9
Seq. ID
Method
                  BLASTX
                  g3695023
NCBI GI
                  292
BLAST score
                  2.0e-26
E value
```

Match length

```
% identity
NCBI Description
                   (AF055850) unknown [Arabidopsis thaliana]
Seq. No.
                   167562
Seq. ID
                   LIB3234-041-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g4584536
                   358
BLAST score
E value
                   4.0e-34
Match length
                   100
% identity
                   63
                   (AL049608) cytochrome p450 like protein [Arabidopsis
NCBI Description
                   thaliana]
                   167563
Seq. No.
Seq. ID
                   LIB3234-041-P1-K1-A10
Method
                   BLASTN
NCBI GI
                   g4757662
BLAST score
                   322
                   0.0e+00
E value
Match length
                   374
% identity
                   97
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F10B6 from
                   chromosome I, complete sequence
Seq. No.
                   167564
Seq. ID
                   LIB3234-041-P1-K1-A11
Method
                  BLASTX
NCBI GI
                   g1864017
BLAST score
                   530
E value
                   3.0e-54
Match length
                   104
% identity
                   97
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   167565
Seq. ID
                  LIB3234-041-P1-K1-A12
Method
                  BLASTN
                   g2656031
NCBI GI
BLAST score
                   349
                   0.0e+00
E value
Match length
                   369
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
Seq. No.
                  167566
                  LIB3234-041-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1841399
BLAST score
                  441
E value
                  8.0e-44
Match length
                  97
% identity
                  89
                  (Z34661) AtTFIIB2 [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

Method

BLASTN

```
LIB3234-041-P1-K1-A3
Seq. ID
Method
                  BLASTN
                  g2564048
NCBI GI
                                                est of
BLAST score
                   343
E value
                  0.0e+00
                  379
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKD15, complete sequence [Arabidopsis thaliana]
                  167568
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  528
E value
                  5.0e-54
Match length
                  108
% identity
                  96
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  167569
Seq. ID
                  LIB3234-041-P1-K1-A6
Method
                  BLASTX
                  g1531762 🗼
NCBI GI
BLAST score
                  195
E value
                  5.0e-15
Match length
                  51
                  75
% identity
                   (Y07765) S-adenosylmethionine decarboxylase (Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167570
Seq. ID
                  LIB3234-041-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q3738288
BLAST score
                  652
E value
                  1.0e-68
                  123
Match length
% identity
                  98
                  (AC005309) auxin-responsive GH3-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  167571
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  g3241916
BLAST score
                  286
E value
                  1.0e-160
                  323
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15N18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167572
Seq. ID
                  LIB3234-041-P1-K1-B11
```

BLAST score

```
NCBI GI
                  q1490552
BLAST score
                  207
E value
                  1.0e-113
Match length
                  283
% identity
                  93
                  Arabidopsis thaliana S-adenosylmethionine decarboxylase
NCBI Description
                   (SAMdc) mRNA, complete cds
Seq. No.
                  167573
Seq. ID
                  .LIB3234-041-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g3413718
BLAST score
                  159
                  1.0e-46
E value
Match length
                  113
% identity
                  87
                  (AC004747) alpha-vacuolar processing enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi 3643591 (AC005395) alpha-vacuolar processing
                  enzyme [Arabidopsis thaliana]
Seq. No.
                  167574
Seq. ID
                  LIB3234-041-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q3249107
BLAST score
                  484
E value
                  7.0e-49
Match length
                  101
% identity
                  92
                  (AC003114) Contains similarity to phloem-specific lectin
NCBI Description
                  PP2 gb Z17331 from Cucubita maxima. [Arabidopsis thaliana]
Seq. No.
                  167575
Seq. ID
                  LIB3234-041-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q3335171
                  475
BLAST score
                  8.0e-48
E value
Match length
                  117
                  78
% identity
                  (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167576
Seq. ID
                  LIB3234-041-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  q3985950
BLAST score
                  140
                  9.0e-73
E value
                  386
Match length
% identity
                  95
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPI10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167577
                  LIB3234-041-P1-K1-B7
Seq. ID
                  BLASTX
Method
                  g1561730
NCBI GI
```

% identity



```
1.0e-10
E value
Match length
                  61
                  46
% identity
NCBI Description
                  (U65491) Dreg-3 protein [Drosophila melanogaster]
Seq. No.
                  167578
                  LIB3234-041-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3395432
BLAST score
                  261
E value
                  9.0e-23
Match length
                  90
% identity
                  56
NCBI Description
                  (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  167579
Seq. ID
                  LIB3234-041-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g131360
BLAST score
                  232
E value
                  2.0e-19
Match length
                  60
% identity
                  78
                  PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
NCBI Description
                  >gi 81727 pir S02115 photosystem II protein psbK precursor
                  - white mustard chloroplast >gi_12209_emb_CAA31909
                   (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
Seq. No.
                  167580
                  LIB3234-041-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82040
BLAST score
                  469
                  3.0e-47
E value
Match length
                  97
% identity
                  25
                  ubiquitin precursor - flax (fragment) >gi 168304 (M57895)
NCBI Description
                  ubiquitin [Linum usitatissimum]
Seq. No.
                  167581
Seq. ID
                  LIB3234-041-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1498053
BLAST score
                  474
                  1.0e-47
E value
Match length
                  113
% identity
                  82
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
Seq. No.
                  167582
Seq. ID
                  LIB3234-041-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  g2623294
BLAST score
                  278
                  1.0e-155
E value
Match length
                  371
```

Seq. ID

```
NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167583
Seq. ID
                  LIB3234-041-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g633890
BLAST score
                  272
E value
                  5.0e-24
Match length
                  82
% identity
                  67
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                  vulgare]
                  167584
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g4580389
BLAST score
                  63
                  4.0e-09
E value
Match length
                  58
% identity
                  60
                  (AC007171) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167585
                  LIB3234-041-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g4773885
NCBI GI
BLAST score
                  495
                  4.0e-50
E value
                  95
Match length
% identity
                  98
                  (AF076243) putative aspartic protease [Arabidopsis
NCBI Description
                  thaliana]
                  167586
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-C8
Method
                  BLASTX
                  q4539005
NCBI GI
BLAST score
                  231
E value
                  3.0e-19
Match length
                  120
                  42
% identity
NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]
                  167587
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2924258
BLAST score
                  413
                  1.0e-40
E value
                  124
Match length
                  65
% identity
NCBI Description (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
Seq. No.
                  167588
```

LIB3234-041-P1-K1-D1

NCBI GI

```
Method
                  BLASTN
NCBI GI
                  q3869069
BLAST score
                   353
                  0.0e+00
E value
Match length
                  365
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167589
Seq. ID
                  LIB3234-041-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  q3985933
BLAST score
                  224
E value
                  1.0e-123
                  264
Match length
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9E15, complete sequence [Arabidopsis thaliana]
                  167590
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  a4204277
BLAST score
                  596
                  5.0e-62
E value
Match length
                  110
% identity
                  100
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  167591
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q881615
BLAST score
                  618
E value
                  1.0e-64
Match length
                  124
% identity
                  96
NCBI Description
                  (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
                  >gi 3096921 emb CAA18831.1 (AL023094) fatty acid elongase
                  1 [Arabidopsis thaliana]
Seq. No.
                  167592
Seq. ID
                  LIB3234-041-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  q881614
BLAST score
                  42
E value
                  2.0e-14
Match length
                  138
% identity
NCBI Description
                  Arabidopsis thaliana fatty acid elongase 1 (Fael) gene,
                  complete cds
Seq. No.
                  167593
Seq. ID
                  LIB3234-041-P1-K1-D5
Method
                  BLASTX
```

g1628583

```
BLAST score
                  360
E value
                  2.0e-34
Match length
                  128
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  167594
Seq. ID
                  LIB3234-041-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  q3985933
BLAST score
                  353
E value
                  0.0e + 00
Match length
                  376
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9E15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167595
Seq. ID
                  LIB3234-041-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                  77
                  2.0e-21
E value
Match length
                  72
                  76
% identity
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
NCBI Description
                   - spinach >gi 1066153_dbj_BAA07177_ (D37963) cysteine
                  synthase [Spinacia oleracea]
Seq. No.
                  167596
                  LIB3234-041-P1-K1-E12
Seq. ID
Method
                  BLASTN
                  q4580745
NCBI GI
BLAST score
                  104
                  2.0e-51
E value
Match length
                  361
                  95
% identity
                  Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
NCBI Description
                  complete sequence
                  167597
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2494842
BLAST score
                  265
E value
                  3.0e-23
                  97
Match length
                  52
% identity
                  GLUCOSYLTRANSFERASE ALG6 >gi 2131171 pir S61985 ALG6
NCBI Description
                  protein - yeast (Saccharomyces cerevisiae) >gi 1150997
                  (U43491) hypothetical protein UNA544 [Saccharomyces
                  cerevisiae] >gi 1420090 emb CAA99190 (Z74910) ORF YOR002w
                  [Saccharomyces cerevisiae]
```

Seq. No.

```
LIB3234-041-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g544424
BLAST score
                   55
E value
                   9.0e-39
Match length
                   85
% identity
                   100
                   GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi 4567224 gb AAD23639.1 AC007119 5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                   167599
Seq. ID
                   LIB3234-041-P1-K1-E5
Method
                   BLASTN
NCBI GI
                   q2337888
BLAST score
                   207
E value
                   1.0e-113
Match length
                   354
% identity
                   97
                   Genomic sequence for Arabidopsis thaliana BAC F14J16,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   167600
                   LIB3234-041-P1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3985949
                   304
BLAST score
E value
                   1.0e-170
                   368
Match length
% identity
                   95
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MOB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167601
Seq. ID
                   LIB3234-041-P1-K1-E8
                   BLASTN
Method
NCBI GI
                   g511598
BLAST score
                   345
E value
                   0.0e + 00
                   377
Match length
                   26
% identity
                  Arabidopsis thaliana cell wall protein (APTR-1) gene,
NCBI Description
                   complete cds
                   167602
Seq. No.
                   LIB3234-041-P1-K1-F10
Seq. ID
                   BLASTX
Method
                   g112682
NCBI GI
BLAST score
                   156
                   2.0e-10
E value
                   78
Match length
                   50
% identity
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
```

cruciferin precursor (CRB) - Arabidopsis thaliana
>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
storage protein [Arabidopsis thaliana]

```
Seq. No.
                   167603
Seq. ID
                   LIB3234-041-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g1084476
BLAST score
                   322
E value
                   5.0e-37
Match length
                   94
                   78
% identity
NCBI Description
                   catalase (EC 1.11.1.6) - maize >gi 311239 emb CAA42720
                   (X60135) catalase-1 [Zea mays]
Seq. No.
                   167604
Seq. ID
                   LIB3234-041-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g2117612
BLAST score
                   352
E value
                   2.0e-33
Match length
                   62
% identity
                   98
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
Seq. No.
                   167605
Seq. ID
                  LIB3234-041-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   561
E value
                   6.0e-58
                   109
Match length
                   98
% identity
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  167606
                  LIB3234-041-P1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1669668
BLAST score
                  306
E value
                  3.0e-28
Match length
                  88
% identity
                  72
NCBI Description
                  (X97131) EF1-alpha [Forsythia x intermedia]
Seq. No.
                  167607 ...
                  LIB3234-041-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3873743
BLAST score
                  251
E value
                  1.0e-21
Match length
                  112
% identity
                  46
NCBI Description
                  (Z66519) similar to Thiamine pyrophosphate enzymes; cDNA
                  EST EMBL: D36315 comes from this gene; cDNA EST EMBL: D33464
```

comes from this gene [Caenorhabditis elegans]

```
167608
Seq. No. ..
                  LIB3234-041-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  221
                  5.0e-18
E value
Match length
                  43
% identity
                  93
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >qi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
                  167609
Seq. No.
                  LIB3234-041-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548655
BLAST score
                  361
E value
                  2.0e-34
Match length
                  83
% identity
                  90
                  50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C)
NCBI Description
                  >qi 541897 pir C53394 ribosomal protein L12.C, chloroplast
                  - Arabidopsis thaliana >qi 468773 emb CAA48183 (X68046)
                  ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.
                  167610
                  LIB3234-041-P1-K1-F8
Seq. ID
Method
                  BLASTN
                  q4557061
NCBI GI
BLAST score
                  140
                  8.0e-73
E value
                  164
Match length
                  96
% identity
                  Arabidopsis thaliana chromosome II BAC F23M2 genomic
NCBI Description
                  sequence, complete sequence
                  167611
Seq. No.
                  LIB3234-041-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4063552
BLAST score
                  594
                  8.0e-62
E value
                  126
Match length
% identity
                  (AF035908) ATP synthase beta subunit [Muntingia calabura]
NCBI Description
Seq. No.
                  167612
Seq. ID
                  LIB3234-041-P1-K1-G10
                  BLASTN
Method
                  g4756963
NCBI GI
                  107
BLAST score
                  4.0e-53
E value
```

Match length

```
% identity
                  88
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                   (ESSA project)
Seq. No.
                  167613
Seq. ID
                  LIB3234-041-P1-K1-G11 ~
Method
                  BLASTN
NCBI GI
                  q4220510
BLAST score
                  333
E value
                  0.0e + 00
Match length
                  373
% identity
                  97
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                   (ESSAII project)
                  167614
Seq. No.
Seq. ID
                  LIB3234-041-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  g4220510
BLAST score
                  277
E value
                  1.0e-154
Match length
                  289
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                   (ESSAII project)
Seq. No.
                  167615
                  LIB3234-041-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206556
BLAST score
                  377
E value
                  2.0e-36
Match length
                  114
% identity
                  68
                  (AF066824) ATP synthase beta subunit [Simaba baileyana]
NCBI Description
                  167616
Seq. No.
                  LIB3234-041-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204299
                  635
BLAST score
E value
                  1.0e-66
                  126
Match length
                  96
% identity
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  167617
Seq. No.
                  LIB3234-041-P1-K1-G4
Seq. ID
                  BLASTX
Method
                  q3335169
NCBI GI
                  665
BLAST score
                  4.0e-70
E value
Match length
                  127
                  97
% identity
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific
```

167618 Seq. No. LIB3234-041-P1-K1-G5 Seq. ID Method BLASTX NCBI GI g4006833 148 BLAST score 2.0e-09 E value 57 Match length % identity 46 NCBI Description (AC005970) putative reverse transcriptase [Arabidopsis thaliana Seq. No. 167619 Seq. ID LIB3234-041-P1-K1-G7 Method BLASTX NCBI GI q3242787 BLAST score 480 E value 2.0e-48 125 Match length 78 % identity NCBI Description (AF055356) respiratory burst oxidase protein E [Arabidopsis thaliana] Seq. No. 167620 Seq. ID LIB3234-041-P1-K1-G8 Method BLASTX NCBI GI q4586053 BLAST score 243 E value 1.0e-20 Match length 125 % identity 46 NCBI Description (AC007020) putative lacasse [Arabidopsis thaliana] Seq. No. 167621 Seq. ID LIB3234-041-P1-K1-G9 Method BLASTN NCBI GI q4586098 BLAST score 349 0.0e+00E value Match length 377 % identity 98 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project) Seq. No. 167622 Seq. ID LIB3234-041-P1-K1-H11 Method BLASTN NCBI GI g3046855 BLAST score 77 E value 1.0e-35 Match length 137 % identity 89 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.

MSL1, complete sequence [Arabidopsis thaliana]

```
LIB3234-041-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120675
BLAST score
                   424
E value
                   7.0e-42
                                                            53 ..
Match length
                   100
% identity
                   81
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                   >qi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                   alba]
Seq. No.
                   167624
                   LIB3234-041-P1-K1-H4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3242700
BLAST score
                   183
                   9.0e-99
E value
                   191
Match length
% identity
                   63
                   Arabidopsis thaliana chromosome II BAC F26B6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   167625
Seq. No.
                   LIB3234-041-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160694
BLAST score
                   492
                   8.0e-50
E value
                   125
Match length
% identity
                   78
                   (U73528) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
                   167626
Seq. No.
Seq. ID
                   LIB3234-041-P1-K1-H6
Method
                   BLASTN
                   g403417
NCBI GI
BLAST score
                   107
                   2.0e-53
E value
Match length
                   118
                   97
% identity
                   Arabidopsis thaliana Columbia bZIP protein GBF4 gene,
NCBI Description
                   complete cds
                   167627
Seq. No.
Seq. ID
                   LIB3234-041-P1-K1-H7
                   BLASTX
Method
                   g3522943
NCBI GI
                   360
BLAST score
                   2.0e-34
E value
Match length
                   124
% identity
                   28
                   (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

Method

BLASTN

```
Seq. ID
                  LIB3234-041-P1-K1-H9
Method
                  BLASTX
                  g3023934
NCBI GI
BLAST score
                  213
E value
                  2.0e-17 :
Match length
                  80
                  50
% identity
                  HISTONE DEACETYLASE 2 (HD2) (YY1 TRANSCRIPTION FACTOR
NCBI Description
                  BINDING PROTEIN) >gi 1667396 (U31758) transcriptional
                  regulator homolog RPD3 [Mus musculus]
Seq. No.
                  167629
                  LIB3234-043-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2088638
BLAST score
                  356
                  0.0e+00
E value
Match length
                  411
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167630
Seq. No.
                  LIB3234-043-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4691223
BLAST score
                  36
                  1.0e-10
E value
                  36
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
NCBI Description
                   (ESSA project)
Seq. No.
                  167631
Seq. ID
                  LIB3234-043-P1-K1-A12
Method
                  BLASTX
NCBÍ GI
                  q4678299
                  622
BLAST score
E value
                  5.0e-65
                  122
Match length
                  99
% identity
                   (AL049655) cysteine proteinase precursor-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  167632
Seq. No.
Seq. ID
                  LIB3234-043-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3869088
                  599
BLAST score
                  2.0e-62
E value
                  117
Match length
                  98
% identity
                  (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
                  167633
Seq. No.
Seq. ID
                  LIB3234-043-P1-K1-A4
```

```
NCBI GI
                   g2264316
BLAST score
                   288
E value
                   1.0e-161
Match length
                   405
% identity _
                   97
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRO11, complete sequence [Arabidopsis thaliana]
                   167634
 Seq. No.
                   LIB3234-043-P1-K1-A9
 Seq. ID
Method
                   BLASTN
NCBI GI
                   g4199934
BLAST score
                   148
                   1.0e-77
E value
                   303
Match length
                   65
 % identity
                   Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   167635
 Seq. No.
                   LIB3234-043-P1-K1-B10
 Seq. ID
Method
                   BLASTX
NCBI GI
                 g4490733
BLAST score
                   468
                   5.0e-47
E value.
Match length
                   96
                   100
 % identity
                  (AL035709) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   167636
                   LIB3234-043-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4559396
BLAST score
                   600
E value
                   2.0e-62
Match length
                   129
 % identity
                   96
NCBI Description (AC006526) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   167637
                   LIB3234-043-P1-K1-B3
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   q2656030
 BLAST score
                   345
                   0.0e+00
 E value
                   406
Match length
 % identity
                   86
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   167638
 Seq. No.
                   LIB3234-043-P1-K1-B4
 Seq. ID
Method
                   BLASTN
NCBI GI
                   q2494110
BLAST score
                   331
E value
                   0.0e + 00
Match length
                   367
```

```
98
% identity
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  167639
Seq. No.
                  LIB3234-043-P1-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3337347
BLAST score
                  43
                  6.0e-15
E value
Match length
                  67
% identity
                  91
                  Arabidopsis thaliana chromosome II BAC F13P17 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167640
Seq. ID
                  LIB3234-043-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g4589445
BLAST score
                  372
                  0.0e+00
E value
Match length
                  396
% identity
                  98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                  MWL2, complete sequence
                  167641
Seq. No.
Seq. ID
                  LIB3234-043-P1-K1-C1
                  BLASTN
Method
                  q3133272
NCBI GI
                  301
BLAST score
                  1.0e-169
E value
Match length
                  405
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T17H7,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167642
Seq. ID
                  LIB3234-043-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g2828188
BLAST score
                  160
E value
                  6.0e-85
Match length
                  232
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3K3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167643
                  LIB3234-043-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3033375
BLAST score
                  281
E value
                  5.0e-25
Match length
                  103
% identity
                  88
                 (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
```

Method

BLASTX

thaliana]

```
167644
Seq. No.
                   LIB3234-043-P1-K1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3894179
BLAST score
                   305
                   1.0e-171
E value
Match length
                   393
% identity
                   94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13H10 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167645
Seq. ID
                   LIB3234-043-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   q4666247
BLAST score
                   66
E value
                   1.0e-28
Match length
                   220
                   83
% identity
NCBI Description Arabidopsis thaliana DNA for germin-like protein precursor,
                  complete cds
Seq. No.
                  167646
Seq. ID
                  LIB3234-043-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  152
                   6.0e-10
E value
Match length
                  102
% identity
                  38
NCBI Description
                 (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  167647
Seq. ID
                  LIB3234-043-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q1143322
                                -5.
BLAST score
                  295
                  7.0e-27
E value
                  102
Match length
% identity
                  61
NCBI Description
                  (U40979) alfa-carboxyltransferase precursor [Glycine max]
Seq. No.
                  167648
Seq. ID
                  LIB3234-043-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g82207
BLAST score
                  602
E value
                  1.0e-62
Match length
                  134
                  87
% identity
NCBI Description hypothetical protein 1708 - common tobacco chloroplast
                  167649
Seq. No.
Seq. ID
                  LIB3234-043-P1-K1-D3
```

BLAST score

```
NCBI GI
                  q4185507
BLAST score
                  466
                  1.0e-46
E value
                  121
Match length
                  81
% identity
                  (AF100163) EZA1 [Arabidopsis thaliana]
NCBI Description
                  167650
Seq. No.
                  LIB3234-043-P1-K1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449332
BLAST score
                  214
E value
                  1.0e-117
Match length
                  331
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSF19, complete sequence [Arabidopsis thaliana]
                  167651
Seq. No.
                  LIB3234-043-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1107501
BLAST score
                  393
                  3.0e-38
E~value
                  99
Match length
% identity
                  80
                  (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
NCBI Description
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                  this gene. [Arabidopsis thaliana]
                  167652
Seq. No.
Seq. ID
                  LIB3234-043-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  g336274
BLAST score
                  90
E value
                  6.0e-43
Match length
                  257
% identity
                  88
                  Alnus incana chloroplast 23S rRNA, 4.5S rRNA, 5S rRNA,
NCBI Description
                  tRNA-Arg, and tRNA-Asn genes
Seq. No.
                  167653
                  LIB3234-043-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1448916
BLAST score
                  359
                  0.0e + 00
E value
Match length
                  399
% identity
                  97
                  Arabidopsis thaliana threonine synthase mRNA, 3' end of cds
NCBI Description
Seq. No.
                  167654
Seq. ID
                  LIB3234-043-P1-K1-E12
Method
                  BLASTN
                  g4580732
NCBI GI
```

BLAST score

```
E value
                   7.0e-21
Match length
                   101
                   88
% identity
                   Genomic sequence for Arabidopsis thaliana BAC F5J5,
NCBI Description
                   complete sequence
                   167655
Seq. No.
                   LIB3234-043-P1-K1-E2
Seq. ID
Method
                   BLASTX
                   q1169515
NCBI GI
BLAST score
                   625
E value
                   2.0e-65
Match length
                   121
% identity
                   EM-LIKE PROTEIN GEA1 >gi 2119768 pir S34819 embryonic
NCBI Description
                   abundant protein Eml - Arabidopsis thaliana
                   \verb|>gi_298070_emb_CAA77509_(Z11158)| Em protein [Arabidopsis thaliana] \\ \verb|>gi_298072_emb_CAA77979_(Z11921)| Em protein \\ |
                   homologue [Arabidopsis thaliana] >gi_3068708 (AF049236) Em1
                   protein [Arabidopsis thaliana]
                   167656
Seq. No.
Seq. ID
                   LIB3234-043-P1-K1-E3
                   BLASTX
Method
                   q3335171
NCBI GI
BLAST score
                   528
E value
                   5.0e-54
Match length
                   122
% identity
                   (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   167657
Seq. ID
                   LIB3234-043-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g2384956
BLAST score
                   231
E value
                   3.0e-19
Match length
                   134
% identity
                   34
                   (AF022985) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   167658
                   LIB3234-043-P1-K1-E7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g12218
BLAST score
                   224
                   1.0e-123
E value
Match length
                   264
% identity
                   96
                   Sinapis alba chloroplast trnG gene for transfer RNA-Gly
NCBI Description
                   167659
Seq. No.
Seq. ID
                   LIB3234-043-P1-K1-E8
Method
                   BLASTX
                   g131360
NCBI GI
```

Match length

```
2.0e-20
E value
                    61
Match length
                    80
% identity
                    PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
NCBI Description
                    >gi 81727 pir S02115 photosystem II protein psbK precursor
                    - white mustard chloroplast >gi 12209 emb CAA31909
                    (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
                    167660
Seq. No.
                    LIB3234-043-P1-K1-F4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g728873
BLAST score
                    168
                    7.0e-12
E value
Match length
                    37
                    81
% identity
NCBI Description
                    L-ASCORBATE PEROXIDASE, CYTOSOLIC (AP)
                    >gi 322534 pir S28856 L-ascorbate peroxidase (EC
                    1.11.1.11), cytosolic - Arabidopsis thaliana

>gi_16173_emb_CAA42168_ (X59600) L-ascorbate peroxidase

[Arabidopsis thaliana] >gi_217833_dbj_BAA03334_ (D14442)
                    ascorbate peroxidase [Arabidopsis thaliana] >gi_1532170
                    (U63815) ascorbate peroxidase [Arabidopsis thaliana]
Seq. No.
                    167661
                    LIB3234-043-P1-K1-F5
Seq. ID
Method
                    BLASTX
NCBI GI
                    q132074
                    193
BLAST score
                    3.0e-15
E value
Match length
                    62
% identity
                    61
NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                    (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    Al precursor - Arabidopsis thaliana
Seq. No.
                    167662
Seq. ID
                    LIB3234-043-P1-K1-F9
Method
                    BLASTX
NCBI GI
                    g117820
BLAST score
                    245
E value
                    8.0e-21
Match length
                    50
                    100
% identity
                    CYTOCHROME B6 >gi 625192 pir CBSP6
NCBI Description
                    plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - spinach chloroplast >gi_12285_emb_CAA30128_
                    (X07106) petB [Spinacia oleracea]
Seq. No.
                    167663
                    LIB3234-043-P1-K1-G12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3157930
BLAST score
                    82
                    7.7e-02
E value
```

```
% identity
                    90
  NCBI Description
                    (AC002131) Strong similarity to
                    amino-cyclopropane-carboxylic acid oxidase gb_L27664 from
                    Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from
                    this gene. [Arabidopsis thaliana]
  Seq. No.
                    167664
  Seq. ID
                    LIB3234-043-P1-K1-G2
 Method
                    BLASTX
  NCBI GI
                    g3327196
 BLAST score
                    281
  E value
                    5.0e-25
 Match length
                    75
  % identity
                    71
 NCBI Description (AB014591) KIAA0691 protein [Homo sapiens]
 Seq. No.
                    167665
 Seq. ID
                    LIB3234-043-P1-K1-G3
 Method
                    BLASTX
 NCBI GI
                    g2245110
 BLAST score
                    271
 E value
                    7.0e-24
 Match length
                    54
 % identity
                    98
 NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   167666
 Seq. ID
                   LIB3234-043-P1-K1-G6
 Method
                   BLASTN
 NCBI GI
                   g2244788
 BLAST score
                   150
 E value
                   9.0e-79
 Match length
                   333
 % identity
                   94
 NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
 Seq. No.
                   167667
Seq. ID
                   LIB3234-043-P1-K1-G7
 Method
                   BLASTX
 NCBI GI
                   g2605714
 BLAST score
                   438
 E value
                   2.0e-43
 Match length
                   107
 % identity
                   81
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
 NCBI Description
                   thaliana]
 Seq. No.
                   167668
 Seq. ID
                   LIB3234-043-P1-K1-G8
Method
                   BLASTN
NCBI GI
                   g3985955
BLAST score
                   303
E value
                   1.0e-170
Match length
                  396
% identity
                  77
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
```

```
MTH16, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     167669
  Seq. ID
                     LIB3234-043-P1-K1-H1
  Method
                     BLASTN
  NCBI GI
                     g4589950
  BLAST score
                     367
                                        . مرجر:
  E value
                     0.0e+00
  Match length
                     408
  % identity
                     97
  NCBI Description
                    Arabidopsis thaliana chromosome II BAC T28P16 genomic
                    sequence, complete sequence
  Seq. No.
                    167670
  Seq. ID
                    LIB3234-043-P1-K1-H11
  Method
                    BLASTN
  NCBI GI
                    g3757512
  BLAST score
                    121
 E value
                    1.0e-61
 Match length
                    171
 % identity
                    62
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F12A24 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   167671
 Seq. ID
                   LIB3234-043-P1-K1-H12
 Method
                   BLASTN
 NCBI GI
                   g4309747
 BLAST score
                   292
 E value
                   1.0e-163
 Match length
                   312
 % identity
                   28
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC T13E11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   167672
Seq. ID
                   LIB3234-043-P1-K1-H2
Method
                   BLASTN
NCBI GI
                   g3402695
BLAST score
                   50
E value
                   4.0e-19
Match length
                   155
% identity
                   87
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T3K9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167673
Seq. ID
                  LIB3234-043-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g4678307
BLAST score
                  580
E value
                  4.0e-60
Match length
                  116
% identity
                  100
NCBI Description
                  (AL049655) vacuolar protein sorting-like protein
                  [Arabidopsis thaliana]
```

NCBI GI

```
Seq. No.
                  167674
                  LIB3234-043-P1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1946354
                  230
BLAST score
E value
                  1.0e-126
                  406
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  167675
Seq. ID
                  LIB3234-046-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q3785999
BLAST score
                  470
E value
                  3.0e-47
Match length
                  107
                  84
% identity
                  (AC005499) putative peptidyl-prolyl cis-trans isomerase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  167676
Seq. ID
                  LIB3234-046-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  66
E value
                  1.0e-28
Match length
                  191
% identity
                  90
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                  167677
Seq. ID
                  LIB3234-046-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  q3327867
BLAST score
                  389
E value
                  0.0e + 00
Match length
                  389
% identity
                  100
                  Arabidopsis thaliana CIP7 mRNA for COP1-Interacting Protein
NCBI Description
                  7, complete cds
Seq. No.
                  167678
Seq. ID
                  LIB3234-046-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  g2154718
BLAST score
                  340
E value
                  0.0e + 00
Match length
                  390
% identity
                  97
NCBI Description A.thaliana nit2 gene, nit1 gene and nit3 gene
Seq. No.
                  167679
                  LIB3234-046-P1-K1-A2
Seq. ID
                  BLASTX
Method
```

g2317902

```
BLAST score
                   714
                   7.0e-76
E value
                   130
Match length
% identity
                   100
                  (U89959) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   167680
Seq. No.
Seq. ID
                   LIB3234-046-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g2262167
BLAST score
                   578
E value
                   7.0e-60
Match length
                   110
                   100
% identity
NCBI Description
                   (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
                   thalianal
Seq. No.
                   167681
Seq. ID
                   LIB3234-046-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   g99992
BLAST score
                   485
E value
                   5.0e-49
Match length
                   129
% identity
                   53
                  protein disulfide-isomerase (EC 5.3.4.1) precursor -
NCBI Description
                   alfalfa (clone B2) >gi 166418 (M82973) putative
                   endomembrane protein; putative [Medicago sativa]
Seq. No.
                   167682
Seq. ID
                  LIB3234-046-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g1531762
BLAST score
                  195
E value
                  5.0e-15
Match length
                  51
% identity
                  75
NCBI Description
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  167683
Seq. ID
                  LIB3234-046-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3808062
BLAST score
                  153
                  4.0e-10
E value
Match length
                  66
% identity
                  44
NCBI Description
                  (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  167684
Seq. ID
                  LIB3234-046-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1814424
BLAST score
                  223
                  3.0e-18
E value
Match length
                  77
```

Method

BLASTN

```
% identity
                  55
NCBI Description (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
                  167685
Seq. No.
                  LIB3234-046-P1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4678299
BLAST score
                  661
                  1.0e-69
E value
                  126
Match length
                  100
% identity
NCBI Description
                  (AL049655) cysteine proteinase precursor-like protein
                  [Arabidopsis thaliana]
                  167686
Seq. No.
                  LIB3234-046-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262116
BLAST score
                  664
                  5.0e-70
E value
Match length
                  129
                 . 98
% identity
NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.
                  167687
                LIB3234-046-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1592675
BLAST score
                  313
                  8.0e-29
E value
Match length
                  108
% identity
                  61
NCBI Description (X91919) LEA76 homologue typel [Arabidopsis thaliana]
Seq. No.
                  167688
Seq. ID
                  LIB3234-046-P1-K1-B12
                  BLASTX
Method
                  q1619602
NCBI GI-
BLAST score
                  369
E value
                  2.0e-35
Match length
                  87
                  79
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                  167689
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1592677
BLAST score
                  193
E value
                  9.0e-15
                  38
Match length
                  100
% identity
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.
                  167690
Seq. ID
                  LIB3234-046-P1-K1-B4
```

Match length

```
g4589969
NCBI GI
BLAST score
                  147
                  6.0e-77
E value
                  262
Match length
                  61
% identity
                  Arabidopsis thaliana chromosome II BAC F1P15 genomic
NCBI Description
                  sequence, complete sequence
                  167691
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q2213606
                  390
BLAST score
                  0.0e + 00
E value
                  390
Match length
                  100
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F21J9,
                  complete sequence [Arabidopsis thaliana]
                  167692
Seq. No.
                  LIB3234-046-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1592677
BLAST score
                   201
                  9.0e-16
E value
                  92
Match length
                   49
% identity
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
                  167693
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-B8
Method
                  BLASTX
NCBI GI
                   q3176874
BLAST score
                   545
E value
                   4.0e-56
Match length
                   121
                  89
% identity
NCBI Description
                   (AF065639) cucumisin-like serine protease [Arabidopsis
                   thaliana]
                   167694
Seq. No.
                  LIB3234-046-P1-K1-B9
Seq. ID
Method
                  BLASTX
                   g2511725
NCBI GI
BLAST score
                   674
E value
                   4.0e-71
Match length
                   128
% identity -
                   100
                   (AF021937) catalase 1 [Arabidopsis thaliana]
NCBI Description
                   167695
Seq. No.
                  LIB3234-046-P1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g112740
BLAST score
                   269
                   1.0e-23
E value
```

BLAST score

```
52
% identity
                  NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)
NCBI Description
                  >qi 81691 pir A25997 napin precursor (napA) - rape
                  >qi 167153 (J02586) prepronapin [Brassica napus] >qi 167155
                  (J02798) napin [Brassica napus]
                  167696
Seq. No.
                  LIB3234-046-P1-K1-C10
Seq. ID
Method
                  BLASTX
                  g2622920
NCBI GI
                  304
BLAST score
E value
                  9.0e-28
Match length
                  123
% identity
                  44
                  (AE000933) dTDP-glucose 4,6-dehydratase [Methanobacterium
NCBI Description
                  thermoautotrophicum]
                  167697
Seq. No.
                  LIB3234-046-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213608
BLAST score
                  233
E value
                  2.0e-19
Match length
                  129
                 ; 36
% identity
NCBI Description (AC000103) F21J9.2 [Arabidopsis thaliana]
                  167698
Seq. No.
                  LIB3234-046-P1-K1-C12
Seq. ID
Method
                  BLASTX
                  g1502428
NCBI GI
                  335
BLAST score
E value
                  2.0e-31
Match length
                  66
% identity
                  100
NCBI Description
                  (U62330) phosphate transporter [Arabidopsis thaliana]
                  >gi_2258116_dbj_BAA21503_ (D86591) inorganic phosphate
                  transporter [Arabidopsis thaliana]
                  >gi_2258118_dbj_BAA21504_ (D86608) inorganic phosphate
                  transporter [Arabidopsis thaliana]
                  167699
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  q4092472
BLAST score
                  36
E value
                  3.0e-11
Match length
                  36
                  100
% identity
                  Arabidopsis thaliana BAC F1K3 from chromosome IV near 21
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
                  167700
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  g4220643
```

```
E value
                   4.0e-19
Match length
                   188
% identity
                   88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MWD22, complete sequence [Arabidopsis thaliana]
                   167701
Seq. No.
Seq. ID
                   LIB3234-046-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1709970
BLAST score
                  . 360
E value
                   2.0e-34
Match length.
                   73
% identity
                   96
NCBI Description
                  60S RIBOSOMAL PROTEIN L10A
Seq. No.
                  167702
Seq. ID
                  LIB3234-046-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g4704824
BLAST score
                   359
E value
                   3.0e-34
Match length
                   117
% identity
                   60
                   (AF139377) stearoyl acyl carrier protein desaturase
NCBI Description
                  Lldd3A20 [Lupinus luteus]
Seq. No.
                  167703
Seq. ID
                  LIB3234-046-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q2244905
BLAST score
                  208
E value
                  2.0e-16
Match length
                  54
% identity
                  80
NCBI Description
                   (Z97339) indole-3-acetate beta-glucosyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                  167704
Seq. ID
                  LIB3234-046-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g4220643
BLAST score
                  356
E value
                  0.0e + 00
Match length
                  384
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167705
Seq. ID
                  LIB3234-046-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g343503
BLAST score
                  183
E value
                  1.0e-13
Match length
                  36
% identity
                  100
```

Metĥod

NCBI GI

BLAST score

BLASTN g4733952

```
(L12250) ribosomal protein S12 [Nicotiana plumbaginifolia]
NCBI Description
                  >qi 1334367 emb CAA27200 (X03481) rps12-like coding
                  sequence [Nicotiana tabacum] >gi 2924276 emb CAA77429_
                  (Z00044) ribosomal protein S12 [Nicotiana tabacum]
                  >qi 2924283 emb CAA77436 (Z00044) ribosomal protein S12
                  [Nicotiana tabacum]
                  167706
Seq. No.
                  LIB3234-046-P1-K1-D1
Seq. ID
                  BLASTX
Method
                  g1107501
NCBI GI
                  378
BLAST score
                  2.0e-36
E value
                  119
Match length
                  66
% identity
                  (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
NCBI Description
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb_{Z17604}, gb_{H76594}, gb_{AA597972} and gb_{AA394824} come from
                  this gene. [Arabidopsis thaliana]
                  167707
Seq. No.
                  LIB3234-046-P1-K1-D11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4510392
                  210
BLAST score
                  1.0e-114
E value
                  387
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T17D12 genomic
NCBI Description
                  sequence, complete sequence
                  167708
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-D12
                  BLASTN
Method
NCBI GI
                  q3135250
BLAST score
                  56
E value
                  1.0e-22
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F27F23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167709
Seq. No.
Seq. ID
                  LIB3234-046-P1-K1-D2
Method
                  BLASTX
                  q4678306
NCBI GI
                  132
BLAST score
E value
                  1.0e-11
                  83
Match length
% identity
                 (AL049655) kinesin-like protein [Arabidopsis thaliana]
NCBI Description
                  167710
Seq. No.
                  LIB3234-046-P1-K1-D3
Seq. ID
```

```
1.0e-156
E value
                  387
Match length
                  93
% identity
                 Arabidopsis thaliana chromosome I BAC F23H11 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  167711
                 LIB3234-046-P1-K1-D4
Seq. ID
Method
                  BLASTN
                  g2564049
NCBI GI
BLAST score
                  392
                  0.0e+00
E value
Match length
                  392
                  100
% identity
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLE2, complete sequence [Arabidopsis thaliana]
                  167712
Seq. No.
                  LIB3234-046-P1-K1-D6
Seq. ID
Method
                  BLASTX
                  q4006827
NCBI GI
                  259
BLAST score
                  2.0e-22
E value
                  130
Match length
% identity
                  44
NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                  167713
                  LIB3234-046-P1-K1-D7
Seq. ID
                  BLASTX
Method
                  q2582381
NCBI GI
BLAST score
                  604
                  6.0e-63
E value
                  127
Match length
                  87
% identity
                 (AF021220) cation-chloride co-transporter [Nicotiana
NCBI Description
                  tabacum]
                  167714
Seq. No.
                  LIB3234-046-P1-K1-D8
Seq. ID
                  BLASTX
Method
                  g112682
NCBI GI
BLAST score
                  158
                  4.0e-23
E value
Match length
                  124
                  55
% identity
                 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  167715
Seq. No.
                  LIB3234-046-P1-K1-D9
Seq. ID
Method
                  BLASTN
                  g4589421
NCBI GI
```

36

BLAST score

```
9.0e-11
E value
Match length
                  70
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K5K13, complete sequence
                  167716
Seq. No.
                  LIB3234-046-P1-K1-E1
Seq. ID
                  BLASTX
Method
                  g1169476
NCBI GI
                  595
BLAST score
                  7.0e-62
E value
                  113
Match length
% identity
                  100
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
                  167717
Seq. No.
                  LIB3234-046-P1-K1-E10
Seq. ID
                  BLASTN
Method
                  g2264316
NCBI GI
                  38
BLAST score
                  6.0e-12
E value
                  156
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167718
                  LIB3234-046-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g1184075
NCBI GI
BLAST score
                  153
                  4.0e-10
E value
                  129
Match length
% identity
                  1
                  (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]
NCBI Description
                  >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon
                  esculentum]
Seq. No.
                  167719
                  LIB3234-046-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g633890
                  287
BLAST score
                  8.0e-26
E value
                  88
Match length
% identity
                  65
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                  vulgare]
                  167720
Seq. No.
                  LIB3234-046-P1-K1-E2
Seq. ID
                  BLASTX
Method
                  g82232
NCBI GI
```

562

BLAST score

Match length

```
E value
                  5.0e-58
                  129
Match length
                  84
% identity
NCBI Description rpoC protein homolog - common tobacco chloroplast
                  167721
Seq. No.
                  LIB3234-046-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2708750
BLAST score
                  316
E value
                  3.0e-29
Match length
                  128
                  55
% identity
NCBI Description
                  (AC003952) putative physical impedence protein [Arabidopsis
Seq. No.
                  167722
                  LIB3234-046-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1077345
BLAST score
                  154
E value
                  3.0e-10
Match length
                  82
% identity
NCBI Description
                  hypothetical protein YLR290c - yeast (Saccharomyces
                  cerevisiae) >gi 596046 (U17243) L8003.16 gene product
                  [Saccharomyces cerevisiae]
                  167723
Seq. No.
                  LIB3234-046-P1-K1-E5
Seq. ID
Method
                  BLASTX
                  q2454184
NCBI GI
BLAST score
                  629
                  7.0e-66
E value
                  127
Match length
% identity
                  99
                  (U80186) pyruvate dehydrogenase El beta subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  167724
                  LIB3234-046-P1-K1-E6
Seq. ID
Method
                  BLASTN
                  q3367500
NCBI GI
BLAST score
                  329
                  0.0e + 00
E value
Match length
                  394 .
% identity
                  96
                 REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                  TO: 93489, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167725
Seq. ID
                  LIB3234-046-P1-K1-E7
Method
                  BLASTX
                  g3402716
NCBÎ GI
BLAST score
                  183
                  1.0e-13
E value
```

```
% identity
NCBI Description
                  (AC004261) unknown protein [Arabidopsis thaliana]
Seq. No.
                  167726
                  LIB3234-046-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2529229
                                                    . .
BLAST score
                  516
E value
                  1.0e-52
Match length
                  127
% identity
                  81
                  (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                  167727
                  LIB3234-046-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q465835
BLAST score
                  443
E value
                  4.0e-44
Match length
                  129
% identity
                  HYPOTHETICAL 272.0 KD PROTEIN C50C3.6 IN CHROMOSOME III
NCBI Description
                  >gi_630577_pir__S44625 C50C3.6 protein - Caenorhabditis
                  elegans >gi_289658 (L14433) putative [Caenorhabditis
                  elegans]
Seq. No.
                  167728
Seq. ID
                  LIB3234-046-P1-K1-F10
Method
                  BLASTX
                  g135406
NCBI GI
BLAST score
                  418
                  3.0e-41
E value
Match length
                  80
                  97
% identity
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin
NCBI Description
                  alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                  167729
                  LIB3234-046-P1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g119143
BLAST score
                  605
                  4.0e-63
E value
Match length
                  115
                  100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_81606_pir__S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453
                  (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1369927 emb CAA34454 (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                  >gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
```

```
167730
Seq. No.
Seq. ID
                   LIB3234-046-P1-K1-F12
Method
                   BLASTX
                   g4204298
NCBI GI
BLAST score
                   558
                   1.0e-57
E value
                   125
Match length
% identity
                   86
                    (AC003027) lcl_prt_seq No definition line found
NCBI Description
                    [Arabidopsis thaliana]
                   167731
Seq. No.
                   LIB3234-046-P1-K1-F4
Seq. ID
Method
                   BLASTX
                   q4586109
NCBI GI
BLAST score
                   314
                    6.0e-29
E value
                    58
Match length
% identity
                   100
                   (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
                   167732
Seq. No.
                   LIB3234-046-P1-K1-F5
Seq. ID
                   BLASTX
Method
                    g2894598
NCBI GI
BLAST score
                    696
E value
                    1.0e-73
Match length
                    131
                   100
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                    167733
Seq. No.
                   LIB3234-046-P1-K1-F7
Seq. ID
                    BLASTX
Method
                                                          4
                    g2832703
NCBI GI
BLAST score
                    381
                    7.0e-37
E value
                    79
Match length
                    95
% identity
                   (AL021713) potassium channel protein KAT2 [Arabidopsis
NCBI Description
                    thaliana]
                    167734
Seq. No.
                    LIB3234-046-P1-K1-F9
Seq. ID
Method
                    BLASTX
                    g4507311
NCBI GI
BLAST score
                    215
E value
                    2.0e-17
Match length
                    103
% identity
                    40
                    suppressor of Ty (S.cerevisiae) 4 homolog 1
NCBI Description
                    >gi 3122873 sp Q16550 SPT4 HUMAN TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1 >gi 1209779 (U43923) similar to
                    Saccharomyces cerevisiae Spt4; protein has potential
                    N-terminal zinc-finger [Homo sapiens] >gi_1401053 (U38818) SUPT4H [Homo sapiens] >gi_1401055 (U38817) SUPT4H [Homo
```

Match length

```
[Mus musculus]
                  167735
Seq. No.
                  LIB3234-046-P1-K1-G1
Seq. ID
                  BLASTN
Method
                  q4220643
NCBI GI
BLAST score
                  363
                  0.0e+00
E value
Match length
                  388
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWD22, complete sequence [Arabidopsis thaliana]
                  167736
Seq. No.
                  LIB3234-046-P1-K1-G10
Seq. ID
                  BLASTX
Method
                  q1168410
NCBI GI
BLAST score
                  639
                  5.0e-67
E value
                  129
Match length
% identity
                  94
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2
NCBI Description
                  >gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi_927505_emb_CAA61947_ (X89829)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
                  167737
Seq. No.
                  LIB3234-046-P1-K1-G11
Seq. ID
                  BLASTN
Method
                  g4586065
NCBI GI
                  95
BLAST score
E value
                  6.0e-46
Match length
                  231
                  85
% identity
                  Arabidopsis thaliana chromosome II BAC T17A11 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  167738
                  LIB3234-046-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264307
BLAST score
                  225
E value
                  1.0e-123
Match length
                  255
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MED24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167739
                  LIB3234-046-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4262250
BLAST score
                  459
                  6.0e-46
E value
```

sapiens] >qi 1401066 (U43154) Supt4h [Mus musculus]

>qi 3779194 (U96809) chromatin structural protein homolog

```
100
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167740
                  LIB3234-046-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1592677
BLAST score
                  382
                  6.0e-37
E value
Match length
                  123
% identity
                  69
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167741
                  LIB3234-046-P1-K1-G7
Seq. ID
Method
                  BLASTN
                  g3659491
NCBI GI
BLAST score
                  385
                  0.0e + 00
E value
Match length
                  385
                  100
% identity
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167742
                  LIB3234-046-P1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2924733
                  135
BLAST score
                   7.0e-70
E value
                   207
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
                  167743
Seq. No.
                  LIB3234-046-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1916613
BLAST score
                   517
                   9.0e-53
E value
                   108
Match length
                   100
% identity
                  (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]
NCBI Description
                   167744
Seq. No.
                  LIB3234-046-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3264778
BLAST score
                   562
E value
                   4.0e-58
                   118
Match length
                   93
% identity
                   (AF072536) H-protein promoter binding factor-1 [Arabidopsis
NCBI Description
                   thaliana]
```

167745

Seq. No.

Method

```
Seq. ID
                   LIB3234-046-P1-K1-H11
Method
                   BLASTN
NCBI GI
                   q3449327
BLAST score
                   340
E value
                   0.0e+00 ·
                   379 -
Match length
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCA23, complete sequence [Arabidopsis thaliana]
                   167746
Seq. No.
                   LIB3234-046-P1-K1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3395441
BLAST score
                   431
                   1.0e-42
E value
                   110
Match length
 % identity
                   75
                   (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   167747
                   LIB3234-046-P1-K1-H2
 Seq. ID
                   BLASTX
Method
                   g4204298
NCBI GI
BLAST score
                   540
                   2.0e-55
 E value
Match length
                   112
                   92
 % identity
                   (AC003027) lcl_prt_seq No definition line found
 NCBI Description
                   [Arabidopsis thaliana]
 Seq. No.
                   167748
                   LIB3234-046-P1-K1-H3
 Seq. ID
                   BLASTN
Method
NCBI GI
                   g4519187
                   115
BLAST score
                   5.0e-58
E value
                   315
Match length
                   94
 % identity
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                   K1G2, complete sequence
                   167749
 Seq. No.
                   LIB3234-046-P1-K1-H4
 Seq. ID
                   BLASTX
 Method
                   g1628583
 NCBI GI
 BLAST score
                   674
                   4.0e-71
 E value
                   129
 Match length
                   100
 % identity
 NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   167750
 Seq. No.
                   LIB3234-046-P1-K1-H5
 Seq. ID
```

BLASTN

E value

```
g3510339
NCBI GI
BLAST score
                  400
                  0.0e+00
E value
Match length
                  400
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3K7, complete sequence [Arabidopsis thaliana]
                  167751
Seq. No.
                  LIB3234-046-P1-K1-H6
Seq. ID
                  BLASTN
Method
                  g3241927
NCBI GI
BLAST score
                  227
                  1.0e-125
E value
                  271
Match length
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTE17, complete sequence [Arabidopsis thaliana]
                  167752
Seq. No.
                  LIB3234-046-P1-K1-H8
Seq. ID
                  BLASTX
Method
                  g4490330
NCBI GI
BLAST score
                  558
                  1.0e-57
E value
Match length
                  128
                  87
% identity
                  (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  167753
Seq. No.
                  LIB3234-046-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1313927
                   45
BLAST score
                   4.0e-16
E value
Match length
                  168
                  83
% identity
                  B.oleracea mRNA for IFA binding protein (sp10)
NCBI Description
                  167754
Seq. No.
                  LIB3234-047-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q3241926
BLAST score
                   85
                   2.0e-40
E value
Match length
                   157
                   89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSG15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167755
                   LIB3234-047-P1-K1-A10
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4757414
                   322
BLAST score
                   0.0e + 00
```

```
Match length
                    354
 % identity
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MYF24, complete sequence
Seq. No.
                    167756
 Seq. ID
                   LIB3234-047-P1-K1-A2
 Method
                   BLASTX
 NCBI GI
                    g1352663
 BLAST score
                    478
 E value
                    4.0e-48
 Match length
                   91
                   99
 % identity
 NCBI Description
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC
                   SUBUNIT >gi_1076388_pir__S52659 phosphoprotein phosphatase
                    (EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana
                   >gi 466441 (M96841) Ser/Thr protein phosphatase
                    [Arabidopsis thaliana]
                   >gi_4559341_gb AAD23003.1_AC007087_22 (AC007087)
                   serine/threonine protein phosphatase PP2A-3 catalytic
                   subunit [Arabidopsis thaliana]
                   >gi_4567320_gb AAD23731.1 AC005956 20 (AC005956)
                   serine/threonine protein phosphatase [Arabidopsis thaliana]
 Seq. No.
                   167757
 Seq. ID
                   LIB3234-047-P1-K1-A4
 Method
                   BLASTX
 NCBI GI
                   q1084351
 BLAST score
                   155
 E value
                   9.0e-15
 Match length
                   83
 % identity
                   58
 NCBI Description
                   napin - rape >gi 468018 (U04943) napin [Brassica napus]
                   >gi_468020 (U04944) napin [Brassica napus]
 Seq. No.
                   167758
 Seq. ID _
                   LIB3234-047-P1-K1-A5
Method :
                   BLASTX
 NCBI GI
                   g1903360
 BLAST score
                   184
 E value
                   8.0e-14
Match length
                   76
 % identity
                   54
NCBI Description
                   (ACO00104) Similar to Arabidopsis 2A6 (gb_X83096). EST
                   gb_T76913 comes from this gene. [Arabidopsis thaliana]
Seq. No.
                   167759
Seq. ID
                   LIB3234-047-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g3687228
BLAST score
                   504
E value
                   5.0e-51
Match length
                   112
% identity
                   95
NCBI Description
                   (AC005169) putative malate dehydrogenase [Arabidopsis
```

thaliana]

Seq. ID

```
Seq. No.
                  167760
                  LIB3234-047-P1-K1-A7
Seq. ID
Method
                  BLASTN
                  g3236234
NCBI GI
                  35
BLAST score
                  3.0e-10
E value
                  122
Match length
% identity
                  82
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  167761
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-A9
                  BLASTX
Method
NCBI GI
                  q2583125
BLAST score
                  52
                  5.0e-55
E value
                  118
Match length
                  96
% identity
                  (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167762
Seq. ID
                  LIB3234-047-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g2351062
BLAST score
                  404
                  0.0e+00
E value
Match length
                  412
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167763
Seq. ID
                  LIB3234-047-P1-K1-B10
Method
                  BLASTN
                  g4544435
NCBI GI
                  184
BLAST score
E value
                  4.0e-99
                  333
Match length
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC F14M13 genomic
NCBI Description
                  sequence, complete sequence
                  167764
Seq. No.
                  LIB3234-047-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4519195
                  68
BLAST score
E value
                  8.0e-30
                  172
Match length
% identity
                  45
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MQC12, complete sequence
                  167765
Seq. No.
                  LIB3234-047-P1-K1-B12
```

```
Method
                  BLASTX
                  g3786005
NCBI GI
BLAST score
                  372
                  8.0e-36
E value
                  87
Match length
                  63
% identity
                  (AC005499) putative phosphoethanolamine
NCBI Description
                  cytidylyltransferase [Arabidopsis thaliana]
                  167766
Seq. No.
                  LIB3234-047-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1168972
BLAST score
                  258
                  2.0e-22
E value
                  56
Match length
                  95
% identity
                  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
NCBI Description
                  PRECURSOR >gi_480969_pir__S37557 clpA protein - rape
                  (fragment) >gi_406311_emb_CAA53077 (X75328) clpA [Brassica
                  napus]
                  167767
Seq. No.
                  LIB3234-047-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  a3212102
BLAST score
                  297
E value
                  1.0e-166
                  373
Match length
                  100
% identity
                  Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  167768
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q120675
BLAST score
                  450
E value
                  6.0e-45
Match length
                  89
                  94
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                  >gi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                  alba]
                  167769
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-B5
Method
                  BLASTX
                  q3335169
NCBI GI
                  533
BLAST score
                  1.0e-54
E value
Match length .
                  119
% identity
                  83
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
```

>gi 4455197 emb_CAB36520.1 (AL035440) embryo-specific

BLAST score

421

protein 1 (ATS1) [Arabidopsis thaliana]

```
Seq. No.
                  167770
                  LIB3234-047-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  q2160133
NCBI GI
BLAST score
                  287
                  9.0e-26
E value
                  119
Match length
                  54
% identity
                  (AC000375) Strong similarity to Arabidopsis
NCBI Description
                  gb X91953, F19K23.3, F19K23.15. ESTs
                  gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this
                  gene. [Arabidopsis thaliana]
                  167771
Seq. No.
                  LIB3234-047-P1-K1-B8
Seq. ID
Method
                  BLASTX
                  g3377797
NCBI GI
                  477
BLAST score
                  5.0e-48
E value
                  121
Match length
                  77
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                  167772
Seq. No.
                  LIB3234-047-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1216389
BLAST score
                  510
E value
                  4.0e-52
Match length
                  95
                  99
% identity
                  (U39289) myrosinase-associated protein [Brassica napus]
NCBI Description
                  >gi_1589009_prf__2209432A myrosinase-associated
                  protein: ISOTYPE=5 [Brassica napus]
                  167773
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                  572
                  3.0e-59
E value
Match length
                  127
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  167774
Seq. ID
                  LIB3234-047-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g4510383
```

NCBI GI

g228416

```
1.0e-41
E value
                  111
Match length
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                  167775
Seq. No.
                  LIB3234-047-P1-K1-C3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3327922
BLAST score
                  119
                  3.0e-60
E value
Match length
                  388
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T31E10 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167776
                  LIB3234-047-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160158
BLAST score
                  466
E value
                  9.0e-47
                - 109
Match length
                  83
% identity
                  (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                  (gb_EF1G_XENLA). ESTs gb T20564,gb T45940,gb T04527 come
                  from this gene. [Arabidopsis thaliana]
                  167777
Seq. No.
                  LIB3234-047-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g2924779
NCBI GI
                  277
BLAST score
                  6.0e-25
E value
                  84
Match length
                  69
% identity
                  (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
NCBI Description
                  thaliana] >gi_2981616_dbj_BAA25248_ (AB008854)
                  3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                  >gi 2981618 dbj BAA25249 (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
                  167778
Seq. No.
                  LIB3234-047-P1-K1-D1
Seq. ID
Method
                  BLASTN
                  g3449313
NCBI GI
                  75
BLAST score
                  5.0e-34
E value
                  226
Match length
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21P3, complete sequence [Arabidopsis thaliana]
                  167779
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-D11
Method
                  BLASTX
```

```
BLAST score
                  478
                  3.0e-48
E value
                  118
Match length
% identity
                  87
NCBI Description
                  oleosin [Brassica napus]
                  167780
Seq. No.
                  LIB3234-047-P1-K1-D12
Sea. ID
Method
                  BLASTX
                  g3269286
NCBI GI
BLAST score
                  498
                  1.0e-50
E value
Match length
                  120
% identity
                  89
NCBI Description
                  (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  167781
                  LIB3234-047-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1864017
BLAST score
                  521
E value
                  3.0e-53
Match length
                  100
% identity
                  99
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
Seq. No.
                  167782
                  LIB3234-047-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2118220
                  405
BLAST score
                  1.0e-39
E value
Match length
                  97
                  56
% identity
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
NCBI Description
                  (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16
                  kDa proteolipid [Arabidopsis thaliana]
                  >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar
                  H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                  >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
                  ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
                  >gi 4589976 gb AAD26493.1 AC007195 7 (AC007195) vacuolar
                  H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.
                  167783
                  LIB3234-047-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1345973
BLAST score
                  311
                  7.0e-29
E value
Match length
                  61
% identity
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
```

1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)

Method

NCBI GI

BLAST score

BLASTX g115767

568

omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

```
Seq. No.
                  167784
                  LIB3234-047-P1-K1-D7
Seq. ID
                  BLASTX
Method
                  g544134
NCBI GI
                  261
BLAST score
E value
                  1.0e-22
Match length
                  90
                  51
% identity
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
NCBI Description
                  >gi 99720 pir S22863 hypothetical protein - Arabidopsis
                  thaliana >gi 421844 pir A46260 RecA functional analog
                  DRT100 - Arabidopsis thaliana (fragment)
                  167785
Seq. No.
                  LIB3234-047-P1-K1-D8
Seq. ID
Method
                  BLASTX
                  g2199574
NCBI GI
BLAST score
                  560
                  9.0e-58
E value
                  106
Match length
                  99
% identity
NCBI Description
                  (AF004293) aquaporin [Brassica rapa]
                  167786
Seq. No.
                  LIB3234-047-P1-K1-E1
Seq. ID
Method
                  BLASTN
                  g3449312
NCBI GI
BLAST score
                  286
E value
                  1.0e-160
Match length
                  337
                  96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K16L22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167787
Seq. ID
                  LIB3234-047-P1-K1-E10
Method
                  BLASTN
                  q4589439
NCBI GI
                  344
BLAST score
                  0.0e + 00
E value
Match length
                  348
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQM1, complete sequence
                  167788
Seq. No.
                  LIB3234-047-P1-K1-E11
Seq. ID
```

Seq. ID

```
9.0e-59
E value
Match length
                  110
% identity
                  98
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  167789
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-E2
Method
                  BLASTX
                  g729857
NCBI GI
BLAST score
                  170
                  3.0e-12
E value
Match length
                  87
% identity
                  38
                  SERINE/THREONINE-PROTEIN KINASE IRE1 PRECURSOR
NCBI Description
                  >gi 539088 pir A47541 protein kinase IRE1 (EC 2.7.1.-)
                  precursor - yeast (Saccharomyces cerevisiae) >gi_393281
                  (L19640) ERN1 [Saccharomyces cerevisiae]
Seq. No.
                  167790
                  LIB3234-047-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2454183
BLAST score
                  60
                  4.0e-25
E value
Match length
                  124
% identity
                  87
                  Arabidopsis thaliana pyruvate dehydrogenase El beta subunit
NCBI Description
                  mRNA, nuclear gene encoding plastid protein, complete cds
Seq. No.
                  167791
Seq. ID
                  LIB3234-047-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g4586109
BLAST score
                  169
E value
                  5.0e-12
Match length
                  41
                  71
% identity
NCBI Description
                  (AL049638) putative protein [Arabidopsis thaliana]
                  167792
Seq. No.
                  LIB3234-047-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3335171
BLAST score
                  549
E value
                  2.0e-56
Match length
                  121
% identity
                  87
                  (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167793
```

LIB3234-047-P1-K1-E7

```
Method
                  BLASTX
NCBI GI
                  q3924596
BLAST score
                  212
E value
                  5.0e-17
Match length
                  106
% identity
                  43
                  (AF069442) putative phospho-ser/thr phosphatase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  167794
                  LIB3234-047-P1-K1-E8
Seq. ID
Method
                  BLASTN
                  q304040
NCBI GI
BLAST score
                  152
E value
                  5.0e-80
                  172
Match length
% identity
                  97
                  Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene
NCBI Description
Seq. No.
                  167795
                  LIB3234-047-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  285
E value
                  1.0e-25
Match length
                  62
% identity
                  90
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi 541882 pir JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi 471091 dbj BAA04505 (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
   •:
                  thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  167796
Seq. No.
                  LIB3234-047-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3047082
BLAST score
                  143
                  4.0e-19
E value
Match length
                  104
% identity
                  50
                  (AF058914) similar to Vigna radiata pectinacetylesterase
NCBI Description
                  precursor (GB:X99348) [Arabidopsis thaliana]
Seq. No.
                  167797
Seq. ID
                  LIB3234-047-P1-K1-F11
Method
                  BLASTN
                  g4589428
NCBI GI
BLAST score
                  187
                  1.0e-101
E value
Match length
                  378
% identity
                  98
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

NCBI Description

MFH8, complete sequence Seq. No. 167798 Seq. ID LIB3234-047-P1-K1-F12 BLASTX Method g3132471 NCBI GI BLAST score 192 9.0e-42 E value Match length 91 99 % identity NCBI Description (AC003096) putative protein phosphatase 2C [Arabidopsis thaliana] Seq. No. 167799 LIB3234-047-P1-K1-F2 Seq. ID Method BLASTX NCBI GI q4115387 BLAST score 365 E value 6.0e-35 Match length 71 100 % identity (AC005967) putative NADP-dependent NCBI Description glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] Seq. No. 167800 LIB3234-047-P1-K1-F3 Seq. ID Method BLASTN NCBI GI q3869063 BLAST score 346 0.0e + 00E value Match length 374 98 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17022, complete sequence [Arabidopsis thaliana] 167801 Seq. No. Seq. ID LIB3234-047-P1-K1-F4 Method BLASTX NCBI GI g625977 BLAST score 534 E value 1.0e-54 Match length 107 96 % identity NCBI Description p40 protein homolog - Arabidopsis thaliana >gi 402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana] Seq. No. 167802 Seq. ID LIB3234-047-P1-K1-F5 Method BLASTX NCBI GI g2586127 BLAST score 253 8.0e-22 E value Match length 99 % identity 51

(U89510) b-keto acyl reductase [Hordeum vulgare]

```
167803
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3335171
                  555
BLAST score
E value
                  3.0e-57
                  122
Match length
                  88
% identity
                  (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
NCBI Description
                  167804
Seq. No.
                  LIB3234-047-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4038039
BLAST score
                  294
                  1.0e-26
E value
Match length
                  72
                  79
% identity
                   (AC005936) putative proteinase inhibitor II [Arabidopsis
NCBI Description
                   thaliana]
                   167805
Seq. No.
                  LIB3234-047-P1-K1-G10
Seq. ID .
                  BLASTN ..
Method
                   q4538990
NCBI GI
BLAST score
                   84
                   1.0e-39
E value
                   183
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
NCBI Description
                   (ESSA project)
                  167806
Seq. No.
                  LIB3234-047-P1-K1-G12
Seq. ID
                   BLASTN
Method
                  g3449312
NCBI GI
                   261
BLAST score
                   1.0e-145
E value
Match length
                   342
                   94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K16L22, complete sequence [Arabidopsis thaliana]
                   167807
Seq. No.
                   LIB3234-047-P1-K1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2894574
                   495
BLAST score
E value
                   3.0e-50
                   96
Match length
% identity
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
NCBI Description
                   >gi 2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
```

167808

Seq. No.

E value

4.0e-84

```
LIB3234-047-P1-K1-G3
Seq. ID
Method
                  BLASTX
                  g118926
NCBI GI
BLAST score
                   276
                   1.0e-24
E value
                  100
Match length
                   53
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                   dessication-related protein [Craterostigma plantagineum]
                   >gi_227781_prf__1710351E abscisic acid responsive protein E
                   [Craterostigma plantagineum]
                   167809
Seq. No.
                  LIB3234-047-P1-K1-G4
Seq. ID
                  BLASTX
Method
                  g4512619
NCBI GI
BLAST score
                   484
                   7.0e-49
E value
                  101
Match length
                   95
% identity
                   (AC004793) This gene is a member of the formyl transferase
NCBI Description
                   family PF_00551 and may be a pseudogene of gb_X74767
                   phosphoribosylglycinamide formyl transferase (PUR3) from
                   Arabidopsis thaliana since our sequence differs from
                   PUR3... >gi 4753662 emb CAA52779.2 (X74767)
                   phosphoribosylglycinamide formyltransferase [Arabidopsis
                   thaliana]
                   167810
Seq. No.
                   LIB3234-047-P1-K1-G7
Seq. ID
Method
                   BLASTN
                  g3150396
NCBI GI
BLAST score
                   196
E value
                   1.0e-106
Match length
                   258
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T27E13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167811
                   LIB3234-047-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g82200
BLAST score
                   343
                   2.0e-32
E value
Match length
                   131
                   69
% identity
NCBI Description
                  hypothetical protein 1244 - common tobacco chloroplast
                   167812
Seq. No.
Seq. ID
                   LIB3234-047-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   q4512656
BLAST score
                   159
```

```
Match length
                   314
                  88
% identity
NCBI Description, Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
                  167813
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-H5
                  BLASTN
Method
                  q3510347
NCBI GI
BLAST score
                   53
                   7.0e-21
E value
                  113
Match length
                   87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167814
                  LIB3234-047-P1-K1-H6
Seq. ID
                   BLASTN
Method
                  q4757414
NCBI GI
BLAST score
                   390
                   0.0e + 00
E value
                   402
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYF24, complete sequence
                   167815
Seq. No.
Seq. ID
                  LIB3234-047-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q2292907
BLAST score
                   246
                   3.0e-21
E value
Match length
                   87
% identity
                   31
                  (Y10099) P-glycoprotein homologue [Hordeum vulgare]
NCBI Description
                   167816
Seq. No.
                  LIB3234-047-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2655008
BLAST score
                   377
                   2.0e-36
E value
                   118
Match length
                   56
% identity
                   (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
NCBI Description
                   esculentum]
                   167817
Seq. No.
                  LIB3234-048-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3335169
BLAST score
                   186
                   6.0e-57
E value
                  123
Match length
% identity
                   89
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
```

. . .

```
protein 1 (ATS1) [Arabidopsis thaliana]
 Seq. No.
                   167818
 Seq. ID
                   LIB3234-048-P1-K1-A11
Method
                   BLASTX
 NCBI GI
                   g1216389
BLAST score
                   123
E value
                   2.0e-56
Match length
                   114
% identity
                   97
NCBI Description
                   (U39289) myrosinase-associated protein [Brassica napus]
                   >gi 1589009 prf 2209432A myrosinase-associated
                   protein:ISOTYPE=5 [Brassica napus]
Seq. No.
                   167819
Seq. ID
                   LIB3234-048-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   q4335711
BLAST score
                   44
                   1.0e-15
E value
Match length
                   146
% identity
                   85
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F9013 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167820
Seq. ID
                   LIB3234-048-P1-K1-A2
Method
                   BLASTN
NCBI GI
                   g2160132
BLAST score
                   186
E value
                   1.0e-100
Match length
                   314
% identity
                   92
                  Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167821
Seq. ID
                  LIB3234-048-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  g2583106
BLAST score
                  173
E value
                  2.0e-92
Match length
                  357
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4L23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167822
Seq. ID
                  LIB3234-048-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3135264
BLAST score
                  332
E value
                  4.0e-31
Match length
                  116
% identity
                  61
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]
```

>gi 4455197_emb_CAB36520.1 (AL035440) embryo-specific

```
Seq. No.
                    167823
 Seq. ID
                    LIB3234-048-P1-K1-A6
 Method
                    BLASTX
 NCBI GI
                    g114649
 BLAST score
                    313
 E value
                    7.0e-29
 Match length
                    81
 % identity
                   85
 NCBI Description
                   ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
                   >gi 67899_pir__LWLVA H+-transporting ATP synthase (EC
                   3.6.1.34) lipid-binding protein - liverwort (Marchantia
                   polymorpha) chloroplast >gi_11653_emb_CAA28066_ (X04465)
                   atpH [Marchantia polymorpha]
 Seq. No.
                   167824
 Seq. ID
                   LIB3234-048-P1-K1-A7
 Method
                   BLASTX
 NCBI GI
                   g485514
 BLAST score
                   151
 E value
                   8.0e-10
Match length
                   53
 % identity
                   51
NCBI Description
                   ADR11-2 protein - soybean (fragment)
                   >gi_296443_emb_CAA49341_ (X69640) auxin down regulated
                   [Glycine max]
Seq. No.
                   167825
Seq. ID
                   LIB3234-048-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g2618688
BLAST score
                   386
E value
                   2.0e-37
Match length
                   118
% identity
                   69
NCBI Description
                  (AC002510) putative esterase D [Arabidopsis thaliana]
Seq. No.
                   167826
Seq. ID
                   LIB3234-048-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g3036810
BLAST score
                   219
E value
                   7.0e-18
Match length
                   62
% identity
NCBI Description
                   (AL022373) putative Myc-type transcription factor
                   [Arabidopsis thaliana]
Seq. No.
                   167827
Seq. ID
                  LIB3234-048-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  g2264321
BLAST score
                  65
E value
                  4.0e-28
Match length
                  348
% identity
                  90
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

NCBI GI

BLAST score

MXM12, complete sequence [Arabidopsis thaliana] Seq. No. -.. 167828 Seq. ID LIB3234-048-P1-K1-B2 . Method BLASTX NCBI GI q2623962 BLAST score 396 E value 2.0e-38 Match length 81 % identity . NCBI Description (Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens] Seq. No. 167829 Seq. ID LIB3234-048-P1-K1-B3 Method BLASTX NCBI GI q136636 BLAST score 316 E value 4.0e-29 Match length 59 % identity 98 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi 1076424 pir_S43781 ubiquitin-conjugating enzyme UBC1 -Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C. $\overline{6}$.3.2. $\overline{19}$) > \overline{g} i 29 $\overline{8}$ 1894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana] Seq. No. 167830 Seq. ID LIB3234-048-P1-K1-B4 Method BLASTN NCBI GI g3327922 BLAST score 67 3.0e-29 E value Match length 348 % identity 91 Arabidopsis thaliana chromosome II BAC T31E10 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] Seq. No. 167831 Seq. ID LIB3234-048-P1-K1-B5 Method BLASTX NCBI GI g1526424 BLAST score 462 E value 2.0e-46 Match length 105 % identity (D64140) LEA protein in group 3 [Arabidopsis thaliana] NCBI Description Seq. No. 167832 Seq. ID LIB3234-048-P1-K1-B6 Method BLASTN

g4510338

BLAST score

```
E value
                   0.0e + 00
Match length
                   370
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F2H17 genomic
                   sequence, complete sequence
                   167833
Seq. No.
                   LIB3234-048-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1209258
BLAST score
                   302
E value
                   1.0e-27
Match length
                   76
% identity
                   79
NCBI Description
                   (L31937) protease inhibitor II [Brassica rapa]
Seq. No.
                   167834
                   LIB3234-048-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g129082
BLAST score
                   355
E value
                   8.0e-34
Match length
                   114
% identity
                   69
                   OLEOSIN BN-III >gi_81692_pir__S22475 oleosin BN-III - rape
NCBI Description
                   >gi_17839_emb_CAA43941_ (X61937) oleosin BN-III [Brassica
napus] >gi_742387_prf__2009397A oleosin [Brassica napus]
Seq. No.
                   167835
Seq. ID
                   LIB3234-048-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   q3193308
BLAST score
                   336
E value
                   1.0e-31
Match length
                   118
% identity
                   (AF069300) similar to Medicago truncatula MtN2 (GB:Y15293)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   167836
Seq. ID
                   LIB3234-048-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g1363488
BLAST score
                   340
E value
                   6.0e-32
Match length
                   68
% identity
                   99
NCBI Description
                   IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410)
                   IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_
                   (AC006340) auxin-induced IAA8 protein [Arabidopsis
                   thalianal
Seq. No.
                   167837
Seq. ID
                   LIB3234-048-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g112741
```

```
6.0e-25
E value
Match length
                  72
                  82
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  167838
Seq. ID
                  LIB3234-048-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q2956690
BLAST score
                  296
E value
                  7.0e-27
Match length
                  89
% identity
                  75
                  (AJ223306) PSBY [Arabidopsis thaliana] >gi 3414928
NCBI Description
                  (AF079800) PsbY precursor [Arabidopsis thaliana]
Seq. No.
                  167839
Seq. ID
                  LIB3234-048-P1-K1-C12
Method
                  BLASTN
                  g4220633
NCBI GI
BLAST score
                  70
E value
                  5.0e-31
Match length
                  156
% identity
                  92
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K7J8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167840
Seq. ID
                  LIB3234-048-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q543841
BLAST score
                  523
                  2.0e-53
E value
Match length
                  102
% identity
NCBI Description
                  ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875
                  ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                  (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                  >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                  thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)
                  ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                  167841
Seq. ID
                  LIB3234-048-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q2558511
BLAST score
                  103
E value
                  9.0e-51
Match length
                  107
% identity
NCBI Description Arabidopsis thaliana mRNA for proton pump interactor,
```

NCBI GI

E value

BLAST score

g3420043

1.0e-179

319

partial Seq. No. 167842 Seq. ID LIB3234-048-P1-K1-C5 Method BLASTN NCBI GI q3046856 BLAST score 308 E value 1.0e-173 Match length 371 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana] Seq. No. 167843 Seq. ID LIB3234-048-P1-K1-C6 Method BLASTX NCBI GI a136739 BLAST score 602 E value 9.0e-63 Match length 124 % identity 95 NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi 67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) potato >gi_218001_dbj_BAA00570 (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum] Seq. No. 167844 Seq. ID LIB3234-048-P1-K1-C8 Method BLASTX NCBI GI g2129648 BLAST score 532 E value 1.0e-54 Match length 98 % identity 100 MYB-related protein 33,3K - Arabidopsis thaliana NCBI Description >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein [Arabidopsis thaliana] Seq. No. 167845 Seq. ID LIB3234-048-P1-K1-D10 Method BLASTX NCBI GI g2129670 BLAST score 229 E value 1.0e-22 Match length 103 % identity 61 NCBI Description phosphoinositide-specific phospholipase C - Arabidopsis thaliana >gi_857374_dbj_BAA09432_ (D50804) phosphoinositide specific phospholipase C [Arabidopsis thaliana] Seq. No. 167846 Seq. ID LIB3234-048-P1-K1-D11 Method BLASTN

```
Match length
                      319
  % identity
                      100
  NCBI Description
                      Arabidopsis thaliana chromosome II BAC F23F1 genomic
                      sequence, complete sequence [Arabidopsis thaliana]
                                                                    . . . .
  Seq. No.
                     167847
  Seq. ID
                     LIB3234-048-P1-K1-D2
  Method
                     BLASTX
  NCBI GI
                     g112682
  BLAST score
                     571
  E value
                      4.0e-59
  Match length
                     122
  % identity
                     88
  NCBI Description
                     12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir S08510
                     cruciferin precursor (CRB) - Arabidopsis thaliana
                     >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                     thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                     storage protein [Arabidopsis thaliana]
  Seq. No.
                     167848
  Seq. ID
                     LIB3234-048-P1-K1-D3
  Method
                     BLASTX
  NCBI GI
                     g4204298
  BLAST score
                     465
· E value
                     1.0e-46
  Match length
                     120
  % identity ~
                     7.2
  NCBI Description
                     (AC003027) lcl_prt_seq No definition line found
                     [Arabidopsis thaliana]
  Seq. No.
                     167849
  Seq. ID
                     LIB3234-048-P1-K1-D4
  Method
                     BLASTN
  NCBI GI
                     g2828187
  BLAST score
                     96
  E value
                     1.0e-46
 Match length
                     236
  % identity
  NCBI Description
                     Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                     K21C13, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     167850
  Seq. ID
                     LIB3234-048-P1-K1-D5
 Method
                     BLASTX
 NCBI GI
                     g82201
 BLAST score
                     214
 E value
                     3.0e-17
 Match length
                     104
 % identity
                     36
 NCBI Description
                    hypothetical protein 131 - common tobacco chloroplast
                    >gi_11879_emb_CAA77392_ (Z00044) hypothetical protein
[Nicotiana tabacum] >gi_1223680_emb_CAA77401_ (Z00044)
                    hypothetical protein [Nicotiana tabacum]
                    >gi_225249_prf__1211235CH ORF 131 [Nicotiana tabacum]
 Seq. No.
                    167851
 Seq. ID
                    LIB3234-048-P1-K1-D6
```

Seq. ID

```
Method
                  BLASTN
NCBI GI
                  q4558674
BLAST score
                  134
                  3.0e-69
E value
Match length
                  265
                  92
% identity
                  Arabidopsis thaliana chromosome II BAC F7B19 genomic
NCBI Description
                  sequence, complete sequence
                  167852
Seq. No.
                  LIB3234-048-P1-K1-D8
Seq. ID
Method
                  BLASTX
                  g129083
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
Match length
                  78
                  50
% identity
                  OLEOSIN BN-V >qi 280390 pir S25089 oleosin Bn-V - rape
NCBI Description
                  (fragment) >gi 808944 emb CAA45313 (X63779) oleosin BN-V
                  [Brassica napus]
                  167853
Seq. No.
                  LIB3234-048-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  g4588906 **
NCBI GI
BLAST score
                  387
                  1.0e-37
E value
Match length
                  98
                  77
% identity
                  (AF118149) ribosomal protein S7 [Secale cereale]
NCBI Description
Seq. No.
                  167854
                  LIB3234-048-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4185511
BLAST score
                  459
E value
                  5.0e-46
Match length
                  102
                  83
% identity
NCBI Description
                  (AF102822) actin depolymerizing factor 4 [Arabidopsis
                  thaliana]
                  167855
Seq. No.
Seq. ID
                  LIB3234-048-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1076331
                  632
BLAST score
E value
                  3.0e-66
Match length
                  116
% identity
                  100
NCBI Description
                  histidine transport protein - Arabidopsis thaliana
                  >gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter
                  1-1 [Arabidopsis thaliana] >gi_744157_prf__2014244A His
                  transporter [Arabidopsis thaliana]
                  167856
Seq. No.
```

LIB3234-048-P1-K1-E11

Method

BLASTX

```
Method
                   BLASTX
NCBI GI
                   q2446981
BLAST score
                   496
E value
                   2.0e-50
Match length
                   96
                   98
% identity
                   (AB005560) AtGDI2 [Arabidopsis thaliana]
NCBI Description
                   >qi 2569936 emb CAA04727 (AJ001397) GDI2 [Arabidopsis
                   thaliana]
                   167857
Seq. No.
                   LIB3234-048-P1-K1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g951453
BLAST score
                   300
                   2.0e-27
E value
                   121
Match length
% identity
                   52
                   (M95746) initiation factor (iso)4f p82 subunit [Triticum
NCBI Description
                   aestivum]
                   167858
Seq. No.
                   LIB3234-048-P1-K1-E2
Seq. ID
                   BLASTN .
Method
                  g3256065
NCBI GI
BLAST score
                   273
E value
                   1.0e-152
                   313
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana mRNA for chloroplast NAD-dependent
                  malate dehydrogenase
Seq. No.
                   167859
                   LIB3234-048-P1-K1-E3
Seq. ID
                   BLASTX
Method
NCBI GÏ
                   g3372645
BLAST score
                   350
                   3.0e-33
E value
Match length
                   119.
% identity
                   49
                  (AF060491) cinnamyl alcohol dehydrogenase [Pinus radiata]
NCBI Description
                   167860
Seq. No.
Seq. ID
                   LIB3234-048-P1-K1-E4
Method
                   BLASTX
                   g129082
NCBI GI
BLAST score
                   364
E value
                   8.0e-35
Match length
                   115
% identity
                   70
                  OLEOSIN BN-III >gi_81692_pir__S22475 oleosin BN-III - rape
NCBI Description
                   >gi_17839_emb_CAA43941_ (X61937) oleosin BN-III [Brassica
napus] >gi_742387_prf__2009397A oleosin [Brassica napus]
Seq. No.
                   167861
Seq. ID
                   LIB3234-048-P1-K1-E6
```

BLAST score

208

```
g129082
NCBI GI
BLAST score
                   374
E value
                   6.0e-36
Match length
                   117
% identity
                   71
                   OLEOSIN BN-III >gi 81692 pir S22475 oleosin BN-III - rape
NCBI Description
                   >gi_17839_emb_CAA43941_ (X61937) oleosin BN-III [Brassica
napus] >gi_742387_prf__2009397A oleosin [Brassica napus]
                   167862
Seq. No.
                   LIB3234-048-P1-K1-E7
Seq. ID
Method
                   BLASTX
                   q3461848
NCBI GI
BLAST score
                   540
E value
                   2.0e-55
Match length
                   121
% identity
                   89
                   (AC005315) putative ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   167863
                   LIB3234-048-P1-K1-F10
Seq. ID
                   BLASTN
Method
                   g511598
NCBI GI
                   368
BLAST score
E value
                   0.0e+00
Match length
                   368
% identity
                   28
                   Arabidopsis thaliana cell wall protein (APTR-1) gene,
NCBI Description
                   complete cds
                   167864
Seq. No.
                   LIB3234-048-P1-K1-F11
Seq. ID
                   BLASTX
Method
                   g112746
NCBI GI
BLAST score
                   378
                   2.0e-36
E value
                   101
Match length
% identity
                   74
                   NAPIN B PRECURSOR (1.7S SEED STORAGE PROTEIN)
NCBI Description
                   >gi 99818 pir S15382 napin napB - rape
                   >gi 17835 emb CAA41150 (X58142) napin [Brassica napus]
                   167865
Seq. No.
                   LIB3234-048-P1-K1-F12
Seq. ID
Method
                   BLASTX
                   g2149640
NCBI GI
                   632
BLAST score
                   3.0e-66
E value
Match length
                   122
                   99
% identity
                   (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                   167866
Seq. No.
                   LIB3234-048-P1-K1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4006888
```

NCBI GI

```
1.0e-16
 E value
                    82
 Match length
 % identity
                    50
 NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
                    167867
 Seq. No.
                    LIB3234-048-P1-K1-F4
 Seq. ID
                    BLASTN
Method
                    g600854
 NCBI GI
                    72
 BLAST score
                    3.0e-32
 E value
                    130
 Match length
                    96
 % identity
 NCBI Description Arabidopsis thaliana bZIP protein mRNA, complete cds
                    167868
 Seq. No.
                    LIB3234-048-P1-K1-F5
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g112742
 BLAST score
                    113
                    1.0e-39
 E value
                    111
 Match length
                    77
 % identity
 NCBI Description NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN)
                    >gi 81687 pir S10018 napin (clone BngNAP1) - rape
                    >gi_1084352_pir__S52027 napin - rape
                    >ģi_17833_emb_CAA35580_ (X17542) napin (AA 1-180) [Brassica
                    napus] >qi 468022 (U04945) napin [Brassica napus]
 Seq. No.
                    167869
                    LIB3234-048-P1-K1-F6
 Seq. ID
                    BLASTN
 Method
                    g557693
 NCBI GI
 BLAST score
                    248
                    1.0e-137
 E value
                    252
 Match length
 % identity
                    100
 NCBI Description Arabidopsis thaliana Columbia GTP binding protein beta
                    subunit (AGB1) mRNA, complete cds
                    167870
 Seq. No.
                    LIB3234-048-P1-K1-F7
 Seq. ID
                    BLASTX
 Method
                    g266693
 NCBI GI
                    543
 BLAST score
                    7.0e-56
 E value
 Match length
                    120
 % identity
                    OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis
 NCBI Description
                    thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
                     (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
                    167871
 Seq. No.
 Seq. ID
                    LIB3234-048-P1-K1-F8
                    BLASTN
 Method
```

g2564044

```
BLAST score
                   90
E value
                   5.0e-43
Match length
                   232
% identity
                   94
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19P17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167872
Seq. ID
                   LIB3234-048-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g4507311
BLAST score
                   199
E value
                   2.0e-15
Match length
                   103
% identity
                   38
NCBI Description
                   suppressor of Ty (S.cerevisiae) 4 homolog 1
                   >gi 3122873 sp Q16550 SPT4 HUMAN TRANSCRIPTION INITIATION
                   PROTEIN SPT4 HOMOLOG 1 >gi 1209779 (U43923) similar to
                   Saccharomyces cerevisiae Spt4; protein has potential
                   N-terminal zinc-finger [Homo sapiens] >qi 1401053 (U38818)
                   SUPT4H [Homo sapiens] >qi 1401055 (U38817) SUPT4H [Homo
                   sapiens] >gi 1401066 (U43154) Supt4h [Mus musculus]
                   >gi 3779194 (U96809) chromatin structural protein homolog
                   [Mus musculus]
Seq. No.
                   167873
Seq. ID
                   LIB3234-048-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g134025
BLAST score
                   446
E value
                   2.0e-44
Match length
                   110
% identity
                   81
NCBI Description
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi 70913 pir R3NT8
                   ribosomal protein S8 - common tobacco chloroplast
                   >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8
[Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal
                   protein S8 [Nicotiana tabacum]
Seq. No.
                   167874
Seq. ID
                   LIB3234-048-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q1707857
BLAST score
                   484
E value
                   6.0e-49
Match length
                   120
% identity.
                   75
NCBI Description
                   (Y09291) obtusifoliol 14-alpha-demethylase [Triticum
                   aestivum]
Seq. No.
                   167875
                   LIB3234-048-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2384671
BLAST score
                   302
E value
                   9.0e-36
Match length
```

NCBI GI

```
88
% identity
NCBI Description
                  (AF012657) putative potassium transporter AtKT2p
                  [Arabidopsis thaliana]
                  167876
Seq. No.
                  LIB3234-048-P1-K1-G2
Seq. ID
                  BLASTN
Method
                  g3659491
NCBI GI
                  193
BLAST score
                  1.0e-104
E value
                  315
Match length
                  99
% identity
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167877
                  LIB3234-048-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q112681
BLAST score
                  264
                  4.0e-23
E value
                  95
Match length
                  56
% identity
                 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  167878
                  LIB3234-048-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g421826
NCBI GI
BLAST score
                  529
                  4.0e-54
E value
Match length
                  124
% identity
                  81
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi 298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
                  167879
Seq. No.
                  LIB3234-048-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421826
BLAST score
                  271
                  6.0e-24
E value
                  95
Match length
                  59
% identity
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis
                  thaliana]
                  ·167880
Seq. No.
                  LIB3234-048-P1-K1-G9
Seq. ID
Method
                  BLASTX
```

q2982437

```
200
BLAST score
E value
                   6.0e-26
Match length
                  101
% identity
                  67
                   (AL022224) terpene cyclase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  167881
Seq. No.
                  LIB3234-048-P1-K1-H2
Seq. ID
                  BLASTX
Method
                  g1706256
NCBI GI
BLAST score
                   351
                   2.0e-33
E value
Match length
                   108
% identity
                   61
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN-10) >gi 733577 (U23453) similar to
                   peptidyl-prolyl cis-trans isomerase (PPIASE) (CYCLOPHILIN)
                   [Caenorhabditis elegans] >gi 1155225 (U34954) cyclophilin
                   isoform 10 [Caenorhabditis elegans]
                  167882
Seq. No.
                  LIB3234-048-P1-K1-H3
Seq. ID
Method
                  BLASTX
                   g2252857
NCBI GI
BLAST score
                   315
                   4.0e-29
E value
                   101
Match length
                   68
% identity
                   (AF013294) similar to acidic ribosomal protein p1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   167883
                LIB3234-048-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1628583
BLAST score
                   567
                 1.0e-58
E value
Match length
                   113
% identity
                   96
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   167884
Seq. No.
                   LIB3234-049-P1-K1-A1
Seq. ID
                   BLASTX
. Method
NCBI GI
                   q1352463
BLAST score
                   452
E value
                   4.0e-45
                   109
Match length
% identity
                   83
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi 1161312
NCBI Description
                   (U04876) myo-inositol-1-phosphate synthase [Arabidopsis
                   thaliana]
```

167885

Seq. No.

- -

```
LIB3234-049-P1-K1-A10
 Seq. ID
 Method
                    BLASTX .
                    g267081
_ NCBI GI
 BLAST score
                    675
                    3.0e-71
 E value
                    126 -
 Match length
                    100
 % identity
                    TUBULIN BETA-7 CHAIN >gi 320188 pir JQ1591 tubulin beta-7
 NCBI Description
                    chain - Arabidopsis thaliana >gi 166906 (M84704) beta-7
                    tubulin [Arabidopsis thaliana] >gi 3980381 (AC004561)
                    tubulin beta-7 chain [Arabidopsis thaliana]
                    167886
 Seq. No.
 Seq. ID
                    LIB3234-049-P1-K1-A11
 Method
                    BLASTX
                    g2605714
 NCBI GI
 BLAST score
                    465
                    1.0e-46
 E value
 Match length
                    113
 % identity
                    82
                    (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    167887
 Seq. ID
                    LIB3234-049-P1-K1-A12
 Method
                    BLASTX
 NCBI GI
                    g4539316
 BLAST score
                    275
                    7.0e-40
 E value
                    96
 Match length
 % identity
                    86
                    (AL035679) putative fructose-bisphosphate aldolase
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    167888
                    LIB3234-049-P1-K1-A2
 Seq. ID
 Method .
                    BLASTN
 NCBI GI
                    g4199934
 BLAST score
                    181
                    3.0e-97
 E value
 Match length
                    303
                    99
 % identity
                    Genomic sequence for Arabidopsis thaliana BAC T3P18,
 NCBI Description
                    complete sequence [Arabidopsis thaliana]
                    167889
 Seq. No.
                    LIB3234-049-P1-K1-A3
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g4206762
 BLAST score
                    89
 E value
                    2.0e-42
 Match length
                    257
                    94
 % identity
                    Arabidopsis thaliana cell wall-plasma membrane linker
 NCBI Description
                    protein homolog (CWLP) mRNA, complete cds
```

167890

Seq. No.

```
LIB3234-049-P1-K1-A4
Seq. ID
Method ·
                  BLASTX
NCBI GI
                  q2829904
BLAST score
                  244
E value
                  1.0e-26
                  116
Match length
                  63
% identity
                 (AC002311) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167891
Seq. ID
                  LIB3234-049-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q1490554
BLAST score
                  93
E value
                  4.0e-10
Match length
                  49
% identity
                  72
                  (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  167892
                  LIB3234-049-P1-K1-A6
Seq. ID
                  BLASTN
Method
                  q633027
NCBI GI
BLAST score
                  257
E value
                  1.0e-142
Match length
                  285
                  98
% identity
NCBI Description Arabidopsis thaliana mRNA for protein phosphatase 2C
                  167893
Seq. No.
                  LIB3234-049-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135858
BLAST score
                  408
E value
                  5.0e-40
Match length
                  100
% identity
                  80
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                  >gi 99760 pir S22201 tonoplast intrinsic protein alpha -
                  Arabidopsis thaliana >gi 16182 emb CAA45114 (X63551)
                  tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
                  thaliana] >qi 166623 (M84343) tonoplast intrinsic protein
                  [Arabidopsis thaliana] >gi_445128_prf 1908432A tonoplast
                  intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.
                  167894
                  LIB3234-049-P1-K1-B12
Seq. ID
Method
                  BLASTN
                  g4584519
NCBI GI
BLAST score
                  374
E value
                  0.0e+00
Match length
                  374
                  100
% identity
NCBI Description 'Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18
                  (ESSA project)
```

Seq. ID

```
Seq. No.
                  167895
Seq. ID
                  LIB3234-049-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g2583131
BLAST score
                  141
E value
                  3.0e-09
Match length
                  62
% identity
                  52
NCBI Description
                 (AC002387) putative pectinesterase [Arabidopsis thaliana]
Seq. No.
                  167896
                  LIB3234-049-P1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4314374
BLAST score
                  32
                  2.0e-08
E value
Match length
                  326
% identity
                  18
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167897
                  LIB3234-049-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3135250
BLAST score
                  141
                  2.0e-73
E value
Match length
                  343
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC F27F23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167898
                  LIB3234-049-P1-K1-C10
Seq. ID
Method
                  BLASTN
                  g2618683
NCBI GI
BLAST score
                  91
E value
                  1.0e-43
Match length
                  323
% identity
                  88
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167899
                  LIB3234-049-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267082
BLAST score
                  145
E value
                  6.0e-27
Match length
                  121
% identity
                  60
                  TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8
NCBI Description
                  chain - Arabidopsis thalīana >gī_166908 (M84705) beta-8
                  tubulin [Arabidopsis thaliana]
                  167900
Seq. No.
```

LIB3234-049-P1-K1-C2

```
Method
                  BLASTX
NCBI GI
                  q4538906
BLAST score
                  452
E value
                  3.0e-45
Match length
                  91
                  97
% identity
                  (ALO49482) choline kinase GmCK2p-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167901
                  LIB3234-049-P1-K1-C3
Seq. ID
Method
                  BLASTX
                  g4538906
NCBI GI
BLAST score
                  250
E value
                  2.0e-21
Match length
                  101
% identity
                  58
                  (AL049482) choline kinase GmCK2p-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  167902
Seq. No.
                  LIB3234-049-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4417310
BLAST score
                  593
E value
                  1.0e-61
Match length
                  130
% identity
                  88
                  (ACO06446) putative Athila retroelement ORF1 protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  167903
                  LIB3234-049-P1-K1-C7
Seq. ID
                  BLASTN
Method
                  g4760411
NCBI GI
BLAST score
                  344
                  0.0e+00
E value
Match length
                  367
                  89
% identity
                  Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
NCBI Description
                  complete sequence
                  167904
Seq. No.
                  LIB3234-049-P1-K1-C8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g436919
                  268
BLAST score
                  1.0e-149
E value
                  268
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana Landsburg lipoxygenase 1 gene,
                  complete cds
                  167905
Seq. No.
                  LIB3234-049-P1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4006885
```

NCBI GI

q629500

```
BLAST score
                   81
                   8.0e-38 ·
E value
Match length
                   202
                   92
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No ...
Seq. No.
                   167906
                   LIB3234-049-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g226120
BLAST score
                   222
E value
                   3.0e-18
Match length
                   122
% identity
                   39
NCBI Description vicilin gene B [Saguinus oedipus]
                   167907
Seq. No.
                   LIB3234-049-P1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1531762
BLAST score
                   195
                   5.0e-15
E value
Match length
                   51
% identity
                   75
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                   thaliana]
                   167908
Seq. No.
                   LIB3234-049-P1-K1-D11
Seq. ID
                   BLASTX
Method
                   q112740
NCBI GI
                   260
BLAST score
                   1.0e-22
E value
Match length
                   115
% identity
                   51
                   NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)
NCBI Description
                   >gi 81691 pir A25997 napin precursor (napA) - rape
                   >gi 16715\overline{3} (J\overline{02}586) prepronapin [Brassica napus] >gi 167155
                   (J0\overline{2}798) napin [Brassica napus]
                   167909
Seq. No.
                   LIB3234-049-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1169598
BLAST score
                   369
                   2.0e-35
E value
Match length
                   81
                   85
% identity
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                   desaturase [Arabidopsis thaliana]
                   167910
Seq. No.
                   LIB3234-049-P1-K1-D2
Seq. ID
Method
                   BLASTX
```

```
BLAST score
                  585
E value
                  1.0e-60
Match length
                  107
% identity
                  100
                  1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) -
NCBI Description
                  Arabidopsis thaliana >qi 166578 (M95594)
                  1-aminocyclopropane-1-carboxylate synthase [Arabidopsis
                  thaliana]
                  167911
Seq. No.
                  LIB3234-049-P1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                  320
E value
                  1.0e-180
Match length
                  386
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  167912
Seq. No.
                  LIB3234-049-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3287693
BLAST score
                  304
E value
                  9.0e-28
Match length
                  81
% identity
                  70
                  (AC003979) Similar to LIM17 gene product gb 1653769 from
NCBI Description
                  the genome of Synechocystis sp. gb D90916. [Arabidopsis
                  thaliana]
                  167913
Seq. No.
Seq. ID
                  LIB3234-049-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  474
E value
                  1.0e-47
Match length
                  104
% identity
                  83
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  167914
Seq. No.
Seq. ID
                  LIB3234-049-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q2827002
BLAST score
                  479
                  3.0e-48
E value
                  116
Match length
```

```
% identity
NCBI Description
                  (AF005993) HSP70 [Triticum aestivum]
Seq. No.
                  167915
Seq. ID
                  LIB3234-049-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g2465924
BLAST score
                  359
E value
                  0.0e + 00
Match length
                  382
% identity
                  98
NCBI Description
                  Arabidopsis thaliana receptor-like serine/threonine kinase
                  (RKF2) mRNA, complete cds
Seq. No.
                  167916
                  LIB3234-049-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2652938
BLAST score
                  508
E value
                  1.0e-51
Match length
                  112
% identity
                  45
NCBI Description (Z47554) orf [Zea mays]
Seq. No.
                  167917
                  LIB3234-049-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204315
BLAST score
                  682
E value
                  4.0e-72
Match length
                  128 .
% identity
                  100
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  167918
Seq. No.
                  LIB3234-049-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706749
BLAST score
                  495
E value
                  4.0e-50
Match length
                  102
% identity
                  99
NCBI Description
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
                   (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi 780814 (U24177)
                  3-ketoacyl-acyl carrier protein synthase I [Arabidopsis
                  thaliana]
Seq. No.
                  167919
                  LIB3234-049-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g586036
BLAST score
                  593
E value
                  1.0e-61
Match length
                  130
% identity
                  92
                  SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 1 (SRP54)
NCBI Description
                  >gi 629560 pir S42550 signal recognition particle 54K
```

```
Seq. No.
                  167920
                                                                       LIB3234-049-P1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3212846
BLAST score
                  383
E value
                  0.0e + 00
Match length
                  391
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167921
                  LIB3234-049-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128180
BLAST score
                  600
E value
                  2.0e-62
Match length
                  126
% identity
                  (AC004521) citrate synthetase [Arabidopsis thaliana]
NCBI Description
                  167922
Seq. No.
                  LIB3234-049-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3212846
BLAST score
                  352
E value
                  0.0e + 00
Match length
                  380
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167923
                  LIB3234-049-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1169273
                  203
BLAST score
E value
                  6.0e-16
Match length
                  116
                  42
% identity
                  DEOXYCYTIDINE KINASE (DCK) >gi 1083283 pir A55122
NCBI Description
                  deoxycytidine kinase (EC 2.7.1.74) - mouse
                  >gi 456677 emb CAA54787 (X77731) deoxycytidine kinase [Mus
                  musculus]
                  167924
Seq. No.
                  LIB3234-049-P1-K1-E6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3885325
BLAST score
                  178
                  8.0e-96
E value
                  194
Match length
                  98
% identity
```

protein - Arabidopsis thaliana >gi_304111 (L19997) signal recognition particle 54 kDa subunit [Arabidopsis thaliana]

NCBI Description Arabidopsis thaliana chromosome II BAC T20P8 genomic

Seq. ID

Method

NCBI GI BLAST score

E value

Match length

sequence, complete sequence [Arabidopsis thaliana] 167925 Seq. No. Seq. ID LIB3234-049-P1-K1-E7 Method BLASTX q3776558 NCBI GI 471 BLAST score 2.0e-47 E value 109 Match length % identity (ACO05388) Identical to gb L14814 DNA for tissue-specific NCBI Description acyl carrier protein isoform 2 from A. thaliana. ESTs gb AA597351, gb T41805, gb_H36871, gb_R30210, gb_AA042549, gb Z47650, gb H76304 and gb AA597348 come from this gene. [Arabidopsi Seq. No. 167926 LIB3234-049-P1-K1-F1 Seq. ID Method BLASTX NCBI GI q3643610 BLAST score 532 2.0e-54 E value Match length 103 100 % identity NCBI Description (AC005395) putative serine/threonine protein kinase [Arabidopsis thaliana] Seq. No. 167927 LIB3234-049-P1-K1-F11 Seq. ID BLASTX Method NCBI GI q2493045 594 BLAST score 9.0e-62 E value 120 Match length 98 % identity ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description >gi_1655484_dbj_BAA13601_ (D88376) delta-prime subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] 167928 Seq. No. LIB3234-049-P1-K1-F12 Seq. ID BLASTN Method NCBI GI g2570223 326 BLAST score 0.0e+00E value Match length 391 98 % identity Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 167929

LIB3234-049-P1-K1-F2

BLASTN

368

376

g2264318

0.0e+00

```
99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167930
                  LIB3234-049-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3184283
BLAST score
                  575
E value
                  1.0e-59
Match length
                  128
% identity
                  91
                   (AC004136) putative TBP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167931
                  LIB3234-049-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2098711
BLAST score
                  237
E value
                  6.0e-20
Match length
                  129
% identity
                  41
                  (U82976) pectinesterase [Citrus sinensis]
NCBI Description
Seq. No.
                  167932
Seq. ID
                  LIB3234-049-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3808062
BLAST score
                  164
E value
                  6.0e-12
Match length
                  68
% identity
                  46
                  (AB019195) PV100 [Cucurbita maxima]
NCBI Description
Seq. No.
                  167933
                  LIB3234-049-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3298532
BLAST score
                  349
E value
                  0.0e + 00
Match length
                  369
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T26B15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167934
Seq. ID
                  LIB3234-049-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g4006833
BLAST score
                  288
E value
                  7.0e-37
Match length
                  128
% identity
                  (AC005970) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thalianal
```

.

```
167935
Seq. No.
Seq. ID
                  LIB3234-049-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q166765
BLAST score
                 . 534
                 9.0e-55
E value
Match length
                  102
                  100
% identity
                 (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]
NCBI Description
                  167936
Seq. No.
                  LIB3234-049-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3157930
BLAST score
                  602
E value
                  1.0e-62
Match length
                  114
% identity
                  98
                  (AC002131) Strong similarity to
NCBI Description
                  amino-cyclopropane-carboxylic acid oxidase gb L27664 from
                  Brassica napus. ESTs gb Z48548 and gb Z48549 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  167937
Seq. ID
                  LIB3234-049-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  g3449321
BLAST score
                  58
                  7.0e-24
E value
                  202
Match length
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MTG10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167938
                  LIB3234-049-P1-K1-G4
Seq. ID
                  BLASTX
Method
                  g3445207
NCBI GI
                  728
BLAST score
                  2.0e-77
E value
                  130
Match length
                  99
% identity
                  (AC004786) unknown protein [Arabidopsis thaliana]
NCBI Description
                  167939
Seq. No.
                  LIB3234-049-P1-K1-G5
Seq. ID
                  BLASTN
Method
                  g4092470
NCBI GI
BLAST score
                  43
E value
                  6.0e-15
Match length
                  71
                  90
% identity
                  Arabidopsis thaliana BAC T24G23 from chromosome IV near 21
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167940
                  LIB3234-049-P1-K1-G8
Seq. ID
```

```
Method
                  BLASTX
NCBI GI
                  g4309730
BLAST score
                   502
                   5.0e-51
E value
Match length
                  113
                  86
% identity
                   (ACOO6439) putative lipid transfer protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  167941
                  LIB3234-049-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4325282
BLAST score
                   304
                   9.0e-28
E value
Match length
                   60
% identity
                   92
NCBI Description
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
                  >gi 4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
Seq. No.
                  167942
Seq. ID
                  LIB3234-049-P1-K1-H1
Method
                  BLASTX
                  g3335169
NCBI GI
BLAST score
                  335
E value
                  1.0e-31
Match length
                  63
% identity
                  97
NCBI Description
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  167943
Seq. ID
                  LIB3234-049-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  q2924729
BLAST score
                  132
E value
                  4.0e-68
Match length
                  286
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNA5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167944
Seq. ID
                  LIB3234-049-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  q4455801
BLAST score
                  205
E value
                  1.0e-112
Match length
                  209
% identity
                  100
NCBI Description
                  Arabidopsis thaliana prxr3 gene, exons 1-4
Seq. No.
                  167945
Seq. ID
                  LIB3234-049-P1-K1-H3
Method
                  BLASTX
```

Method

BLASTN

```
g2583108
NCBI GI
BLAST score
                   414
                   7.0e-41
E value
                   100
Match length
                   85
% identity
                   (ACO02387) putative surface protein [Arabidopsis thaliana]
NCBI Description
Seq. No. -
                   167946
                   LIB3234-049-P1-K1-H4
Seq. ID
                   BLASTX
Method
                   q112682
NCBI GI
BLAST score
                   592
E value
                   2.0e-61
                   125
Match length
                   89
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsīs thaliana
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
                   167947
Seq. No.
                   LIB3234-049-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160146
                   277
BLAST score
                   1.0e-24
E value
Match length
                   65
% identity
                   86
                   (ACO00375) Strong similarity to Arabidopsis gb_X91953,F21M12.3,F21M12.1. EST gb_H36326 comes from this
NCBI Description
                   gene. [Arabidopsis thaliana]
Seq. No.
                   167948
                   LIB3234-049-P1-K1-H6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4584351
BLAST score
                   352
E value
                   0.0e + 00
Match length
                   368
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC T12H3 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   167949
                   LIB3234-049-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4650842
BLAST score
                   646
E value
                   7.0e-68
Match length
                   128
% identity
NCBI Description
                   (AB026185) elongation factor 2 [Lithospermum erythrorhizon]
                   167950
Seq. No.
                   LIB3234-049-P1-K1-H9
Seq. ID
```

```
NCBI GI
                   g2281081
BLAST score '
                   334
E value -
                   0.0e + 00
Match length
                   350
% identity
                   99
                   Arabidopsis thaliana chromosome II BAC F18019 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167951
                   LIB3234-050-P1-K1-A10
Seq. ID
Method
                   BLASTN
                   g3402695
NCBI GI
BLAST score
                   271
E value
                   1.0e-151
Match length
                   350
% identity
                   100
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T3K9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   167952
Seq. ID
                   LIB3234-050-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   g4467094
BLAST score
                   366
E value
                   0.0e+00
Match length
                   370
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
                   (ESSA project)
Seq. No.
                   167953
Seq. ID
                   LIB3234-050-P1-K1-A2
Method
                   BLASTX
                   g1706186
NCBI GI
BLAST score
                   280
E value
                   5.0e-25
Match length
                   119
% identity
                   46
NCBI Description
                  HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1)
                   (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC
                   RETROVIRAL LEUKEMIA RECEPTOR) (ERR) (ECOTROPIC RETROVIRUS
                   RECEPTOR) >gi 110721 pir A32742 murine ecotropic
                   retrovirus receptor protein - mouse >gi 532612 (M26687)
                   ecotropic retrovirus receptor [Mus musculus]
Seq. No.
                   167954
                   LIB3234-050-P1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4468976
BLAST score
                   377
                   0.0e+00
E value
Match length
                   377
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18
                   (ESSA project)
```

167955

Seq. No.

```
LIB3234-050-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129753
BLAST score
                  632
                  3.0e-66
E value
                  121
Match length
                  100
% identity
                  threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                  thaliana (fragment) >gi_1448917 (L41666) threonine synthase
                  [Arabidopsis thaliana]
Seq. No.
                  167956
                  LIB3234-050-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4510360
BLAST score
                  373
                  0.0e + 00
E value
                  373
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
NCBI Description
                  sequence, complete sequence
                  167957
Seq. No.
                  LIB3234-050-P1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q633027
BLAST score
                  189
                  1.0e-102
E value
                  361
Match length
                  89
% identity
NCBI Description Arabidopsis thaliana mRNA for protein phosphatase 2C
                  167958
Seq. No.
                  LIB3234-050-P1-K1-A7
Seq. ID
                  BLASTN
Method
                  g3449318
NCBI GI
BLAST score
                  82
                  3.0e - 38
E value
Match length
                  150
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLF18, complete sequence [Arabidopsis thaliana]
                  167959
Seq. No.
                  LIB3234-050-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  g3918
NCBI GI .
BLAST score
                  412
E value
                  2.0e-40
Match length
                  122
% identity
                  61
                  (X58378) mitochondrial elongation factor G [Saccharomyces
NCBI Description
                  cerevisiae]
                  167960
Seq. No.
                  LIB3234-050-P1-K1-B12
Seq. ID
```

BLASTN

Method

NCBI GI

```
NCBI GI
                   g4262221
BLAST score
                   279
E value
                   1.0e-156
                   370
Match length
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC F10A8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                  167961
Seq. No.
                  LIB3234-050-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3808062
BLAST score
                  148
                  2.0e-09
E value
Match length
                  61
                   46
% identity
NCBI Description
                  (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  167962
                  LIB3234-050-P1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  184
E value
                  4.0e-99
Match length -
                  343
% identity
                  100
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  167963
Seq. ID
                  LIB3234-050-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g4503269
BLAST score
                  190
E value
                  2.0e-14
Match length
                  110
% identity
                  42
                  deoxycytidine kinase >gi_118447_sp_P27707_DCK_HUMAN
NCBI Description
                  DEOXYCYTIDINE KINASE (DCK) >gi_\overline{105829}pir_A38585
                  deoxycytidine kinase (EC 2.7.1.74) - human >gi 181510
                   (M60527) deoxycytidine kinase [Homo sapiens]
                  167964
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  g3309276
BLAST score
                  170
E value
                  1.0e-90
Match length
                  272
% identity
                  99
NCBI Description
                  Arabidopsis thaliana BAC T26N6 from chromosome IV at 19.3
                  cM, complete sequence
                  167965
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-B8
Method
                  BLASTX
```

g1592677

BLAST score

371

```
BLAST score
                  193
E value
                  8.0e-15
Match length
                  38
% identity
                  100
NCBI Description
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
                  167966
Seq. No.
                  LIB3234-050-P1-K1-B9 -
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129532
BLAST score
                  269
E value
                  1.0e-23
Match length
                  83
% identity
                  66
NCBI Description
                  acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -
                  Arabidopsis thaliana >gi 1107507 emb CAA63746 (X93461)
                  acyl-[acyl-carrier protein] desaturase [Arabidopsis
                  thaliana]
                  167967
Seq. No.
                  LIB3234-050-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2262155
BLAST score
                  229
E value
                  1.0e-126
Match length
                  289
% identity
                  97
NCBI Description
                  DNA sequence of Arabidopsis thaliana BAC F5J6 from
                  chromosome IV, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167968
Seq. ID
                  LIB3234-050-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g4432829
BLAST score
                  207
E value
                  1.0e-113
Match length
                  373
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T1B3 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167969
Seq. ID
                  LIB3234-050-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3287691
BLAST score
                  165
E value
                  2.0e-11
Match length
                  65
% identity
                  55
NCBI Description
                  (AC003979) Contains similarity to RING zinc finger protein
                  gb_X95455 from Gallus gallus. [Arabidopsis thaliana]
                  167970
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-C3
Method
                  BLASTN
                  g4159712
NCBI GI
```

Match length

```
0.0e+00
E value
Match length
                  371
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWI23, complete sequence
                  167971
Seq. No.
                  LIB3234-050-P1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2651294
BLAST score
                  305
                  1.0e-171
E value
Match length
                  377
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T2P4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  167972
                  LIB3234-050-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678285
BLAST score
                  410
E value
                  3.0e-40
Match length
                  122
% identity
                  61
                  (AL049660) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  167973
Seq. ID
                  LIB3234-050-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  517
E value
                  8.0e-53
Match length
                  121
% identity
NCBI Description
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  167974
                  LIB3234-050-P1-K1-D1
Seq. ID
Method
                  BLASTN
                  q4455348
NCBI GI
BLAST score
                  370
                  0.0e+00
E value
                  370
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8
                  (ESSAII project)
Seq. No.
                  167975
Seq. ID
                  LIB3234-050-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  q4159703
BLAST score
                  134
                  3.0e-69
E value
                  270
```

```
87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5F14, complete sequence
Seq. No.
                  167976
Seq. ID
                  LIB3234-050-P1-K1-D3
                  BLASTX
Method
NCBI GI
                  g1617268
BLAST score
                  597
E value
                  4.0e-62
Match length
                  122
% identity
                  90
                 (Z72153) acyl CoA synthetase [Brassica napus]
NCBI Description
Seq. No.
                  167977
                  LIB3234-050-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q72827
BLAST score
                  157
E value
                  1.0e-10
Match length
                  63
% identity
                  13
NCBI Description IgA Fc receptor precursor - Streptococcus agalactiae
Seq. No.
                  167978
                  LIB3234-050-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4335752
BLAST score
                  324
E value
                  4.0e-30
Match length
                  104
% identity
                  56
                  (AC006284) putative myb transcription factor-like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  167979
                  LIB3234-050-P1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3808062
BLAST score
                  149
E value
                  1.0e-09
Match length
                  62
                  45
% identity
NCBI Description
                 (AB019195) PV100 [Cucurbita maxima]
                  167980
Seq. No.
                  LIB3234-050-P1-K1-D7
Seq. ID
                  BLASTX
Method
                  g399091
NCBI GI
BLAST score
                  485
E value
                  5.0e-49
Match length
                  120
% identity
                  80
NCBI Description
                  PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
                  (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                  (H+-PPASE) >gi 282878 pir A38230 inorganic pyrophosphatase
```

(EC 3.6.1.1), H+-translocating pyrophosphate-energized -

NCBI Description

```
H+-phosphatase [Arabidopsis thaliana]
Seq. No.
                  167981
Seq. ID
                  LIB3234-050-P1-K1-D8
Method
                  BLASTX
NCBI GI
                   q3445209
BLAST score
                   518
                   6.0e-53
E value
Match length
                   121
                   78
% identity
NCBI Description
                   (AC004786) putative serine carboxypeptidase I [Arabidopsis
Seq. No.
                   167982
Seq. ID
                  LIB3234-050-P1-K1-D9
Method
                  BLASTX
NCBI GI
                   q3603456
BLAST score
                   477
                   4.0e-48
E value
Match length
                   98
                   29
% identity
                  (AF088848) polyubiquitin [Capsicum chinense]
NCBI Description
                  167983
Seq. No.
Seq. ID
                   LIB3234-050-P1-K1-E10
Method
                   BLASTN
NCBI GI
                   q3482964
BLAST score
                   359
E value
                   0.0e + 00
Match length
                   371
% identity
                   99
                  Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
NCBI Description
                   (ESSAII project)
Seq. No.
                   167984
                  LIB3234-050-P1-K1-E11
Seq. ID
Method
                  BLASTN
                   q3482964
NCBI GI
BLAST score
                   177
E value
                   6.0e-95
Match length
                   333
                   88
% identity
                  Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
NCBI Description
                   (ESSAII project)
Seq. No.
                   167985
                  LIB3234-050-P1-K1-E12
Seq. ID
                  BLASTN
Method
                   g4159708
NCBI GI
BLAST score
                   360
E value
                  0.0e + 00
Match length
                   372
% identity
                   93
```

Arabidopsis thaliana >qi 166634 (M81892) vacuolar

MKP6, complete sequence

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

Method

```
Seq. No.
                   167986
 Seq. ID
                   LIB3234-050-P1-K1-E2
 Method
                   BLASTN
 NCBI GI
                   g4757678
 BLAST score
                  . 33
 E'value
                   5.0e-09
 Match length
                   96
 % identity
                   90
 NCBI Description Arabidopsis thaliana chromosome I BAC F9H16 genomic
                   sequence, complete sequence
 Seq. No.
                   167987
 Seq. ID
                   LIB3234-050-P1-K1-F1
 Method
                   BLASTX
 NCBI GI
                   g131297
 BLAST score
                   674
 E value
                   3.0e-71
 Match length
                   124
 % identity
                   98
 NCBI Description PHOTOSYSTEM II D2 PROTEIN (PHOTOSYSTEM Q(A) PROTEIN)
                   >gi_72667_pir__F2SPD2 photosystem II protein D2 - spinach
                   chloroplast >gi_12280_emb_CAA25863_ (X01724) D2 protein
                   [Spinacia oleracea] > gi_473511 (M27308) D2 photosystem II
                   protein [Spinacia oleracea] >gi 552887 (M36833) 32 Kd-like
                  protein [Spinacia oleracea]
Seq. No.
                  167988
Seq. ID
                  LIB3234-050-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  425
E value
                  5.0e-42
Match length
                  96
% identity
                  81
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.~) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  167989
Seq. ID
                  LIB3234-050-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q4585972
BLAST score
                  284
E value
                  2.0e-25
Match length
                  94
% identity
NCBI Description (AC005287) Putative ATPase [Arabidopsis thaliana]
Seq. No.
                  167990
Seq. ID
```

LIB3234-050-P1-K1-F3

BLASTX

BLAST score

101

```
NCBI GI
                    g128733
 BLAST score
                    270
 E value
                    8.0e-24
 Match length
                    51
 % identity
 NCBI Description
                    NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4-LIKE
                    >gi_97653_pir__S14968 ndhD-like protein - Synechocystis sp
                    >gi_581748_emb_CAA37837_ (X53842) ndhD-like ORF
                    [Synechocystis sp.]
 Seq. No.
                    167991
 Seq. ID
                   LIB3234-050-P1-K1-F4
 Method
                   BLASTX
 NCBI GI
                   g4512673
 BLAST score
                   332
 E value
                   4.0e-31
 Match length
                   64
 % identity
                   100
NCBI Description
                   (AC006931) putative phosphoprotein phosphatase [Arabidopsis
                   thaliana]
 Seq. No.
                   167992
 Seq. ID
                   LIB3234-050-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g166570
BLAST score
                   220
E value
                   6.0e-18
Match length
                   101
% identity
                   47
NCBI Description
                  (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                   167993
Seq. ID
                   LIB3234-050-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   q4262250
BLAST score
                   607
E value
                   2.0e-63
Match length
                   117
% identity
                   100
NCBI Description
                  (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                   167994
Seq. ID
                   LIB3234-050-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g3695374
BLAST score
                   407
                   7.0e-40
E value
Match length
                   73
% identity
                   97
NCBI Description
                  (AF096370) contains similarity to NAM (no apical meristem)
                  -like proteins [Arabidopsis thaliana]
Seq. No.
                  167995
                  LIB3234-050-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3298532
```

Match length

338

```
2.0e-49
 E value
                    205
 Match length
                    88
  % identity
 NCBI Description
                    Arabidopsis thaliana chromosome II BAC T26B15 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
                    167996
  Seq. No.
                    LIB3234-050-P1-K1-G12
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4249382
  BLAST score
                    393
  E value
                    3.0e-38
 Match length
                    95
                    81
  % identity
  NCBI Description
                    (AC005966) Strong similarity to gi 3337350 F13P17.3
                    putative permease from Arabidopsis thaliana BAC
                    gb AC004481. [Arabidopsis thaliana]
  Seq. No.
                    167997
  Seq. ID
                    LIB3234-050-P1-K1-G2
  Method
                    BLASTN
  NCBI GI
                    g2264315
                                                                     . .
  BLAST score
                    367
· E value
                    0.0e+00
 Match length
                    371
  % identity
                    100
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
  NCBI Description
                    MRN17, complete sequence [Arabidopsis thaliana]
                    167998
  Seq. No.
                    LIB3234-050-P1-K1-G3
  Seq. ID
                    BLASTX
  Method
                    g3335171
  NCBI GI
  BLAST score
                    535
                    7.0e-55
  E value
                    114
  Match length
                    89
  % identity
                    (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
  NCBI Description
                    167999
  Seq. No.
                    LIB3234-050-P1-K1-G4
  Seq. ID
                    BLASTX
  Method
                    g3319355
  NCBI GI
  BLAST score
                    581
                    3.0e-60
  E value
  Match length
                    125
                    100
  % identity
                    (AF077407) similar to chaperonin containing TCP-1 complex
  NCBI Description
                    gamma chain [Arabidopsis thaliana]
  Seq. No.
                    168000
                    LIB3234-050-P1-K1-G5
  Seq. ID
                    BLASTN
  Method
                    g3426033
  NCBI.GI
                    311
  BLAST score
  E value
                    1.0e-175
```

```
% identity
                   92
 NCBI Description Arabidopsis thaliana chromosome II BAC F12C20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No..
                   168001
                   LIB3234-050-P1-K1-G6
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q3808062
 BLAST score
                   143
. E value
                   6.0e-09
 Match length
                   61
 % identity
                   44
 NCBI Description (AB019195) PV100 [Cucurbita maxima]
 Seq. No.
                   168002
                   LIB3234-050-P1-K1-G7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q4581140
 BLAST score
                   325
 E value
                   3.0e-30
 Match length
                   121
 % identity
                   57
 NCBI Description (AC006919) unknown protein [Arabidopsis thaliana]
                   168003
 Seq. No.
                   LIB3234-050-P1-K1-G9
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4325282
                   272
 BLAST score
                   4.0e-24
 E value
 Match length
                   72
                   72
 % identity
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
 NCBI Description
                   >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                   168004
 Seq. No.
                   LIB3234-050-P1-K1-H1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g207905
                   276
 BLAST score
                   2.0e-24
 E value
                   124
 Match length
 % identity
                   41
                   (M18027) alpha globulin B [Artificial gene]
 NCBI Description
                   168005
 Seq. No.
                   LIB3234-050-P1-K1-H10
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g4490324
 BLAST score
                   301
                   1.0e-169
 E value
                   313
 Match length
                   99
 % identity
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
                    (ESSA project)
```

NCBI GI

g136739

```
168006
Seq. No.
Seq. ID
                  LIB3234-050-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2117612
BLAST score
                  687
                  1.0e-72
E value
Match length
                  124
                  99
% identity
                  catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
NCBI Description
                  168007
Seq. No.
                  LIB3234-050-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1168391
BLAST score
                  173
                  1.0e-12
E value
Match length
                  96
                  38
% identity
NCBI Description
                  ALLERGEN ARA H 1, CLONE P41B (ARA H I) >qi 602436 (L34402)
                  Ara h I [Arachis hypogaea]
Seq. No.
                  168008
Seq. ID
                  LIB3234-050-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  g3983533
BLAST score
                  214
                  1.0e-117
E value
Match length
                  318
% identity
                  97
NCBI Description Arabidopsis thaliana BAC T24G3 from chromosome V near 70
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168009
                  LIB3234-050-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913648
BLAST score
                  246
E value
                  5.0e-21
                  96
Match length
% identity
                  55
NCBI Description FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)
Seq. No.
                  168010
Seq. ID
                  LIB3234-050-P1-K1-H5
Method
                  BLASTN
                  g4314374
NCBI GI
BLAST score
                  45 -
E value
                  1.0e-16
Match length
                  244
% identity
                  10
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168011
Seq. ID
                  LIB3234-050-P1-K1-H6
Method
                  BLASTX
```

```
BLAST score
                  345
                  1.0e-32
E value
Match length
                  112
% identity
                  62
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
                  168012
Seq. No.
                  LIB3234-050-P1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4115930
                  290
BLAST score
                  1.0e-162
E value
Match length
                  366
                  94
% identity
NCBI Description Arabidopsis thaliana BAC T4B21
                  168013
Seq. No.
                  LIB3234-050-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  g4689108
NCBI GI
BLAST score
                  176
                  8.0e-13
E value
Match length
                  82
                  44
% identity
                  (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]
NCBI Description
                  168014
Seq. No.
                  LIB3234-052-P1-K1-A1
Seq. ID
Method
                  BLASTN
                  g336917
NCBI GI
BLAST score
                  56
                  1.0e-22
E value
Match length
                  104
% identity
                  95
NCBI Description Epifagus virginiana chloroplast complete genome
                  168015
Seq. No.
                  LIB3234-052-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2262155
                  378
BLAST score
                  0.0e + 00
E value
                  378
Match length
                  100
% identity
                  DNA sequence of Arabidopsis thaliana BAC F5J6 from
NCBI Description
                  chromosome IV, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168016
                  LIB3234-052-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827559
                  361
BLAST score
```

2.0e-34

E value

% identity

```
83
Match length
                  82
% identity
                  (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3292808_emb_CAA19798_ (AL031018) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  168017
                LIB3234-052-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  431
E value
                  1.0e-42
Match length
                  97
                  81
% identity
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  168018
Seq. No.
                  LIB3234-052-P1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1502428
BLAST score
                  335
E value
                  2.0e-31
Match length
                  66
                  100
% identity
NCBI Description
                  (U62330) phosphate transporter [Arabidopsis thaliana]
                  >gi_2258116_dbj_BAA21503_ (D86591) inorganic phosphate
                  transporter [Arabidopsis thaliana]
                  >gi_2258118_dbj_BAA21504_ (D86608) inorganic phosphate
                  transporter [Arabidopsis thaliana]
Seq. No.
                  168019
                  LIB3234-052-P1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4049332
BLAST score
                  284
E value
                  1.0e-158
Match length
                  329
% identity
                  100
                 Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
NCBI Description
                  (ESSAII project)
Seq. No.
                  168020
                  LIB3234-052-P1-K1-A4
Seq. ID
Method
                  BLASTN
                  q2827698
NCBI GI
                  33
BLAST score
E value
                  6.0e-09
Match length
                  164
```

```
NCBI Description Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11
                  (ESSAII project)
                  168021
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-A5
                  BLASTX
Method
                  *q3420004
NCBI GI
BLAST score
                  160
                  6.0e-11
E value
Match length
                  73
                  40
% identity
                  (AF000305) steroid sulfotransferase 1 [Brassica napus]
NCBI Description
                  168022
Seq. No.
                  LIB3234-052-P1-K1-A7
Seq. ID
Method
                  BLASTX
                  g267069
NCBI GI
BLAST score
                  526
                  8.0e-54
E value
Match length
                  97
                  100
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  168023
                  LIB3234-052-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3128205 .
BLAST score
                  521
                  3.0e-53
E value
                  120
Match length
% identity
                  87
                  (AC004077) putative pyruvate dehydrogenase complex E1 beta
NCBI Description
                  subunit [Arabidopsis thaliana]
                  168024
Seq. No.
                  LIB3234-052-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  566
                  2.0e-58
E value
Match length
                  127
% identity
                  86
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  168025
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  q4581138
BLAST score
                  54
```

2.0e-21

E value

```
114
 Match length
 % identity
                   87
                   Arabidopsis thaliana chromosome II BAC F1011 genomic
. NCBI Description
                   sequence, complete sequence
 Seq. No.
                   168026
                   LIB3234-052-P1-K1-B11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q4454482
 BLAST score
                   472
 E value
                   2.0e-47
 Match length
                   122
 % identity
                   73
 NCBI Description (AC006234) hypothetical protein [Arabidopsis thaliana]
                   168027
 Seq. No.
                   LIB3234-052-P1-K1-B2
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g2351061
 BLAST score
                   380
                 0.0e+00
 E value
 Match length
                   388
 % identity
                   99
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MAF19, complete sequence [Arabidopsis thaliana]
                   168028
 Seq. No.
 Seq. ID
                   LIB3234-052-P1-K1-B4
 Method
                   BLASTN
                   q3169169
 NCBI GI
                   270
 BLAST score
                   1.0e-150
 E value
 Match length
                   349
 % identity
                   93
 NCBI Description Arabidopsis thaliana chromosome II BAC F21P24 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   168029
 Seq. No.
 Seq. ID
                   LIB3234-052-P1-K1-B5
 Method
                   BLASTN
 NCBI GI
                   g1931636
 BLAST score
                   165
 E value
                   5.0e-88
 Match length
                   219
 % identity
 NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
 Seq. No.
                   168030
 Seq. ID
                   LIB3234-052-P1-K1-B6
 Method
                   BLASTN
 NCBI GI
                   q511598
 BLAST score
                   375
 E value
                   0.0e+00
 Match length
                   375
 % identity
                   27
 NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene,
```

complete cds

```
Seq. No.
                  168031
Seq. ID
                  LIB3234-052-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  q4159703
BLAST score
                  149
                  3.0e-78
E value
Match length
                  347
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K5F14, complete sequence
Seq. No.
                  168032
Seq. ID
                  LIB3234-052-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2239089
BLAST score
                  145
                  3.0e-09
E value
Match length
                  53
% identity
                  47
                  (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                  [Dianthus caryophyllus] >gi 3288180 emb CAB11466 (298758)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                  [Dianthus caryophyllus]
Seq. No.
                  168033
                  LIB3234-052-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961107
BLAST score
                  140
                  1.0e-08
E value
Match length
                  69
                  39
% identity
                  (AF042383) TLS-associated protein with SR repeats [Mus
NCBI Description
                  musculus] >gi 2961149 (AF047448) TLS-associated protein
                  TASR [Homo sapiens]
Seq. No.
                  168034
                  LIB3234-052-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4454587
BLAST score
                  58
E value
                  7.0e-24
Match length
                  148
% identity
                  89
                  Arabidopsis thaliana BAC F21A20 from chromosome V near 61
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168035
Seq. ID
                  LIB3234-052-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  g2244870
BLAST score
                  71
E value
                  1.0e-31
Match length
                  228
% identity
                  93
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
```

fragment No

```
Seq. No.
                   168036
                   LIB3234-052-P1-K1-C12
Seq. ID
                   BLASTX
Method
                   g140551
NCBI GI
BLAST score
                   212
                   1.0e-18
E value
Match length
                   91
                   63
% identity
                   HYPOTHETICAL 250 KD PROTEIN (ORF 2131)
NCBI Description
                   >gi_81505_pir__S01446 hypothetical protein 2131 - spinach
                   chloroplast >gi_12246_emb_CAA30743_ (X07908) ORF 2131 (AA
                   1-2131) [Spinacia oleracea]
                   168037
Seq. No.
                   LIB3234-052-P1-K1-C3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3449321
BLAST score
                   36
                   9.0e-11
E value
Match length
                   72
                   88
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MTG10, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168038
                   LIB3234-052-P1-K1-C4
Seq. ID
Method
                   BLASTX
                   g1703108
NCBI GI
BLAST score
                   548
E value
                   2.0e-56
Match length
                   101
% identity
                   100
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
NCBI Description
                   thaliana >gi_1049307 (U37281) actin-2 (Arabidopsis
                   thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   168039
Seq. No.
                   LIB3234-052-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160138
BLAST score
                   644
                   1.0e-67
E value
Match length
                   126
% identity
                   51
                   (AC000375) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   168040
Seq. ID
                   LIB3234-052-P1-K1-D1
Method
                   BLASTN
NCBI GI
                   q3193305
BLAST score
                   383
                   0.0e + 00
E value
Match length
                   387
```

```
100
% identity
NCBI Description Arabidopsis thaliana BAC F3D13
                  168041
Seq. No.
                  LIB3234-052-P1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  261
                  1.0e-145
E value
Match length
                  356
% identity
                  91
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  168042
Seq. No.
                  LIB3234-052-P1-K1-D11
Seq. ID
Method
                  BLASTN
                  q2264302
NCBI GI
                  20
BLAST score
                  3.2e-01
E value
Match length
                  378
                  92
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168043
                  LIB3234-052-P1-K1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4335744
BLAST score
                  141
E value
                  7.0e-74
Match length
                  141
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T4M8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168044
Seq. ID
                  LIB3234-052-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  q1699056
BLAST score
                  379
                  0.0e + 00
E value
Match length
                  383
% identity
                  100
                  Arabidopsis thaliana 27 kDa unknown protein mRNA, complete
NCBI Description
                  cds
                  168045
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-D3
Method
                  BLASTX
                  q1709970
NCBI GI
BLAST score
                  452
E value
                  4.0e-45
Match length
                  114
% identity
                  80
```

NCBI Description 60S RIBOSOMAL PROTEIN L10A

```
Seq. No.
                  168046
Seq. ID
                  LIB3234-052-P1-K1-D5
Method
                  BLASTN
                  g4519192
NCBI GI
BLAST score
                  173
E value
                  2.0e-92
Match length -
                  371
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MBK21, complete sequence
Seq. No.
                  168047
Seq. ID
                  LIB3234-052-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4522003
BLAST score
                  477
E value
                  4.0e-48
Match length
                  112
% identity
NCBI Description
                  (AC007069) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  168048
Seq. ID
                  LIB3234-052-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                  545
E value
                  5.0e-56
Match length
                  124
% identity
                  85
NCBI Description
                  (AC003027) 1cl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  168049
Seq. ID
                  LIB3234-052-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2832620
BLAST score
                  414
                  1.0e-40
E value
Match length
                  115
% identity
                  69
                  (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168050
Seq. ID
                  LIB3234-052-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g3046855
BLAST score
                  219
E value
                  1.0e-120
Match length
                  342
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168051
Seq. ID
                  LIB3234-052-P1-K1-E2
Method
                  BLASTN
```

```
BLAST score
                  157
E value
                  6.0e-83
Match length
                  373
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
NCBI Description
                  (ESSAII project)
Seq. No.
                  168052
Seq. ID
                  LIB3234-052-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  q4217996
BLAST score
                  349
                  0.0e+00
E value
Match length
                  365
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F24H14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168053
                  LIB3234-052-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4519193
BLAST score
                  128
E value
                  1.0e-65
Match length
                  383
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC11, complete sequence
Seq. No.
                  168054
Seq. ID
                  LIB3234-052-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q4249391
BLAST score
                  392
E value
                  4.0e-38
Match length
                  112
                  73
% identity
                  (AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase
NCBI Description
                  from Arabidopsis thaliana BAC gb AC004473. [Arabidopsis
                  thalianal
Seq. No.
                  168055
Seq. ID
                  LIB3234-052-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  185
E value
                  8.0e-14
Match length
                  94
% identity
                  46
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor (Arabidopsis thaliana)
```

```
Seq. No.
                   168056
                   LIB3234-052-P1-K1-E8
Seq. ID
Method
                   BLASTX
                   g3287691
NCBI GI
                   153
BLAST score
E value
                   4.0e-10
Match length
                   65
% identity
                   52
                   (AC003979) Contains similarity to RING zinc finger protein
NCBI Description
                   gb_X95455 from Gallus gallus. [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3234-052-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q82051
BLAST score
                   317
E value
                   3.0e-29
Match length
                   119
% identity
                   lipid body-associated membrane protein - carrot
NCBI Description
                   >gi_259453_bbs_117620 (S47635) lipid body membrane
protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                   180 aa] [Daucus carota]
                   168058
Seq. No.
                   LIB3234-052-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129659
BLAST score
                   86
                   2.0e-15
E value
                   80
Match length
% identity
                   57
                   oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
NCBI Description
                   (L40954) oleosin [Arabidopsis thaliana]
                   168059
Seq. No.
Seq. ID
                   LIB3234-052-P1-K1-F10
Method
                   BLASTX
                   g1345973
NCBI GI
BLAST score
                   435
                   4.0e-43
E value
                   98
Match length
% identity
                   82
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   >gi 541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                   1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
                   168060
Seq. No.
                   LIB3234-052-P1-K1-F11
Seq. ID
                   BLASTX
Method
```

Match length

384

```
BLAST score
                  225
E value
                  2.0e-18
Match length
                  90
% identity
                  43
                  (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
NCBI Description
                  168061
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q4263646
BLAST score
                  644
                  1.0e-67
E value
Match length
                  126
% identity
NCBI Description
                   (AC006136) putative TA1-like reverse transcriptase
                   [Arabidopsis thaliana]
                  168062
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q1762584
BLAST score
                  473
E value
                  1.0e-47
Match length
                  91
                  100
% identity
NCBI Description
                   (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
                   [Arabidopsis thaliana]
Seq. No.
                  168063
Seq. ID
                  LIB3234-052-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g4490749
BLAST score
                  654
E value
                  8.0e-69
Match length
                  125
% identity
                  99
                   (AL035708) 2-dehydro-3-deoxyphosphoheptonate aldolase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  168064
Seq. ID
                  LIB3234-052-P1-K1-F4
                  BLASTN
Method
NCBI GI
                  g3985949
BLAST score
                  378
E value
                  0.0e+00
                  382
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOB24, complete sequence [Arabidopsis thaliana]
                  168065
Seq. No.
Seq. ID
                  LIB3234-052-P1-K1-F5
Method
                  BLASTN
                  g4454447
NCBI GI
BLAST score
                  178
                  2.0e-95
E value
```

```
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F5H14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   168066
Seq. No.
                   LIB3234-052-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4314363
BLAST score
                   610
                   1.0e-63
E value
Match length
                   123
% identity
                   98
NCBI Description
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
                   168067
Seq. No.
                  LIB3234-052-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2245378
BLAST score
                   589
E value
                   3.0e-61
Match length
                  125
% identity
                   91
NCBI Description
                  (U83245) auxin response factor 1 [Arabidopsis thaliana]
Seq. No.
                  168068
Seq. ID
                  LIB3234-052-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g4757411
BLAST score
                   343
E value
                   0.0e + 00
Match length
                   347
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MXC7, complete sequence
Seq. No.
                  168069
Seq. ID
                  LIB3234-052-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  q3046850
BLAST score
                  351
E value
                  0.0e + 00
Match length
                  378
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K24G6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168070
Seq. ID
                  LIB3234-052-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  q2924729
BLAST score
                  267
E value
                  1.0e-148
Match length
                  379
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MNA5, complete sequence [Arabidopsis thaliana]

Method

BLASTX

```
Seq. No.
                    168071
  Seq. ID
                    LIB3234-052-P1-K1-G2
 Method
                    BLASTX
 NCBI GI
                    g2961356
 BLAST score
                    416
 E value
                    6.0e-41
 Match length
                    113
 % identity
                    71
 NCBI Description (AL022140) alcohol dehydrogenase like protein [Arabidopsis
                   thaliana]
 Seq. No.
                   168072
 Seq. ID
                   LIB3234-052-P1-K1-G3
 Method
                   BLASTN
 NCBI GI
                   q3805839
 BLAST score
                   382
 E value
                   0.0e+00
 Match length
                   382
 % identity
                   100
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14
                   (ESSAII project)
 Seq. No.
                   168073
 Seq. ID
                   LIB3234-052-P1-K1-G4
 Method
                   BLASTN
 NCBI GI
                   g3172156
 BLAST score
                   177
 E value
                   7.0e~95
Match length
                   387
 % identity
                   100
NCBI Description Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   168074
Seq. ID
                   LIB3234-052-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g4678299
BLAST score
                   594
E value
                   8.0e-62
Match length
                  116
% identity
                   100
NCBI Description
                  (AL049655) cysteine proteinase precursor-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  168075
Seq. ID
                  LIB3234-052-P1-K1-H10
Method :
                  BLASTX
NCBI GI
                  g2924258
BLAST score
                  524
E value
                  1.0e-53
Match length
                  126
% identity
NCBI Description (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
Seq. No.
                  168076
Seq. ID
                  LIB3234-052-P1-K1-H11
```

```
NCBI GI
                     g3242079
  BLAST score
                     226
  E value
                     1.0e-18
  Match length
                     69
  % identity
                     62
  NCBI Description
                     (AJ006984) proline-rich protein [Capsicum annuum]
  Seq. No.
                     168077
  Seq. ID
                     LIB3234-052-P1-K1-H12
  Method
                     BLASTX
  NCBI GI
                     g2129773
  BLAST score
                     678
  E value
                     1.0e-71
  Match length
                     125
  % identity
                    98
  NCBI Description
                    xyloglucan endotransglycosylase-related protein XTR3 -
                    Arabidopsis thaliana (fragment) >gi_1244752 (U43485)
                    xyloglucan endotransglycosylase-related protein
                    [Arabidopsis thaliana]
  Seq. No.
                    168078
 Seq. ID
                    LIB3234-052-P1-K1-H2
 Method
                    BLASTX
 NCBI GI
                    g4755194
 BLAST score
                    693
 E value
                    2.0e-73
 Match length
                    126
 % identity
 NCBI Description
                    (AC007018) hypothetical protein [Arabidopsis thaliana]
                   >gi_4755195_gb_AAD29062.1_AC007018_10 (AC007018)
                   hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   168079
 Seq. ID
                   LIB3234-052-P1-K1-H3
 Method
                   BLASTX
 NCBI GI
                   q3421378
 BLAST score
                   371
 E value
                   1.0e-35
Match length
                   125
% identity
                   62
NCBI Description
                  (AF080249) kinesin-like heavy chain [Arabidopsis thaliana]
Seq. No.
                   168080
Seq. ID
                   LIB3234-052-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   g4678266
BLAST score
                   379
E value
                   0.0e+00
Match length
                   383
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8
                   (ESSA project)
Seq. No.
                  168081
Seq. ID
                  LIB3234-052-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g3242079
```

```
BLAST score
                   145
 E value
                   3.0e-09
Match length
                   50
 % identity
                   56
NCBI Description (AJ006984) proline-rich protein [Capsicum annuum]
Seq. No.
                   168082
Seq. ID
                   LIB3234-052-P1-K1-H6
Method
                   BLASTN
NCBI GI
                  g3659491
BLAST score
                  355
E value
                  0.0e+00
Match length
                  380
% identity
                  98
NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
```

1, complete sequence [Arabidopsis thaliana] Seq. No. 168083 Seq. ID LIB3234-052-P1-K1-H7

Method BLASTN NCBI GI g3449316 BLAST score 380 E value 0.0e+00 Match length 380 % identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9D7, complete sequence [Arabidopsis thaliana]

Seq. No. 168084 Seq. ID LIB3234-052-P1-K1-H8 Method BLASTN NCBI GI g4662609 BLAST score 72 E value 2.0e-32 Match length 168

% identity 90 NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No. 168085 Seq. ID LIB3234-052-P1-K1-H9 Method BLASTX NCBI GI g82512 BLAST score 538

E value 3.0e-55 Match length 109 % identity 43 NCBI Description

ubiquitin precursor - rice (fragment)

>gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza

Seq. No. 168086

Seq. ID LIB3234-053-P1-K1-A12 Method

BLASTX NCBI GI g1345973 BLAST score 223 E value 2.0e-18

BLAST score

210

```
Match length
                   62
% identity
                   74
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                   1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795 dbj BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  168087
Seq. ID
                  LIB3234-053-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  436
                  2.0e-43
E value
Match length
                  92
% identity
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  168088
Seq. ID
                  LIB3234-053-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g4406784
                  84
BLAST score
E value
                  1.0e-44
                  92
Match length
% identity
                  (AC006532) putative oligopeptide transport protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  168089
                  LIB3234-053-P1-K1-A4
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3449334
BLAST score
                  311
E value
                  1.0e-175
Match length
                  344
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168090
Seq. ID
                  LIB3234-053-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2541876
```

```
E value
                   9.0e-17
Match length
                   81
                   44
% identity
                    (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                    [Nicotiana tabacum]
Seq. No.
                   168091
                   LIB3234-053-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q120667
BLAST score
                   302
E value
                   9.0e-28
Match length
                   75
% identity
                   79
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
thaliana >gi_166706 (M64116) cystolic
                   glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                   thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                   dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   168092
Seq. ID
                   LIB3234-053-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q2058313
BLAST score
                   405
E value
                   1.0e-39
Match length
                   98
% identity
                   78
NCBI Description
                   (X97433) cinnamoyl-CoA reductase [Eucalyptus gunnii]
Seq. No.
                   168093
Seq. ID
                   LIB3234-053-P1-K1-B11
Method
                   BLASTN
                   g4096078
NCBI GI
BLAST score
                   354
E value
                   0.0e + 00
                   378
Match length
                   99
% identity
                   Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   168094
Seq. No.
Seq. ID
                   LIB3234-053-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q2244841
BLAST score
                   273
                   4.0e-24
E value
Match length
                   104
                   56
% identity
                   (297337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   168095
Seq. No.
                   LIB3234-053-P1-K1-B2
Seq. ID
                   BLASTX
Method
```

```
548
BLAST score
E value
                  2.0e-56
Match length
                  104
% identity
                  100
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
              168096
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g4678371
BLAST score
                  229
E value
                  1.0e-126
Match length
                  289
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15
                  (ESSA project)
                  168097
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2244841
BLAST score
                  261
E value
                  6.0e-23
Match length
                  97
                  57
% identity
NCBI Description (297337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168098
Seq. ID
                  LIB3234-053-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  117
E value
                  3.0e-59
Match length
                  319
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  168099
Seq. ID
                  LIB3234-053-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g4558592
BLAST score
                  271
E value
                  5.0e-24
                  112
Match length
% identity
                  54
NCBI Description (AC006555) hypothetical protein [Arabidopsis thaliana]
                  168100
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  g3702724
BLAST score
                  377
E value
                  0.0e+00
                  392
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
```

Seq. No. 168101 Seq. ID LIB3234-053-P1-K1-C10 Method BLASTX NCBI GI g136739 254 BLAST score 8.0e-35 E value Match length 116 % identity 69 NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum] Seq. No. 168102 Seq. ID LIB3234-053-P1-K1-C11 Method BLASTN NCBI GI g2244870 BLAST score 101 E value 2.0e-49 Match length 304 % identity 89 Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description fragment No Seq. No. 168103 Seq. ID LIB3234-053-P1-K1-C5 Method BLASTN NCBI GI g2160132 BLAST score 43 3.0e-15 E value Match length 140 % identity 63 Sequence of BAC F19K23 from Arabidopsis thaliana chromosome NCBI Description 1, complete sequence [Arabidopsis thaliana] 168104 Seq. No. Seq. ID LIB3234-053-P1-K1-C8 Method BLASTX NCBI GI g2947062 BLAST score 148 E value 2.0e-09 Match length 101 % identity 42 NCBI Description (AC002521) unknown protein [Arabidopsis thaliana] Seq. No. 168105 Seq. ID LIB3234-053-P1-K1-C9 Method BLASTX NCBI GI q3176685 BLAST score 338 E value 8.0e-32 Match length 64 % identity (AC003671) Strong similarity to spermidine synthase 1, NCBI Description

K17N15, complete sequence [Arabidopsis thaliana]

```
gb_AA712346 come from this ge
Seq. No.
                   168106
Seq. ID
                   LIB3234-053-P1-K1-D11
Method
                   BLASTN
NCBI GI
                   g2264302
BLAST score
                   89
E value
                   2.0e-42
Match length
                   244
% identity
                   84
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MAC12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168107
Seq. ID
                   LIB3234-053-P1-K1-D2
Method
                   BLASTX
NCBI GI
                  g4678299
BLAST score
                   601
E value
                  1.0e-62
Match length
                   121
% identity
                   98
                   (AL049655) cysteine proteinase precursor-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  168108
Seq. ID
                  LIB3234-053-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g1709970
BLAST score
                  355
E value
                  9.0e-34
Match length
                  101
                  69
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10A
Seq. No.
                  168109
Seq. ID
                  LIB3234-053-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g3668073
BLAST score
                  210
E value
                  1.0e-115
Match length
                  218
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T4C15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168110
Seq. ID
                  LIB3234-053-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2245048
BLAST score
                  410
E value
                  3.0e-40
Match length
                  129
% identity
                  67
```

gb_Y08252 and possibly closer similarity to spermidine synthase 2 gb_Y08253 from Datura stramonium. ESTs gb_N38155, gb_T41738, gb_AA597626, gb_AA712967 and

NCBI Description (Z97342) resistance gene homolog [Arabidopsis thaliana]

```
Seq. No.
                     168111
  Seq. ID
                     LIB3234-053-P1-K1-E10
  Method
                     BLASTN
  NCBI GI
                     g4335711
  BLAST score
                     226
  E value
                     1.0e-124
  Match length
                     375
  % identity
                    99
  NCBI Description
                    Arabidopsis thaliana chromosome II BAC F9013 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    168112
  Seq. ID
                    LIB3234-053-P1-K1-E11
  Method
                    BLASTN
  NCBI GI
                    g4468103
  BLAST score
                    362
 E value
                    0.0e+00
 Match length
                    383
 % identity
                    98
 NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
                    (ESSA project)
 Seq. No.
                    168113
 Seq. ID
                    LIB3234-053-P1-K1-E2
 Method
                    BLASTX
 NCBI GI
                    g1749546
 BLAST score
                    220
 E value
                    6.0e-18
 Match length
                    123
 % identity
                    46
 NCBI Description
                   (D89169) similar to Saccharomyces cerevisiae SCD6 protein,
                   SWISS-PROT Accession Number P45978 [Schizosaccharomyces
                   pombe]
Seq. No.
                   168114
Seq. ID
                   LIB3234-053-P1-K1-E9
Method
                   BLASTN
NCBI GI
                   g4538918
BLAST score
                   338
E value
                   0.0e+00
Match length
                   366
% identity
                   98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18
                   (ESSA project)
Seq. No.
                  168115
Seq. ID
                  LIB3234-053-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  g4519195
BLAST score
                  55
E value
                  4.0e-22
Match length
                  223
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
```

```
Seq. No.
                   168116
 Seq. ID
                   LIB3234-053-P1-K1-F11
 Method
                   BLASTX
 NCBI GI
                   q1491615
 BLAST score
                   511
 E value
                   5.0e-52
 Match length
                   127
 % identity
 NCBI Description
                   (X99923) male sterility 2-like protein [Arabidopsis
                   thaliana
 Seq. No.
                   168117
 Seq. ID
                   LIB3234-053-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q4758634
BLAST score
                   158
E value
                   4.0e-14
Match length
                   84
 % identity
                   42
NCBI Description
                   Sec24p, S. Cerevisiae, homolog of
                   >gi_1723050_sp_P53992_Y079_HUMAN HYPOTHETICAL PROTEIN
                   KIAA0079 (HA3543) >gi_559717_dbj_BAA07558 (D38555) The
                   ha3543 gene product is related to S.cerevisiae protein
                   encoded in chromosome VIII. [Homo sapiens]
                   >gi_4741921_gb_AAD28756.1_ (AF130464) sec24D protein [Homo
                   sapiens]
Seq. No.
                   168118
Seq. ID
                   LIB3234-053-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2702284
BLAST score
                   45
E value
                   5.0e-24
Match length
                   71
% identity
                   92
NCBI Description
                   (AC003033) Argonaute (AG01)-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   168119
Seq. ID
                   LIB3234-053-P1-K1-F5
Method
                   BLASTN
NCBI GI
                   q4454447
BLAST score
                   65
E value
                   3.0e-28
Match length
                   205
% identity
                   91
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168120
Seq. ID
                  LIB3234-053-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  q4757411
BLAST score
                  34
E value
                  1.0e-09
Match length
                  238
% identity
                  79
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MXC7, complete sequence
Seq. No.
                  168121
                  LIB3234-053-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1363488
BLAST score
                  394
                  2.0e-38
E value
Match length
                  78
% identity
                  99
NCBI Description
                  IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410)
                  IAA8 [Arabidopsis thaliana] >gi 4314364 gb AAD15575
                  (AC006340) auxin-induced IAA8 protein [Ārabidopsis
                  thalianal
Seq. No.
                  168122
Seq. ID
                  LIB3234-053-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  q4589435
BLAST score
                  366
E value
                  0.0e + 00
Match length
                  378
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOE17, complete sequence
Seq. No.
                  168123
Seq. ID
                  LIB3234-053-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  g3386593
BLAST score
                  72
E value
                  2.0e-32
Match length
                  213
% identity
                  85
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  168124
Seq. No.
                  LIB3234-053-P1-K1-G3
Seq. ID
Method
                  BLASTX
                  g1076660
NCBI GI
BLAST score
                  308
                  3.0e-28
E value
                  95
Match length
% identity
                  69
                  D13F(MYBST1) protein - potato >gi 786426 bbs 159122
NCBI Description
                  (S74753) MybSt1=Myb-related transcriptional activator
                  {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                  leaf, Peptide, 342 aa] [Solanum tuberosum]
                  168125
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-G4
Method
                  BLASTX
                  g1170503
NCBI GI
BLAST score
                  333
```

7.0e-40

E value

```
Match length
                  90
% identity
                  93
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
NCBI Description
                  >gi 322503 pir JC1452 translation initiation factor
                  eIF-4A1 - Arabidopsis thaliana >gi 16554 emb CAA46188
                   (X65052) eukaryotic translation initiation factor 4A-1
                   [Arabidopsis thaliana]
                  168126
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-G5
Method
                  BLASTX
                  g2160158
NCBI GI
BLAST score
                  365
                  5.0e-35
E value
Match length
                  115
% identity
                  64
NCBI Description
                   (AC000132) Similar to elongation factor 1-gamma
                   (gb EF1G XENLA). ESTs gb T20564, gb T45940, gb T04527 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  168127
Seq. ID
                  LIB3234-053-P1-K1-G6
Method
                  BLASTN
                  q3869069
NCBI GI
BLAST score
                  53
                  2.0e-21
E value
                  113
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168128
Seq. ID
                  LIB3234-053-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  q3150396
BLAST score
                  358
E value
                  0.0e + 00
Match length
                  362
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T27E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168129
                  LIB3234-053-P1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2914688
BLAST score
                  351
E value
                  0.0e+00
Match length
                  371
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168130
                  LIB3234-053-P1-K1-H10
Seq. ID
                  BLASTX
Method
```

```
BLAST score
                   361
E value
                   2.0e-34
Match length
                   106
% identity
                    (ACO02336) putative ribosomal protein S26 [Arabidopsis
NCBI Description
                   thaliana]
                   168131
Seq. No.
Seq. ID
                   LIB3234-053-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g464707
BLAST score
                   420
                   2.0e-41
E value
Match length
                   83
                   100
% identity
                   40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                   protein S18.A - Arabidopsis thaliana
                   >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                    [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                    [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                   thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                   gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
                   protein [Arabidopsis thaliana]
Seq. No.
                   168132
Seq. ID
                   LIB3234-053-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q4038037
BLAST score
                   145
                    4.0e-09
E value
Match length
                   130
% identity
NCBI Description (AC005936) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   168133
Seq. ID
                   LIB3234-053-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g166570
BLAST score
                   241
E value
                   2.0e-20
Match length
                   105
% identity
NCBI Description
                   (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                   168134
                   LIB3234-053-P1-K1-H6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3659491
BLAST score
                   125
```

7.0e-64

E value

```
264
Match length
% identity
                  89
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  168135
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3913425
BLAST score
                  632
E value
                  3.0e-66
                  127
Match length
                  96
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE >gi 2275203 (AC002337) RNA helicase isolog
                  [Arabidopsis thaliana]
                  168136
Seq. No.
Seq. ID
                  LIB3234-053-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4263713
BLAST score
                  287
                  9.0e-26
E value
Match length
                  124
% identity
                  52
                  (AC006223) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168137
Seq. ID
                  LIB3234-053-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g2262135
BLAST score
                  164
E value
                  4.0e-87
Match length
                  216
% identity
                  54
                  Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
NCBI Description
                  cM, complete sequence
Seq. No.
                  168138
Seq. ID
                  LIB3234-054-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g4262232
BLAST score
                  390
E value
                  7.0e-38
Match length
                  111
% identity
NCBI Description
                  (AC006200) putative ribosomal protein L7 [Arabidopsis
                  thaliana]
Seq. No.
                  168139
Seq. ID
                  LIB3234-054-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3859606
BLAST score
                  677
                  1.0e-71
E value
                  123
Match length
                  98
% identity
```

```
NCBI Description
                   (AF104919) contains similarity to cysteine proteases (Pfam:
                    PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]
 Seq. No.
. Seq. ID
                   LIB3234-054-P1-K1-A11
 Method
                   BLASTX
 NCBI GI
                   g2459417
 BLAST score
                    404
 E value
                   2.0e-39
 Match length
                   124
 % identity
                    69
 NCBI Description
                    (AC002332) putative pre-mRNA splicing factor PRP19
                    [Arabidopsis thaliana]
 Seq. No.
                   168141
 Seq. ID
                   LIB3234-054-P1-K1-A12
 Method
                   BLASTX
                   g452470
 NCBI GI
 BLAST score
                   93
                   5.0e-18
 E value
 Match length
                    64
 % identity
                   91
 NCBI Description
                   (U05218) ATP sulfurylase [Arabidopsis thaliana]
 Seq. No.
                   168142
                   LIB3234-054-P1-K1-A4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1170503
 BLAST score
                   433
                   6-0e-43
 E value
 Match length
                   83
 % identity
                   100
                   EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
 NCBI Description
                   >gi 322503 pir JC1452 translation initiation factor
                   eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188
                    (X65052) eukaryotic translation initiation factor 4A-1
                    [Arabidopsis thaliana]
 Seq. No.
                   168143
 Seq. ID
                   LIB3234-054-P1-K1-A5
 Method
                   BLASTX
 NCBI GI
                   g1531762
 BLAST score
                   195
                   5.0e-15
 E value
 Match length
                   51
 % identity
                   75
 NCBI Description
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                   thaliana]
 Seq. No.
                   168144
 Seq. ID
                   LIB3234-054-P1-K1-A6
 Method
                   BLASTX
                   g4468806
 NCBI GI
 BLAST score
                   212
 E value
                   5.0e-17
                   51
Match length
                   78
 % identity
```

```
NCBI Description (AL035601) cytochrome P450 monooxygenase-like protein
                  [Arabidopsis thaliana]
                  168145
Seq. No.
Seq. ID
                  LIB3234-054-P1-K1-A7
Method
                  BLASTN
                  g3869072
NCBI GI
                  36
BLAST score
                  5.0e-11
E value
Match length
                  72
% identity
                  88
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168146
                  LIB3234-054-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  g2894598
NCBI GI
                  532
BLAST score
                  2.0e-54
E value
Match length
                  126
% identity
                  86
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                                                 _
Seq. No.
                  168147
                  LIB3234-054-P1-K1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1448916
                  266
BLAST score
                  1.0e-148
E value
                  352
Match length
% identity
NCBI Description Arabidopsis thaliana threonine synthase mRNA, 3' end of cds
Seq. No.
                  168148
                  LIB3234-054-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  452
                  4.0e-45
E value
Match length
                  90
% identity
                  96
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  168149
Seq. ID
                  LIB3234-054-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4325343
BLAST score
                  606
E value
                  3.0e-63
Match length
                  122
% identity
                  98
NCBI Description (AF128393) contains similarity to homeobox domains (Pfam:
```

NCBI Description

```
168150
Seq. No.
                   LIB3234-054-P1-K1-B3
Seq. ID
Method
                   BLASTN
                   g1707006
NCBI GI
BLAST score
                   365
                   0.0e+00
E value
                   369
Match length
% identity
                   100
                   Arabidopsis thaliana chromosome II BAC T1B8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   168151
Seq. No.
Seq. ID
                   LIB3234-054-P1-K1-B4
                   BLASTN
Method
NCBI GI
                   g1353238
BLAST score
                   36
                   9.0e-11
E value
Match length
                   64
% identity
                   89
                  Arabidopsis thaliana Col-O putative RNA helicase A mRNA,
NCBI Description
                   complete cds
                   168152
Seq. No.
                   LIB3234-054-P1-K1-B5
Seq. ID
                   BLASTN
Method
                   g4063730
NCBI GI
                   146
BLAST score
                   2.0e-76
E value
Match length
                   378
% identity
                   98
                  Arabidopsis thaliana BAC F21J6 from chromosome V,
NCBI Description
                   containing KNAT3 and mapping near 60.5 cM, complete
                   sequence [Arabidopsis thaliana]
Seq. No.
                   168153
Seq. ID
                   LIB3234-054-P1-K1-B6
Method
                   BLASTN
NCBI GI
                   q4063730
BLAST score
                   121
                   2.0e-61
E value
Match length
                   304
% identity
                   92
                  Arabidopsis thaliana BAC F21J6 from chromosome V,
NCBI Description
                   containing KNAT3 and mapping near 60.5 cM, complete
                   sequence [Arabidopsis thaliana]
                   168154
Seq. No.
Seq. ID
                   LIB3234-054-P1-K1-B7
                   BLASTN
Method
NCBI GI
                   g2924651
BLAST score
                   218
                   1.0e-119
E value
                   309
Match length
                   97
% identity
```

PF00046, Score, 36.5, E=6.9e-08, N=1) [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

Seq. No.

168160

K2A18, complete sequence [Arabidopsis thaliana] 168155 Seq. No. LIB3234-054-P1-K1-B8 Seq. ID Method BLASTX NCBI GI q1351272 BLAST score 416 E value 6.0e-41 Match length 99 % identity 83 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana] Seq. No. 168156 Seq. ID LIB3234-054-P1-K1-B9 Method BLASTX NCBI GI q21911 BLAST score 178 E value 5.0e-13 Match length 73 % identity 44 NCBI Description (X62625) vicilin [Theobroma cacao] Seq. No. 168157 Seq. ID LIB3234-054-P1-K1-C1 Method BLASTX NCBI GI q4512697 BLAST score 226 E value 1.0e-18 Match length 84 % identity 56 NCBI Description (AC006569) unknown protein [Arabidopsis thaliana] Seq. No. 168158 Seq. ID LIB3234-054-P1-K1-C10 Method BLASTN NCBI GI q511598 BLAST score 368 E value 0.0e+00Match length 372 % identity 28 NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds Seq. No. 168159 Seq. ID LIB3234-054-P1-K1-C11 Method BLASTX NCBI GI q2662343 BLAST score 508 E value 1.0e~51 Match length 106 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa]

```
Seq. ID
                  LIB3234-054-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   q4581103
BLAST score
                   152
E value
                   5.0e-80
Match length
                   276
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T24I21 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   168161
Seq. ID
                  LIB3234-054-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q4263777
BLAST score
                  529
E value
                   3.0e-54
Match length
                  113
                  87
% identity
NCBI Description
                  (ACO06068) putative serine carboxypeptidase II [Arabidopsis
                  thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative
                  serine carboxypeptidase II [Arabidopsis thaliana]
Seq. No.
                  168162
Seq. ID
                  LIB3234-054-P1-K1-C3
Method
                  BLASTX
NCBF GI
                  q1710780
BLAST score
                  411
E value
                  2.0e-40
Match length
                  110
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917 emb CAA65433
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
Seq. No.
                  168163
Seq. ID
                  LIB3234-054-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q511598
BLAST score
                  343
                  0.0e + 00
E value
Match length
                  375
% identity
                  28
NCBI Description
                  Arabidopsis thaliana cell wall protein (APTR-1) gene,
                  complete cds
Seq. No.
                  168164
Seq. ID
                  LIB3234-054-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g4406764
BLAST score
                  306
                  3.0e-37
E value
Match length
                  86
% identity
                  58
NCBI Description
                  (AC006836) putative uridylyl transferase [Arabidopsis
                  thaliana]
```

Seq. No.

```
Seq. ID
                  LIB3234-054-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  q3985958
BLAST score
                  215
                  1.0e-117
E value
Match length
                  380
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168166
Seq. ID
                  LIB3234-054-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  q3292807
                  345
BLAST score
                  0.0e+00
E value
Match length
                  377
% identity
                  97
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
NCBI Description
                  (ESSAII project)
Seq. No.
                  168167
Seq. ID
                  LIB3234-054-P1-K1-C8
Method
                  BLASTN
                                                                    ---
NCBI GI
                  q3292807
                  294
BLAST score
                  1.0e-164
E value
Match length
                  374
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
NCBI Description
                   (ESSAII project)
Seq. No.
                  168168
Seq. ID
                  LIB3234-054-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q135406
BLAST score
                  519
E value
                  5.0e-53
Match length
                  97
% identity
                  100
NCBI Description
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768_pir_ A32712 tubulin
                  alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
                  168169
Seq. No.
Seq. ID
                  LIB3234-054-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4056502
BLAST score
                  516
E value
                  1.0e-52
Match length
                  102
                  99
% identity
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                  168170
Seq. No.
                  LIB3234-054-P1-K1-D10
Seq. ID
```

```
Method
                  BLASTN
                  g2696018
NCBI GI
BLAST score
                  337
                  0.0e + 00
E value
                  369
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC9, complete sequence [Arabidopsis thaliana]
                  168171
Seq. No.
                  LIB3234-054-P1-K1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2959729
                  308
BLAST score
                  1.0e-173
E value
                  312
Match length
                  100
% identity
                  Arabidopsis thaliana mRNA for GATA transcription factor
NCBI Description
                  168172
Seq. No.
                  LIB3234-054-P1-K1-D2
Seq. ID
                  BLASTN
Method
                  g4115930
NCBI GI
BLAST score
                  290
                  1.0e-162
E value
                  378
Match length
                  94
% identity
NCBI Description Arabidopsis thaliana BAC T4B21
                  168173
Seq. No.
                  LIB3234-054-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  534
E value
                  8.0e-55
                  103
Match length
% identity
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >gi 4455197 emb CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  168174
                  LIB3234-054-P1-K1-D4
Seq. ID
Method
                  BLASTN
                  g3241920
NCBI GI
                  228
BLAST score
                  1.0e-125
E value
Match length
                  374
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168175
Seq. ID
                  LIB3234-054-P1-K1-D5
Method
                  BLASTN
                  g2947056
NCBI GI
```

BLAST score

```
E value
                    0.0e + 00
Match length
                    374
                    87
% identity
                    Arabidopsis thaliana chromosome II BAC T20F6 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    168176
Seq. ID
                    LIB3234-054-P1-K1-D6
Method
                    BLASTX
NCBI GI
                    g1703108
BLAST score
                    543
                    8.0e-56
E value
                    100
Match length
                    100
% identity
                    ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
NCBI Description
                    thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                    thaliana]
Seq. No.
                    168177
Seq. ID
                    LIB3234-054-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    q1737492
BLAST score
                    281
E value
                    4.0e-25
                    91
Match length
% identity
                    67
NCBI Description
                   (U81318) poly(A)-binding protein [Triticum aestivum]
Seq. No.
                    168178
Seq. ID
                    LIB3234-054-P1-K1-D9
                    BLASTX
Method
NCBI GI
                    g2924784
BLAST score
                   . 98
E value
                    1.0e-03
Match length
                    111
                    13
% identity
NCBI Description
                    (AC002334) similar to jasmonate inducible protein
                    [Arabidopsis thaliana]
                    168179
Seq. No.
                    LIB3234-054-P1-K1-E1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3413716
BLAST score
                    364
E value
                    8.0e-35
                    80
Match length
                    50
% identity
NCBI Description
                    (AC004747) unknown protein [Arabidopsis thaliana]
                    >gi_3643589 (AC005395) unknown protein [Arabidopsis
                    thaliana]
                    168180
Seq. No.
Seq. ID
                    LIB3234-054-P1-K1-E10
Method
                    BLASTX
```

```
BLAST score
                   410
                   3.0e-40
E value
                   116
Match length
% identity
                   72
                   (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
NCBI Description
                   Match to gb_X91954 orf gene product from A. thaliana. ESTs
                   gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                   this gene. [Arabidopsis thaliana]
 Seq. No.
                   168181
 Seq. ID
                   LIB3234-054-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   q2914688
BLAST score
                   189
E value
                   1.0e-102
Match length
                   319
 % identity
                   94
                   Arabidopsis thaliana chromosome II BAC F24L7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   168182
 Seq. No.
 Seq. ID
                   LIB3234-054-P1-K1-E2
Method
                   BLASTX
                  -- q4678285
NCBI GI
BLAST score
                   374
                   5.0e-36
E value
Match length
                   122
 % identity
                   58
                   (AL049660) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  · 168183
Seq. ID
                   LIB3234-054-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g1107501
BLAST score
                   408
E value
                   5.0e-40
Match length
                   109
.% identity
                   75
                   (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
NCBI Description
                   Match to gb X91954 orf gene product from A. thaliana. ESTs
                   gb Z17604, gb H76594, gb AA597972 and gb AA394824 come from
                   this gene. [Arabidopsis thaliana]
 Seq. No.
                   168184
 Seq. ID
                   LIB3234-054-P1-K1-E5
Method
                   BLASTN
NCBI GI
                   g3695372
BLAST score
                   272
E value
                   1.0e-151
Match length
                   347
 % identity
                   95
NCBI Description Arabidopsis thaliana BAC F1104
Seq. No.
                   168185
                   LIB3234-054-P1-K1-E6
Seq. ID
Method
                   BLASTN
```

```
BLAST score
                   124
                   2.0e-63
E value
Match length
                   327
% identity
                  Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
NCBI Description
                  K11J9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168186
Seq. ID
                  LIB3234-054-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  q3928074
BLAST score
                   49
E value
                   1.0e-18
Match length
                   60
                   95
% identity
                  Arabidopsis thaliana chromosome II BAC T7F6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168187
Seq. ID
                  LIB3234-054-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q4432811
BLAST score
                   349
E value
                  0.0e + 00
Match length ...
                   361
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F16D14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168188
Seq. ID
                  LIB3234-054-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3128169
BLAST score
                  95
                  1.0e-17
E value
Match length
                   91
% identity
                  54
NCBI Description
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168189
Seq. ID
                  LIB3234-054-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3925363
BLAST score
                  148
                  2.0e-09
E value
Match length
                  120
% identity
                  44
                  (AF067961) homeodomain protein [Malus domestica]
NCBI Description
Seq. No.
                  168190
Seq. ID
                  LIB3234-054-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  g1245181
BLAST score
                  359
                  0.0e+00
E value
Match length
                  374
```

% identity

```
NCBI Description Arabidopsis thaliana sterol delta-7 reductase (ST7R) mRNA,
                  complete cds
                  168191
Seq. No.
                  LIB3234-054-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1109697
BLAST score
                  610
                  1.0e-63
E value
Match length
                  125
% identity
                  92
NCBI Description
                  (X83380) gibberellin 20-oxidase [Arabidopsis thaliana]
                  168192
Seq. No.
Seq. ID
                  LIB3234-054-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q4063568
BLAST score
                  627
                  1.0e-65
E value
                  125
Match length
                  100
% identity
NCBI Description
                  (AF035916) ATP synthase beta subunit [Triplochlamys
                  multiflora]
                  168193
Seq. No.
                  LIB3234-054-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3445209
BLAST score
                  146
E value
                  9.0e-10
Match length
                  38
% identity
NCBI Description
                  (AC004786) putative serine carboxypeptidase I [Arabidopsis
                  thaliana]
Seq. No. Seq. ID
                  168194
                  LIB3234-054-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q3335169
BLAST score
                  583
                  2.0e-60
E value
Match length
                  112
% identity
                  98
NCBI Description
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  168195
Seq. ID
                  LIB3234-054-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q131398
BLAST score
                  479
E value
                  2.0e-48
Match length
                  113
% identity
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
```

Method NCBI GI

```
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                   gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                   come from this gene. [Arabidopsis
Seq. No.
                   168196
                   LIB3234-054-P1-K1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4337186
BLAST score
                   212
E value
                   1.0e-116
Match length
                   376
% identity
                   98
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T28I24 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168197
Seq. ID
                   LIB3234-054-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   574
E value
                   2.0e-59
Match length
                   106
                   99
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   168198
Seq. ID
                   LIB3234-054-P1-K1-G4
Method
                   BLASTN
                   g2696018
NCBI GI
BLAST score
                   346
E value
                   0.0e + 00
Match length
                   358
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                   MXC9, complete sequence [Arabidopsis thaliana]
                   168199
Seq. No.
Seq. ID
                   LIB3234-054-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   q1335862
                   613
BLAST score
                   5.0e-64
E value
                   126
Match length
% identity
                   94
                  (U42608) clathrin heavy chain [Glycine max]
NCBI Description
Seq. No.
                   168200
Seq. ID
                   LIB3234-054-P1-K1-G6
```

- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa

BLASTN

q2618602

Method

NCBI GI

BLASTN

q2924257

```
BLAST score
                     186
 E value
                     1.0e-100
 Match length
                     186
 % identity
                     100
 NCBI Description
                     Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                     MSJ1, complete sequence [Arabidopsis thaliana]
 Seq. No.
 Seq. ID
                     LIB3234-054-P1-K1-G7
 Method
                     BLASTX
 NCBI GI
                     q133729
 BLAST score
                     317
                     2.0e-29
 E value
. Match length
                     80
 % identity
                     79
 NCBI Description
                     CHLOROPLAST 30S RIBOSOMAL PROTEIN S11 >gi 70941 pir R3NT11
                     ribosomal protein S11 - common tobacco chloroplast >gi_11861_emb_CAA77377_ (Z00044) ribosomal protein S11 [Nicotiana tabacum] >gi_225229_prf__1211235BL ribosomal
                     protein S11 [Nicotiana tabacum]
 Seq. No.
                     168202
 Seq. ID
                     LIB3234-054-P1-K1-H1
 Method
                     BLASTN
NCBI GI
                     q2864607
BLAST score
                     247
E value
                     1.0e-137
Match length
                     297
 % identity
                     99
NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                     (ESSAII project)
 Seq. No.
                     168203
Seq. ID
                     LIB3234-054-P1-K1-H10
Method
                     BLASTN
NCBI GI
                     g4589433
BLAST score
                     370
E value
                     0.0e + 00
Match length
                     378
                     99
 % identity
NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                     MNI5, complete sequence
 Seq. No.
                     168204
Seq. ID
                     LIB3234-054-P1-K1-H11
Method
                     BLASTN
NCBI GI
                     q3193305
BLAST score
                     153
E value
                     1.0e-80
Match length
                     327
% identity
                     80
NCBI Description Arabidopsis thaliana BAC F3D13
Seq. No.
                    168205
Seq. ID
                    LIB3234-054-P1-K1-H12
```

BLAST score

639

```
BLAST score
                  65
                  5.0e-28
E value
Match length
                  93
                  92
% identity
NCBI Description Tobacco chloroplast genome DNA
                  168206
Seq. No.
Seq. ID
                  LIB3234-054-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  q1279568
BLAST score
                  41
E value
                  9.0e-14
Match length
                  49
% identity
                  96
NCBI Description Nicotiana acuminata chloroplast JLB region, 1-250bp
Seq. No.
                  168207
Seq. ID
                  LIB3234-054-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q2529680
BLAST score
                  496
E value
                  3.0e-50
Match length
                  114
% identity
                  49
NCBI Description
                  (AC002535) putative protein disulfide-isomerase precursor
                  [Arabidopsis thaliana]
Seq. No.
                  168208
Seq. ID
                  LIB3234-054-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g122781
BLAST score
                  202
E value
                  8.0e-16
Match length
                  52
% identity
                  69
NCBI Description
                  POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229)
                  >gi_82210_pir__A05198 hypothetical protein 229 - common
                  tobacco chloroplast >gi_11844_emb_CAA77364_ (Z00044)
                  hypothetical protein [Nicotiana tabacum]
                  >gi_225212_prf__1211235AT ORF 229 [Nicotiana tabacum]
                  168209
Seq. No.
Seq. ID
                  LIB3234-054-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  g2351061
BLAST score
                  197
E value
                  1.0e-107
Match length
                  351
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168210
Seq. ID
                  LIB3234-054-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1628583
```

```
E value
                   4.0e-67
Match length
                   124
                   98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  168211
Seq. ID
                  LIB3234-054-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g3046855
BLAST score
                  35
E value
                   4.0e-10
Match length
                   67
% identity
                  88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168212
Seq. ID
                  LIB3234-055-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2605714
BLAST score
                  489
E value
                  2.0e-49 ~
Match length
                  115
                  83
% identity
NCBI Description
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                  thaliana]
Seq. No.
                  168213
Seq. ID
                  LIB3234-055-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g2351062
BLAST score
                  383
                  0.0e+00
E value
Match length
                  383
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168214
Seq. ID
                  LIB3234-055-P1-K1-A12
Method
                  BLASTN
                  g4159712
NCBI GI
BLAST score
                  156
                  2.0e-82
E value
Match length
                  291
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
                  168215
Seq. No.
Seq. ID
                  LIB3234-055-P1-K1-A2
Method
                  BLASTX
                  g3850816
NCBI GI
                  378
BLAST score
```

2.0e-36

E value

Seq. ID

```
Match length
                   79
% identity
                   85
                   (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                   sativa]
Seq. No.
                   168216
Seq. ID
                   LIB3234-055-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   q2760165
BLAST score
                   59
E value
                   2.0e-24
Match length
                   301
                   83
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168217
Seq. ID
                   LIB3234-055-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   q4585989
BLAST score
                   175
E value
                   1.0e-12
Match length
                   85
% identity
NCBI Description
                   (AC005287) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   168218
Seq. ID
                   LIB3234-055-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q1345973
BLAST score
                   439
E value
                   1.0e-43
Match length
                   99
% identity
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
NCBI Description
                   1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
                   168219
Seq. No.
Seq. ID
                   LIB3234-055-P1-K1-A8
Method
                   BLASTX
                   q4704766
NCBI GI
BLAST score
                   66
                   3.0e-26
E value
Match length
                   124
% identity
NCBI Description
                   (AF131223) protein disulfide isomerase homolog; PDI
                   [Datisca glomerata]
                   168220
Seq. No.
```

LIB3234-055-P1-K1-B1

```
Method
                    BLASTN
  NCBI GI
                    q2842474
  BLAST score
                    140
  E value
                    3.0e-73
  Match length
                    156
  % identity
                    97
                    Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
  NCBI Description
                    (ESSAII project)
  Seq. No.
                    168221
  Seq. ID
                    LIB3234-055-P1-K1-B10
  Method
                    BLASTX
  NCBI GI
                    q112740
  BLAST score
                    260
                    1.0e-22
  E value
  Match length
                    115
  % identity
                    51
                    NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)
  NCBI Description
                    >gi 81691 pir A25997 napin precursor (napA) - rape
                    >gi 167153 (J02586) prepronapin [Brassica napus] >gi 167155
                    (J02798) napin [Brassica napus]
                    168222
  Seq. No.
  Seq. ID
                    LIB3234-055-P1-K1-B12
  Method
                    BLASTX
  NCBI GI
                    q1711382
BLAST score
                    289
 E value
                    5.0e-26
  Match length
                    97
  % identity
                    48
                    SET PROTEIN >gi_940889 (U30470) SET [Drosophila
  NCBI Description
                    melanogaster]
  Seq. No.
                    168223
  Seq. ID
                    LIB3234-055-P1-K1-B2
  Method
                    BLASTX
  NCBI GI
                    q2129532
  BLAST score
                    330
                    8.0e-31
  E value
  Match length
                    93
                    71
  % identity
                    acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -
  NCBI Description
                    Arabidopsis thaliana >gi 1107507 emb CAA63746 (X93461)
                    acyl-[acyl-carrier protein] desaturase [Arabidopsis
                    thaliana]
  Seq. No.
                    168224
  Seq. ID
                    LIB3234-055-P1-K1-B3
  Method
                    BLASTX
                    q4006924
  NCBI GI
  BLAST score
                    587
                    6.0e-61
  E value
  Match length
                    129
  % identity
                    88
                    (Z99708) beta-galactosidase like protein [Arabidopsis
  NCBI Description
```

thaliana]

Seq. No.

168230

```
168225
    Seq. No.
    Seq. ID
                      LIB3234-055-P1-K1-B4
Method
                      BLASTN
    NCBI GI
                      g4662609
    BLAST score
                      254
    E value.
                      1.0e-141
                      287
    Match Tength
    % identity
    NCBI Description
                      Genomic sequence for Arabidopsis thaliana BAC F10A5,
                      complete sequence
                      168226
    Seq. No.
    Seq. ID
                      LIB3234-055-P1-K1-B5
    Method
                      BLASTN
    NCBI GI
                      g4662609
    BLAST score
                      258
                      1.0e-143
    E value
    Match length
                      287
                      98
    % identity
    NCBI Description
                      Genomic sequence for Arabidopsis thaliana BAC F10A5,
                      complete sequence
    Seq. No.
                      1.68227
  - Seq. ID
                      LIB3234-055-P1-K1-B6
    Method ....
                      BLASTX
    NCBI GI
                      g4734006
    BLAST score
                      152
    E value
                      6.0e-10
                      62
    Match length
    % identity .
                      48
    NCBI Description (AC007178) hypothetical protein [Arabidopsis thaliana]
                      168228
    Seq. No.
                      LIB3234-055-P1-K1-B7
    Seq. ID
    Method
                      BLASTN
                      q2264306
    NCBI GI
    BLAST score
                      304
                      1.0e-170
    E value
                      336
    Match length
    % identity
                      Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
    NCBI Description
                      MBK5, complete sequence [Arabidopsis thaliana]
                      168229
    Seq. No.
    Seq. ID
                      LIB3234-055-P1-K1-B8
    Method
                      BLASTX
    NCBI GI
                      q3023848
    BLAST score
                      612
                      6.0e-64
    E value
                      126
    Match length
    % identity
                      59
                      GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
    NCBI Description
                      PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                      >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis
                      thaliana]
```

E value

```
LIB3234-055-P1-K1-B9
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g498038
  BLAST score
                    235
  E value
                    5.0e-20
  Match length
                    85
. % identity
                    58
                   (L33792) lipid transfer protein [Senecio odorus]
  NCBI Description
                    168231
  Seq. No.
  Seq. ID
                    LIB3234-055-P1-K1-C1
                    BLASTX
  Method
  NCBI GI
                    q498038
  BLAST score
                    504
  E value
                    3.0e-51
  Match length
                    127
                    76
  % identity
                    (L33792) lipid transfer protein [Senecio odorus]
  NCBI Description
                    168232
  Seq. No.
  Seq. ID
                    LIB3234-055-P1-K1-C10
  Method
                    BLASTN
  NCBI GI
                    q4309747
  BLAST score
                    60
  E value
                    3.0e-25
                    179
  Match length
  % identity
                    72
                    Arabidopsis thaliana chromosome II BAC T13E11 genomic
  NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    168233
                    LIB3234-055-P1-K1-C12
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g2244991
  BLAST score
                    195
  E value
                    1.0e-105
  Match length
                    389
  % identity
                    98
                    Arabidopsis thaliana DNA chromosome 4, ESSA I contig
  NCBI Description
                    fragment No
  Seq. No.
                    168234
  Seq. ID
                    LIB3234-055-P1-K1-C2
  Method
                    BLASTX
  NCBI GI
                    g2058311
  BLAST score
                    410
  E value
                    3.0e-40
                    99
  Match length
                    78
  % identity
  NCBI Description
                   (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]
  Seq. No.
                    168235
  Seq. ID
                    LIB3234-055-P1-K1-C3
 Method
                    BLASTN
 NCBI GI
                    g3449332
 BLAST score
                    115
                    7.0e-58
```

Seq. No.

168241

```
317
Match length
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168236
                  LIB3234-055-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3641835
BLAST score
                  289
E value
                  1.0e-162
Match length
                  346
% identity
                  96
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
NCBI Description
                  (ESSAII project)
                  168237
Seq. No.
                  LIB3234-055-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  343
E value
                  2.0e-32
Match length
                  111
                  62
% identity
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168238
                  LIB3234-055-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3461814
BLAST score
                  687
E value
                  1.0e-72
                  128
Match length
% identity
                  99
NCBI Description
                  (AC004138) hypothetical protein [Arabidopsis thaliana]
                  168239
Seq. No.
                  LIB3234-055-P1-K1-C7
Seq. ID
                  BLASTX
Method
                  g1526424
NCBI GI
                  338
BLAST score
                  6.0e-32
E value
                  79
Match length
                  82
% identity
                  (D64140) LEA protein in group 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168240
                  LIB3234-055-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  q1041704
NCBI GI
                  206
BLAST score
                  2.0e-16
E value
Match length
                  78
% identity
                  56
                  (U30478) expansin At-EXP5 [Arabidopsis thaliana]
NCBI Description
```

```
Seq. ID
                   LIB3234-055-P1-K1-C9
 Method
                   BLASTN
 NCBI GI
                  - g4309747
 BLAST score
                   372
 E value
                   0.0e+00
"Match length
                   376
 % identity
                   39
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC T13E11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168242
 Seq. ID
                   LIB3234-055-P1-K1-D10
 Method
                   BLASTX
 NCBI GI
                   g3023848
 BLAST score
                   552
 E value
                   6.0e-57
 Match length
                   108
 % identity
                   57
 NCBI Description
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                   >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis
                   thaliana]
 Seq. No.
                   168243
 Seq. ID
                   LIB3234-055-P1-K1-D11
 Method
                 · BLASTN
 NCBI GI
                   q4586241
 BLAST score
                   155
 E value
                   9.0e-82
 Match length
                   218
                   92
 % identity
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                   (ESSA project)
 Seq. No.
                   168244
 Seq. ID
                   LIB3234-055-P1-K1-D12
 Method
                   BLASTX
 NCBI GI
                   q4263771
 BLAST score
                   283
                   3.0e-25
 E value
 Match length
                   73
 % identity
                   68
 NCBI Description
                   (AC006218) putative nonspecific lipid-transfer protein
                   precursor [Arabidopsis thaliana]
                   >gi_4726121_gb_AAD28321.1 AC006436 12 (AC006436) putative
                   nonspecific lipid-transfer protein precursor [Arabidopsis
                   thaliana]
 Seq. No.
                   168245
 Seq. ID
                   LIB3234-055-P1-K1-D3
 Method
                   BLASTX
 NCBI GI
                   g3850816
 BLAST score
                   415
 E value
                   9.0e-41
Match length
                   80
 % identity
NCBI Description (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
```

sativa] 168246 Seq. No. Seq. ID LIB3234-055-P1-K1-D6 Method BLASTN NCBI GI q4589450 1-20 -BLAST score 174 E value 4.0e-93 Match length 370 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T31K7, complete sequence Seq. No. 168247 Seq. ID LIB3234-055-P1-K1-D7 Method BLASTN NCBI GI q3047074 BLAST score 300 E value 1.0e-168 Match length 370 94 % identity NCBI Description Arabidopsis thaliana BAC F21E10 Seq. No. 168248 Seq. ID LIB3234-055-P1-K1-D9 Method BLASTX NCBI GI q4204298 BLAST score 575 E value 1.0e-59 Match length 128 % identity 88 NCBI Description (AC003027) lcl prt seq No definition line found [Arabidopsis thaliana] Seq. No. 168249 Seq. ID LIB3234-055-P1-K1-E1 Method BLASTN NCBI GI q4589439 BLAST score 237 1.0e-131 E value Match length 305 % identity 93 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MQM1, complete sequence Seq. No. 168250 Seq. ID LIB3234-055-P1-K1-E12 Method BLASTX NCBI GI g267073 BLAST score 572 3.0e-59 E value Match length 104 % identity 100 TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir_ JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) NCBI Description

beta-3 tubulin [Arabidopsis thaliana]

Seq. ID

```
Seq. No.
                   168251
Seq. ID
                  LIB3234-055-P1-K1-E2
                  BLASTN
Method
NCBI GI
                   g2160132
BLAST score
                   374
                   0.0e + 00
E value
                   390
Match length
                   99
% identity
NCBI Description
                  Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
                  168252
Seq. No.
Seq. ID
                  LIB3234-055-P1-K1-E3
Method
                  BLASTX
NCBI GI
                   g3327204
BLAST score
                   372
E value
                   9.0e-36
Match length
                  128
% identity
                   57
                  (AB014595) KIAA0695 protein [Homo sapiens]
NCBI Description
Seq. No.
                  168253
Seq. ID
                  LIB3234-055-P1-K1-E4
                                                   4...
Method
                  BLASTX
NCBI GI
                  g3461828
BLAST score
                   186
                   6.0e-14
E value
                  119
Match length
                  36
% identity
NCBI Description
                  (AC004138) unknown protein [Arabidopsis thaliana]
                  168254
Seq. No.
Seq. ID
                  LIB3234-055-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q3264778
BLAST score
                  365
                   6.0e-35
E value
Match length
                  123
% identity
NCBI Description
                   (AF072536) H-protein promoter binding factor-1 [Arabidopsis
                  thaliana]
Seq. No.
                  168255
Seq. ID
                  LIB3234-055-P1-K1-F11
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  646
                  7.0e-68
E value
                  127
Match length
                  98
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  168256
Seq. No.
```

LIB3234-055-P1-K1-F12

BLAST score

333

```
Method
                  BLASTN
NCBI GI
                  q3193311
BLAST score
                  392
E value
                  0.0e+00
Match length
                  392
% identity
                  100
NCBI Description Arabidopsis thaliana BAC F6N15
Seq. No.
                  168257
Seq. ID
                  LIB3234-055-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1480347
BLAST score
                  207
                  2.0e-16
E value
Match length
                  109
% identity
                  48
NCBI Description
                 (X99419) ferrodoxin NADP oxidoreductase [Pisum sativum]
Seq. No.
                  168258
Seq. ID
                  LIB3234-055-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q3193310
BLAST score
                  621
E value
                  6.0e-65 ·
Match length
                  131
% identity
                  94
NCBI Description
                  (AF069300) contains similarity to Nicotiana tabacum hinl
                  (GB:Y07563) [Arabidopsis thaliana]
Seq. No.
                  168259
Seq. ID
                  LIB3234-055-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q3335169
BLAST score
                  671
E value
                  8.0e-71
                  125
Match length
% identity
                  100
NCBI Description
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  168260
Seq. ID
                  LIB3234-055-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3660471
BLAST score
                  301
E value
                  2.0e-27
                  97
Match length
% identity
                  62
                  (AJ001809) succinate dehydrogenase flavoprotein alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
Seq. No.
                  168261
Seq. ID
                  LIB3234-055-P1-K1-G1
                  BLASTN
Method
NCBI GI
                  g547390
```

E value

. - -

1.0e-43

```
0.0e + 00
 E value
 Match length
                    341
 % identity
                    99
                   Arabidopsis thaliana TRAP mRNA, partial cds
 NCBI Description
                    168262
 Seq. No.
                    LIB3234-055-P1-K1-G11
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g2924731
 BLAST score
                    330
 E value
                    0.0e + 00
                    381
 Match length
                    97
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MSI17, complete sequence [Arabidopsis thaliana]
                    168263
 Seq. No.
 Seq. ID
                    LIB3234-055-P1-K1-G2
 Method
                    BLASTX
 NCBI GI
                    g1107501
 BLAST score
                    378
                    2.0e-36
 E value
. Match length
                    119
                    66
 % identity
                   (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
 NCBI Description
                    Match to gb X91954 orf gene product from A. thaliana. ESTs
                    gb Z17604, gb H76594, gb AA597972 and gb AA394824 come from
                    this gene. [Arabidopsis thaliana]
 Seq. No.
                    168264
 Seq. ID
                    LIB3234-055-P1-K1-G3
                    BLASTX
 Method
 NCBI GI
                    g4204299
 BLAST score
                    649
 E value
                    3.0e-68
                    126
 Match length
 % identity
                    100
                    (AC003027) 1cl prt seq No definition line found
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    168265
 Seq. ID
                   LIB3234-055-P1-K1-G4
                   BLASTX
 Method
 NCBI GI
                   g2160151
                    555
 BLAST score
                   3.0e-57
 E value
                    112
 Match length
 % identity
                    (AC000375) Strong similarity to Brassica aspartic protease
 NCBI Description
                    (gb X77260). [Arabidopsis thaliana]
                   168266
 Seq. No.
 Seq. ID
                   LIB3234-055-P1-K1-G5
                   BLASTX
 Method
                   g4583544
 NCBI GI
 BLAST score
                   440
```

```
Match length
                   90
% identity
                   91
                   (Z95637) acyl-CoA:1-acylglycerol-3-phosphate
NCBI Description
                   acyltransferase [Brassica napus]
Seq. No.
                   168267
Seq. ID
                  LIB3234-055-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3461828
BLAST score
                   154
E value
                   3.0e-10
Match length
                  88
                   40
% identity
NCBI Description
                  (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                  168268
Seq. ID
                  LIB3234-055-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  q2760164
BLAST score
                   380
E value
                  0.0e+00
Match length
                  396
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168269
Seq. ID
                  LIB3234-055-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2342723
BLAST score
                  179
E value
                  3.0e-13
Match length
                  104
% identity
                  36
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168270
Seq. ID
                  LIB3234-055-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q3292836
BLAST score
                  455
E value
                  2.0e-45
Match length
                  94
                  99
% identity
                  (AL031018) gamma-glutamylcysteine synthetase [Arabidopsis
NCBI Description
                  thaliana] >gi 4262277_gb_AAD14544_ (AF068299)
                  gamma-glutamylcysteine synthetase [Arabidopsis thaliana]
Seq. No.
                  168271
Seq. ID
                  LIB3234-055-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  g2564048
BLAST score
                  368
E value
                  0.0e + 00
                  380
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

% identity

NCBI Description

95

```
MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168272
Seq. ID
                   LIB3234-055-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   586
                   7.0e-61
E value
Match length
                   112
% identity
                   99
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   168273
Seq. ID
                   LIB3234-056-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g114330
BLAST score
                   578
E value
                   5.0e-60
Match length
                   115
% identity
                   97
NCBI Description
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
                   >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
                   type 1, plasma membrane - Arabidopsis thaliana >gi 166746
                   (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis
                   thalianal
Seq. No.
                   168274
Seq. ID
                  LIB3234-056-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2289006
BLAST score
                   469
E value
                   4.0e-47
Match length
                  106
% identity
                  88
                   (AC002335) glutathione perosidase isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  168275
Seq. ID
                  LIB3234-056-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  g2864607
BLAST score
                  166
E value
                  2.0e-88
Match length
                  326
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                  (ESSAII project)
Seq. No.
                  168276
Seq. ID
                  LIB3234-056-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2160151
BLAST score
                  336
E value
                  6.0e-40
Match length
                  90
```

22785

(AC000375) Strong similarity to Brassica aspartic protease

Method

NCBI GI

BLASTX

g2924784

(gb X77260). [Arabidopsis thaliana]

```
168277
Seq. No.
                   LIB3234-056-P1-K1-A3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2760164
BLAST score
                   386
                   0.0e+00
E value
                   394
Match length
% identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3234-056-P1-K1-A6
Method
                   BLASTN
NCBI GI
                   q4757401
BLAST score
                   137
E value
                   5.0e-71
Match length
                   375
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MGH6, complete sequence
Seq. No.
                   168279
Seq. ID
                   LIB3234-056-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g1345973
BLAST score
                   570
E value
                   5.0e-59
Match length
                   110
% identity
NCBI Description
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514 (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
Seq. No.
                   168280
Seq. ID
                   LIB3234-056-P1-K1-A8
Method
                   BLASTN
NCBI GI
                   g2760164
BLAST score
                   209
                   1.0e-114
E value
Match length
                   251
% identity
                   97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168281
Seq. ID
                  LIB3234-056-P1-K1-B1
```

Method

BLASTN

```
BLAST score
                   98
                   1.0e-03
E value
Match length
                   114
% identity
                   13
                   (AC002334) similar to jasmonate inducible protein
NCBI Description
                   [Arabidopsis thaliana]
                   168282
Seq. No.
Seq. ID
                   LIB3234-056-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q3819099
BLAST score
                   268
                   1.0e-23
E value
                   129
Match length
% identity
                   46
                   (AJ009825) copper amine oxidase [Cicer arietinum]
NCBI Description
Seq. No.
                   168283
Seq. ID
                   LIB3234-056-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q4650842
BLAST score
                   636
E value
                   1.0e-66
                   126
Match length
% identity
                   96
                   (AB026185) elongation factor 2 [Lithospermum erythrorhizon]
NCBI Description
Seq. No.
                   168284
Seq. ID
                   LIB3234-056-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g133872
BLAST score
                   329
E value
                   1.0e-30
Match length
                   84
% identity
                   73
NCBI Description
                   30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
                   >gi 282838 pir S26494 ribosomal protein S1, chloroplast -
                   spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >gi 170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
Seq. No.
                   168285
Seq. ID
                   LIB3234-056-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g2961390
BLAST score
                   188
E value
                   3.0e-14
Match length
                   47
                   79
% identity
NCBI Description
                   (AL022141) beta-galactosidase like protein [Arabidopsis
                   thaliana]
                   168286
Seq. No.
Seq. ID
                   LIB3234-056-P1-K1-B4
```

E value

5.0e-98

```
NCBI GI
                   q4185128
BLAST score
                   162
E value
                   5.0e-86
Match length
                   311
                   100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II P1 MSF3 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168287
Seq. ID
                   LIB3234-056-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   q2398679
BLAST score
                   460
E value
                   5.0e-46
Match length
                   113
% identity
                   77
NCBI Description
                   (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
                   synthase [Morinda citrifolia]
Seq. No.
                   168288
Seq. ID
                   LIB3234-056-P1-K1-B8
Method
                  BLASTN
NCBI GI
                   g2088638
BLAST score
                   170
E value
                   9.0e-91
Match length
                   246
% identity
                   92
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168289
Seq. ID
                  LIB3234-056-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q70644
BLAST score
                  531
E value
                  2.0e-54
Match length
                  109 -
                  19
% identity
NCBI Description
                  ubiquitin precursor - common sunflower (fragment)
Seq. No.
                  168290
Seq. ID
                  LIB3234-056-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g2828182
BLAST score
                  362
                  0.0e + 00
E value
Match length
                  370
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168291
                  LIB3234-056-P1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2914688
BLAST score
                  182
```

Match length

87

```
Match length
                  289
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168292
                  LIB3234-056-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3406034
BLAST score
                  191
E value
                  1.0e-103
Match length
                  261
% identity
                  94
NCBI Description BAC F18A17 from chromosome V containing TINY at 60.5 cM,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  168293
                  LIB3234-056-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  g4507433
NCBI GI
                  190
BLAST score
E value
                  2.0e-14
Match length
                  114
% identity
                  39
                  testis enhanced gene transcript
NCBI Description
                  >gi_1729891_sp_P55061_TEGT_HUMAN TEGT PROTEIN (TESTIS
                  ENHANCED GENE TRANSCRIPT) >gi_2136254_pir__138334 TEGT
                  (testis enhanced gene transcript) - human
                  >gi_458545_emb_CAA53472_ (X75861) TEGT [Homo sapiens]
                  168294
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q1698690
BLAST score
                  623
E value
                  4.0e-65
Match length
                  131
% identity
NCBI Description
                  (U67317) beta-ketoacyl-ACP synthase II [Cuphea wrightii]
Seq. No.
                  168295
Seq. ID
                  LIB3234-056-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g166570
BLAST score
                  230
E value
                  4.0e-19
Match length
                  103
% identity
NCBI Description
                  (LO4173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                  168296
                  LIB3234-056-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  155
                  1.0e-10
E value
```

```
% identity
                   52
 NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
                   168297
 Seq. No.
 Seq. ID
                   LIB3234-056-P1-K1-C6
 Method
                   BLASTN
 NCBI GI
                   g3927822
 BLAST score
                   229
 E value
                   1.0e-126
Match length
                   295
 % identity
                   97
NCBI Description Arabidopsis thaliana chromosome II BAC F8N16 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168298
 Seq. ID
                   LIB3234-056-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g2244979
BLAST score
                   374
E value
                   8.0e-49
Match length
                   114
% identity
                   92
                  (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  168299
Seq. ID
                  LIB3234-056-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g2435510
BLAST score
                  299
E value
                  1.0e-167
Match length
                  388
% identity
                  93
NCBI Description Arabidopsis thaliana BAC TM017A05
Seq. No.
                  168300
Seq. ID
                  LIB3234-056-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g4586241
BLAST score
                  34
E value
                  1.0e-09
Match length
                  132
% identity
                  86
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                  (ESSA project)
Seq. No.
                  168301
Seq. ID
                  LIB3234-056-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g3819099
BLAST score
                  265
E value
                  3.0e-23
Match length
                  121
% identity
NCBI Description (AJ009825) copper amine oxidase [Cicer arietinum]
Seq. No.
                  168302
```

```
Seq. ID
                  LIB3234-056-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  a3335169
BLAST score
                  692
E value
                  3.0e-73
Match length
                  131
% identity
                  98
NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  q4159708
BLAST score
                  370
E value
                  0.0e+00
Match length
                  378
% identity
                  93
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MKP6, complete sequence
Seq. No.
                  168304
Seq. ID.
                  LIB3234-056-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  q4115912
BLAST score
                  45
E value
                  4.0e-16
Match length
                  148
% identity
                  45
NCBI Description
                  Arabidopsis thaliana BAC F3H7
Seq. No.
                  168305
Seq. ID
                  LIB3234-056-P1-K1-D7
                  BLASTX
Method
NCBI GI
                  g2501296
BLAST score
                  253
E value
                  9.0e-22
                  118
Match length
% identity
                  41
                  DNA GYRASE SUBUNIT B >gi 1652801 dbj BAA17720 (D90908) DNA
NCBI Description
                  gyrase B subunit [Synechocystis sp.]
Seq. No.
                  168306
Seq. ID
                  LIB3234-056-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3157937
BLAST score
                  562
                  5.0e-58
E value
                  117
Match length
                  88
% identity
NCBI Description
                  (AC002131) Identical to aspartic proteinase cDNA gb U51036
                  from A. thaliana. ESTs gb N96313, gb T21893, gb R30158,
                  gb T21482, gb T43650, gb R64749, gb R65157, gb T88269,
                  gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
```

gb AA728734, gb

Seq. ID

```
168307
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-E1
Method
                  BLASTN
                  g4589439
NCBI GI
BLAST score
                  186
E value
                  1.0e-100
Match length
                  270
                  94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQM1, complete sequence
Seq. No.
                  168308
                  LIB3234-056-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4220644
BLAST score
                  48
E value
                  7.0e-18
Match length
                  261
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXL8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168309
                  LIB3234-056-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1531762
BLAST score
                  170
E value
                  4.0e-12
Match length
                  47
% identity
                  74
NCBI Description
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  168310
Seq. ID
                  LIB3234-056-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1654140
BLAST score
                  467
E value
                  7.0e-47
Match length
                  129
                  67
% identity
NCBI Description
                  (U37840) lipoxygenase [Lycopersicon esculentum]
Seq. No.
                  168311
Seq. ID
                  LIB3234-056-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g135467
BLAST score
                  590
E value
                  3.0e-61
Match length
                  107
                  100
% identity
                  TUBULIN BETA-4 CHAIN >gi_2129546_pir__$68122 beta-tubulin 4
NCBI Description
                  - Arabidopsis thaliana >gi 166640 (M21415) beta-tubulin
                  [Arabidopsis thaliana]
                  168312
Seq. No.
```

22792

LIB3234-056-P1-K1-E4

NCBI GI

```
Method
                    BLASTN
 NCBI GI
                    q3763944
 BLAST score .
                    116
 E value
                    2.0e-58
 Match length
                    324
 % identity
                   98
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                   (ESSAII project)
 Seq. No.
                   168313
 Seq. ID
                   LIB3234-056-P1-K1-E5
 Method
                   BLASTX
 NCBI GI
                   q82263
 BLAST score
                   280
 E value
                   6.0e-25
 Match length
                   62
 % identity
                   81
 NCBI Description
                   ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
                   cl precursor (clone pC(1)3II) - potato
 Seq. No.
                   168314
 Seq. ID
                   LIB3234-056-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   g3869067
BLAST score
                   271
E value
                   1.0e-151
Match length
                   404
 % identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCK7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168315
Seq. ID
                   LIB3234-056-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g4204298
BLAST score
                   510
E value
                   5.0e-52
Match length
                   96
% identity
                   100
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   168316
Seq. ID
                  LIB3234-056-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3522936
BLAST score
                  575
E value
                  2.0e-59
Match length
                  118
% identity
                  97
NCBI Description
                  (AC004411) putative alcohol dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  168317
Seq. ID
                  LIB3234-056-P1-K1-F1
Method
                  BLASTN
```

g2924257

```
BLAST score
                  52
                  3.0e-20
E value
Match length
                 - 179
% identity
                  93
NCBI Description Tobacco chloroplast genome DNA
                  168318
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q170354
BLAST score
                  542
E value
                  1.0e-55
                  111
Match length
% identity
                  20
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
                  168319
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2829914
BLAST score
                  111
E value
                  9.0e-34
                  80
Match length
                  97
% identity
NCBI Description (AC002291) putative peroxidase [Arabidopsis thaliana]
Seq. No.
                  168320
Seq. ID
                  LIB3234-056-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1335862
BLAST score
                  610
E value
                  1.0e-63
Match length
                  124
% identity
                  96
NCBI Description (U42608) clathrin heavy chain [Glycine max]
                  168321
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  261
                  1.0e-145
E value
Match length
                  325
% identity
                  94
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
                  168322
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                  237
                  7.0e-20
E value
                  113
Match length
% identity
                  42
```

NCBI Description vicilin gene B [Saguinus oedipus]

```
Seq. No.
                   168323
Seq. ID
                   LIB3234-056-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   q548847
BLAST score
                   387
E value
                   2.0e-37
Match length
                   77
% identity
                  . 99
NCBI Description
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
                   >gi_1086182_pir__S39501 ribosomal protein S12 -
                   curled-leaved tobacco >gi_225248 prf 1211235CG ribosomal
                   protein S12 [Nicotiana tabacum]
Seq. No.
                   168324
Seq. ID
                   LIB3234-056-P1-K1-F9
Method
                   BLASTN
NCBI GI
                   g4713943
BLAST score
                   55
                   4.0e-22
E value
Match length
                   156
% identity
                   90
                  Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,
NCBI Description
                   complete sequence
Seq. No.
                   168325
Seq. İD
                  LIB3234-056-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g4454447
                  89
BLAST score
E value
                   5.0e-43
Match length
                   93
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168326
Seq. ID
                  LIB3234-056-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  g4455262
BLAST score
                  157
E value
                  5.0e-83
Match length
                  336
% identity
                  87
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                  (ESSAII project)
Seq. No.
                  168327
Seq. ID
                  LIB3234-056-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  g3402747
BLAST score
                  204
E value
                  1.0e-111
Match length
                  215
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22
```

(ESSAII project)

```
Seq. No.
                   168328
Seq. ID
                   LIB3234-056-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   g3402747
BLAST score
                   39
E value
                   1.0e-12
Match length
                   67
% identity
                   97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22
                   (ESSAII project)
Seq. No.
                   168329
Seq. ID
                   LIB3234-056-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g1107501
BLAST score
                   204
E value
                   2.0e-16
Match length
                   79
% identity
                   57
NCBI Description
                   (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
                   Match to gb_X91954 orf gene product from A. thaliana. ESTs
                   gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]
                                                                               .
.
Seq. No.
                   168330
                   LIB3234-056-P1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4206762
BLAST score
                   124
                   2.0e-63
E value
                   234
Match length
% identity
                   92
                  Arabidopsis thaliana cell wall-plasma membrane linker
NCBI Description
                   protein homolog (CWLP) mRNA, complete cds
                  168331
Seq. No.
Seq. ID
                  LIB3234-056-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  g4678266
BLAST score
                   48
E value
                   4.0e-18
Match length
                  115
% identity
                   91
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8
NCBI Description
                   (ESSA project)
Seq. No.
                  168332
Seq. ID
                  LIB3234-056-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  q4468103
BLAST score
                  382
E value
                  0.0e+00
                  390
Match length
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
NCBI Description
```

(ESSA project)

BLAST score

150

```
Seq. No.
                  168333
Seq. ID
                  LIB3234-056-P1-K1-G8
Method
                  BLASTX
                                                . . . .
NCBI GI
                  g4510397
BLAST score
                  649
                  3.0e-68
E value
                  127
Match length
% identity
                  97
NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
Seq. No.
                  168334
Seq. ID
                  LIB3234-056-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2924514
BLAST score
                  422
                  1.0e-41
E value
                  82
Match length
% identity
                  98
NCBI Description (AL022023) protein kinase-like [Arabidopsis thaliana]
Seq. No.
                  168335
Seq. ID
                  LIB3234-056-P1-K1-H1
                  BLASTX 6
Method
NCBI GI
                  q4510397
BLAST score
                  702
E value
                  2.0e-74
Match length
                  132
                  99
% identity
NCBI Description
                 (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
Seq. No.
                  168336
                  LIB3234-056-P1-K1-H10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4455262
BLAST score
                  375
E value
                  0.0e+00
                  383
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                  (ESSAII project)
Seq. No.
                  168337
Seq. ID
                  LIB3234-056-P1-K1-H11
Method
                  BLASTN
                  g3402745
NCBI GI
BLAST score
                  116
E value
                  1.0e-58
                  204
Match length
                  89
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
                  (ESSAII project)
                  168338
Seq. No.
                  LIB3234-056-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4415934
```

```
7.0e-10
E value
                  87
Match length
                   45
% identity
                   (AC006418) putative auxin response factor 1 (Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  168339
Seq. ID
                  LIB3234-056-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q4558592
BLAST score
                   481
                  2.0e-48
E value
                  129
Match length
                  75
% identity
                  (AC006555) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  168340
Seq. No.
                  LIB3234-056-P1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4558592
BLAST score
                  74
                  2.0e-22
E value
                  122
Match length
% identity.
                  64.
                  (AC006555) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168341
                  LIB3234-056-P1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g481131
BLAST score
                  563
E value
                  4.0e-58
Match length
                  108
% identity
                  100
                  sucrose transport protein SUC2 - Arabidopsis thaliana
NCBI Description
                  >gi_407092_emb_CAA53150_ (X75382) sucrose-proton symporter
                   [Arabidopsis thaliana]
                  168342
Seq. No.
                  LIB3234-056-P1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2827529
                  347
BLAST score
E value
                  8.0e-33
Match length
                  114
% identity
                  69
                  (AL021633) putative protein [Arabidopsis thaliana]
NCBI Description
                  168343
Seq. No.
                  LIB3234-057-P1-K1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1345973
BLAST score
                  398
                  8.0e-39
E value
                  94
Match length
                  79
% identity
```

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
omega-3 fatty acid desaturase [Arabidopsis thaliana]
>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
desaturase [Arabidopsis thaliana]

```
168344
Seq. No.
Seq. ID
                  LIB3234-057-P1-K1-A3
                  BLASTN
Method
                  q4469002
NCBI GI
BLAST score
                  218
                  1.0e-119
E value
Match length
                  246
% identity
                  96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                   (ESSA project)
Seq. No.
                  168345
Seq. ID
                  LIB3234-057-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  g2351068
BLAST score
                  368
E value
                  0.0e+00
Match length
                  372
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRH10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168346
Seq. ID
                  LIB3234-057-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q2499973
BLAST score
                  385
E value
                  3.0e-37
Match length
                  95
% identity
                  83
                  PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
NCBI Description
                  >gi 1465366 emb CAA66701 (X98078) photosystem II
                   [Arabidopsis thaliana]
                  168347
Seq. No.
Seq. ID
                  LIB3234-057-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3822036
BLAST score
                  289
                  5.0e-26
E value
Match length
                  124
                  47
% identity
```

Seq. No. 168348

NCBI Description

Seq. ID LIB3234-057-P1-K1-A8

Method BLASTX NCBI GI g4490333

(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

```
BLAST score
                   401
E value
                   3.0e-39
Match length
                   92
% identity
                   86
NCBI Description (AL035656) EF-Hand containing protein-like [Arabidopsis
                   thaliana]
Seq. No.
                   168349
Seq. ID
                   LIB3234-057-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   q1592677
BLAST score
                   289
E value
                   5.0e-26
Match length
                   103
% identity
                   60
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.
                   168350
Seq. ID
                   LIB3234-057-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g266989
BLAST score
                   475
E value
                   7.0e-48
Match length
                   125
% identity
                   75
                  GTP-BINDING PROTEIN SAR1B >gi_322517_pir__$28603
NCBI Description
                   GTP-binding protein - Arabidopsis thaliana >gi 166734
                   (M95795) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  168351
Seq. ID
                  LIB3234-057-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2842481
BLAST score
                  177
E value
                  6.0e-13
Match length
                  107
% identity
                  46
NCBI Description
                  (AL021749) extensin-like protein [Arabidopsis thaliana]
Seq. No.
                  168352
Seq. ID
                  LIB3234-057-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  54
                  2.0e-21
E value
Match length
                  200
% identity
                  94
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                  168353
Seq. ID
                  LIB3234-057-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2769642
BLAST score
                  514
E value
                  2.0e-52
Match length
                  125
% identity
                  75
```

```
NCBI Description
                   (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon
                    esculentum]
   £.
 Seq. No.
                    168354
 Seq. ID
                    LIB3234-057-P1-K1-B3
 Method
                    BLASTX
 NCBI GI
                    g3808062
 BLAST score
                    143
 E value
                    7.0e-09
 Match length
                    61
 % identity
                    44
                    (AB019195) PV100 [Cucurbita maxima]
 NCBI Description
 Seq. No.
                   168355
 Seq. ID
                   LIB3234-057-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   g2244747
BLAST score
                   344
E value
                   0.0e + 00
Match length
                   379
% identity
                   98
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   168356
Seq. ID
                   LIB3234-057-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g1362003
BLAST score
                   635
E value
                   1.0e-66
Match length
                   125
% identity
NCBI Description
                   protein phosphatase 2A B regulatory chain 55K - Arabidopsis
                   thaliana >gi_710330 (U18129) 55 kDa B regulatory subunit of
                   phosphatase \overline{2}A [Arabidopsis thaliana]
Seq. No.
                   168357
Seq. ID
                   LIB3234-057-P1-K1-B7
Method
                   BLASTN
NCBI GI
                   q4314374
BLAST score
                   229
E value
                   1.0e-126
Match length
                   323
% identity
                   25
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F10A12 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168358
Seq. ID
                   LIB3234-057-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g3600054
BLAST score
                   478
E value
                  3.0e-48
Match length
                  109
% identity
                  84
NCBI Description
                  (AF080120) No definition line found [Arabidopsis thaliana]
```

NCBI GI

```
Seq. No.
                   168359
Seq. ID
                  LIB3234-057-P1-K1-C10
Method
                  BLASTX
NCBI GI
                   g2511725
BLAST score
                   649
E-value
                  3.0e-68
Match length
                   124
% identity
                  100
NCBI Description
                  (AF021937) catalase 1 [Arabidopsis thaliana]
Seq. No.
                  168360
Seq. ID
                  LIB3234-057-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  g3510347
BLAST score
                  288
E value
                  1.0e-161
                   378
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168361
Seq. ID
                  LIB3234-057-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  q4539466
BLAST score
                  190
E value
                  2.0e-14
Match length
                  70
% identity
                  51
NCBI Description
                  (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                  168362
Seq. ID
                  LIB3234-057-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  g3242700
BLAST score
                  293
E value
                  1.0e-164
                  377
Match length
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC F26B6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168363
Seq. ID
                  LIB3234-057-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  g4589950
BLAST score
                  179
                  5.0e-96
E value
Match length
                  355
                  94
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T28P16 genomic
                  sequence, complete sequence
                  168364
Seq. No.
Seq. ID
                  LIB3234-057-P1-K1-C5
Method
                  BLASTX
```

g3236248

Method

BLASTX

```
BLAST score
                      545
E value
                      5.0e-56
Match length
                      124
% identity
                      84
NCBI Description
                     (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                      168365
                     LIB3234-057-P1-K1-C7
Seq. ID
Method
                     BLASTN
                      q2924257
NCBI GI
BLAST score
                      30
                      3.0e-07
E value
Match length
                      148
% identity
                      91
NCBI Description
                     Tobacco chloroplast genome DNA
Seq. No.
                      168366
                     LIB3234-057-P1-K1-C8
Seq. ID
Method
                     BLASTX
NCBI GI
                      g3913437
BLAST score
                      613
E value
                      5.0e-64
Match length
                      123
% identity
                      95
                      PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                     \label{eq:helicase} \begin{array}{lll} \texttt{HELICASE} > & \texttt{gi\_1402875\_emb\_CAA66825\_} & \texttt{(X98130)} & \texttt{RNA helicase} \\ \texttt{[Arabidopsis thaliana]} > & \texttt{gi\_1495271\_emb\_CAA66613\_} & \texttt{(X97970)} \end{array}
                      RNA helicase [Arabidopsis thaliana]
Seq. No.
                      168367
Seq. ID
                     LIB3234-057-P1-K1-C9
Method
                     BLASTN
NCBI GI
                     q3046855
BLAST score
                      48
                      6.0e-18
E value
                     271
Match length
                     83
% identity
                     Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                     MSL1, complete sequence [Arabidopsis thaliana]
                     168368
Seq. No.
                     LIB3234-057-P1-K1-D10
Seq. ID
Method
                     BLASTX
NCBI GI
                     g122781
BLAST score
                     267
                     2.0e-23
E value
Match length
                     70
                     71
% identity
                     POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229)
NCBI Description
                     >gi 82210 pir A05198 hypothetical protein 229 - common
                     tobacco chloroplast >gi 11844 emb CAA77364 (Z00044)
                     hypothetical protein [Nicotiana tabacum]
                     >gi_225212_prf__1211235AT ORF 229 [Nicotiana tabacum]
Seq. No.
                     168369
Seq. ID
                     LIB3234-057-P1-K1-D12
```

Seq. ID

```
NCBI GI
                   g2129653
BLAST score
                   286
                   1.0e-25
E value
                   125
Match length
                   58
% identity
NCBI Description
                   myosin heavy chain MYA2 - Arabidopsis thaliana
                   >gi_499047_emb_CAA84066_ (Z34293) myosin [Arabidopsis
                   thaliana]
Seq. No.
                   168370
Seq. ID
                   LIB3234-057-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q4321496
BLAST score
                   149
E value
                   9.0e-37
Match length
                   122
% identity
                   66
                   (AF049898) gibberellin 20-oxidase-1; 20ox-1 [Lycopersicon
NCBI Description
                   esculentum]
                   168371
Seq. No.
Seq. ID
                   LIB3234-057-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q4582446
BLAST score
                   499
E value
                   1.0e-50
Match length
                   123
% identity
NCBI Description
                   (AC007071) putative RING finger protein [Arabidopsis
                   thaliana]
Seq. No.
                   168372
Seq. ID
                   LIB3234-057-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g116527
BLAST score
                   514
E value
                   2.0e-52
Match length
                   112
% identity
                   87
                   PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)
NCBI Description
                   >gi_1143166 (U32397) ClpP protease [Nicotiana tabacum]
>gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease
                   proteolytic subuni [Nicotiana tabacum]
                   168373
Seq. No.
Seq. ID
                   LIB3234-057-P1-K1-D6
Method
                   BLASTX
                   q4490333
NCBI GI
BLAST score
                   82
                   2.0e-49
E value
Match length
                   124
% identity
                   85
NCBI Description
                   (AL035656) EF-Hand containing protein-like [Arabidopsis
                   thaliana]
Seq. No.
                   168374
```

LIB3234-057-P1-K1-D7

E value

7.0e-40

```
Method
                  BLASTN
                  q2924257
NCBI GI
BLAST score
                  68
                  8.0e-30
E value
Match length
                  214
% identity
                  91
                  Tobacco chloroplast genome DNA
NCBI Description
                  168375
Seq. No.
Seq. ID
                  LIB3234-057-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                  545
                  5.0e-56
E value
Match length
                  104
                  99
% identity
NCBI Description
                  (AC003027) 1cl prt seq No definition line found
                  [Arabidopsis thaliana]
                  168376
Seq. No.
Seq. ID
                  LIB3234-057-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2244835
BLAST score
                  300
                  2.0e-30
E value
                  71
Match length
                  100
% identity
NCBI Description
                 (Z97337) protein kinase homolog [Arabidopsis thaliana]
                  168377
Seq. No.
Seq. ID
                  LIB3234-057-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  g2494106
BLAST score
                  189
                  1.0e-102
E value
Match length
                  335
                  91
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  168378
                  LIB3234-057-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220645
BLAST score
                  126
E value
                  2.0e-64
Match length
                  366
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYA6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168379
Seq. ID
                  LIB3234-057-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1170503
BLAST score
                  407
```

```
Match length
                   81
% identity
                   96
                   EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
NCBI Description
                   >gi 322503 pir JC1452 translation initiation factor
                   eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188
                   (X65052) eukaryotic translation initiation factor 4A-\overline{1}
                   [Arabidopsis thaliana]
Seq. No.
                   168380
                   LIB3234-057-P1-K1-E2
Seq. ID
Method
                   BLASTX
                   g2623303
NCBI GI
BLAST score
                   118
E value
                   5.0e-06
Match length
                   119
% identity
                   75
NCBI Description
                  (AC002409) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   168381
                   LIB3234-057-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   548
E value
                   2.0e-56
Match length
                   106
% identity
                   98
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   168382
                   LIB3234-057-P1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4519671
                   224
BLAST score
E value
                   2.0e-18
                   69
Match length
                   70
% identity
                  (AB017693) transfactor [Nicotiana tabacum]
NCBI Description
Seq. No.
                   168383
Seq. ID
                   LIB3234-057-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   g4757401
BLAST score
                   369
                   0.0e+00
E value
                   381
Match length
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGH6, complete sequence
                   168384
Seq. No.
Seq. ID
                   LIB3234-057-P1-K1-E7
                  BLASTN
Method
NCBI GI
                   g3075383
                   348
BLAST score
                  0.0e+00
E value
                   375
Match length
                   98
% identity
```

Method.

BLASTX

```
NCBI Description Arabidopsis thaliana chromosome II BAC T1D16 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  168385
Seq. No.
                  LIB3234-057-P1-K1-E8
Seq. ID
Method
                  BLASTX
                  q2244749
NCBI GI
                  549
BLAST score
                  2.0e-56
E value
Match length
                  106
% identity
                  98
NCBI Description
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                  168386
                  LIB3234-057-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1864017
                  547
BLAST score
                  3.0e-56
E value
Match length
                  109
% identity
                  96
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  168387
                .. LIB3234-057-P1-K1-F1
Seq. ID
Method
                  BLASTN
                . g1931636
NCBI GI
BLAST score
                  144
                  3.0e-75
E value
Match length
                  351
% identity
                  85
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
Seq. No.
                  168388
Seq. ID
                  LIB3234-057-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1755162
BLAST score
                  625
E value
                  2.0e-65
Match length
                  122
                  97
% identity
                  (U75192) germin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168389
Seq. ID
                  LIB3234-057-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g2583106
BLAST score
                  259
E value
                  1.0e-144
Match length
                  356
                  93
% identity
                  Arabidopsis thaliana chromosome II BAC F4L23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168390
                  LIB3234-057-P1-K1-F3
Seq. ID
```

```
NCBI GI
                   g2129642
BLAST score
                   600
                   2.0e-62<sup>--</sup>
E value
Match length
                   116
                  95
% identity
NCBI Description
                  major latex protein type 3 - Arabidopsis thaliana
                  >gi_1107495 emb CAA63027 (X91961) major latex protein
                  type3 [Arabidopsis thaliana]
Seq. No.
                  168391
Seq. ID
                  LIB3234-057-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q2642430
BLAST score
                  207
E value
                  2.0e-16
Match length
                  37
% identity
                  100
                  (AC002391) putative AP2 domain containing protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  168392
Seq. ID
                  LIB3234-057-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  651
E value
                  2.0e-68
Match length
                  122
% identity
                  98
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi_4490713_emb_CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  168393
Seq. ID
                  LIB3234-057-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3860277
BLAST score
                  434
E value
                  5.0e-43
Match length
                  86
% identity
                  98
NCBI Description
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
                  thaliana] >gi_4314394_gb AAD15604 (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  168394
Seq. ID
                  LIB3234-057-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  289
                  5.0e-26
E value
Match length
                  91
                  64
% identity
NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
```

Seq. No.

Seq. ID

168400

LIB3234-057-P1-K1-G5

(L40954) oleosin [Arabidopsis thaliana] Seq. No. 168395 Seq. ID LIB3234-057-P1-K1-F9 Method BLASTX NCBI GI q4106930 BLAST score 69 E value 5.0e-20 Match length 80 % identity NCBI Description (AF114794) succinate:cytochrome c oxidoreductase subunit 2 [Porphyra purpurea] Seq. No. 168396 Seq. ID LIB3234-057-P1-K1-G1 Method BLASTN NCBI GI g4691223 BLAST score 140 E value 8.0e-73 Match length 383 % identity 98 NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project) Seq. No. 168397 Seq. ID LIB3234-057-P1-K1-G10 Method BLASTX g2827529 NCBI GI BLAST score · 280 5.0e-25 E value 80 Match length % identity 78 NCBI Description (AL021633) putative protein [Arabidopsis thaliana] Seq. No. 168398 Seq. ID LIB3234-057-P1-K1-G2 Method BLASTX NCBI GI q2832625 BLAST score 213 E value 4.0e-17 Match length 62 % identity 63 NCBI Description (AL021711) putative protein [Arabidopsis thaliana] Seq. No. 168399 Seq. ID LIB3234-057-P1-K1-G4 Method BLASTN NCBI GI g4432793 BLAST score 145 E value 8.0e-76 Match length 165 97 % identity NCBI Description Arabidopsis thaliana chromosome II BAC T19K21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Method

BLASTX

```
Method
                   BLASTN
NCBI GI ~
                   q2739359
BLAST score
                   73
E value
                   8.0e-33
Match length
                   200
% identity
                   86
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T9J22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3234-057-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q4432845
BLAST score
                   145
E value
                   3.0e-09
Match length
                   63
% identity
                   56
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   168402
Seq. ID
                   LIB3234-057-P1-K1-G8
Method
                   BLASTN
NCBI GI
                   g3985957
BLAST score
                   367
E value
                   0.0e + 00
Match length
                   371
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168403
Seq. ID
                   LIB3234-057-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3023799
BLAST score
                   157
                   1.0e-10
E value
Match length
                   63
% identity
                   48
NCBI Description
                   DIHYDRONEOPTERIN ALDOLASE (DHNA) >qi 1118003 (U40768)
                   dihydroneopterin aldolase [Staphylococcus haemolyticus]
>gi_1586495_prf__2204217C dihydroneopterin aldolase
                   [Staphylococcus haemolyticus]
                   168404
Seq. No.
Seq. ID
                   LIB3234-057-P1-K1-H10
Method
                   BLASTN
NCBI GI
                   g2160132
                   92
BLAST score
E value
                   3.0e-44
Match length
                   231
                   86
% identity
                   Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168405
Seq. ID
                   LIB3234-057-P1-K1-H11
```

```
NCBI GI
                    q860891
BLAST score
                    456
E value
                    1.0e-45
Match length
                    92
% identity
                    95
NCBI Description
                    (X87636) PSII cytochome b559 alpha chain [Beta vulgaris]
                    >gi 860897 emb CAA60972 (X87637) PSII cytochrome b599
                    alpha chain [Beta vulgaris]
Seq. No.
                    168406
Seq. ID
                    LIB3234-057-P1-K1-H12
Method
                    BLASTN
                    q2656032
NCBI GI
BLAST score
                    192
E value
                    1.0e-104
Match length
                    318
% identity
                    100
NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
Seq. No.
                    168407
Seq. ID
                    LIB3234-057-P1-K1-H2
Method
                    BLASTX
NCBI GI
                    q1345973
BLAST score
                    421
                    2.0e-41
E value
Match length
                    95
% identity
                    81
                    OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                    >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                    omega-3 fatty acid desaturase [Arabidopsis thaliana]
                    >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                    microsomal omega-3 fatty acid desaturase [Arabidopsis
                    thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                    desaturase [Arabidopsis thaliana]
Seq. No.
                    168408
                    LIB3234-057-P1-K1-H3
Seq. ID
Method
                    BLASTN
NCBI GI
                    q4220641
                    234
BLAST score
                    1.0e-129
E value
                    361
Match length
% identity
                    89
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MUL3, complete sequence [Arabidopsis thaliana]
Seq. No.
                    168409
Seq. ID
                    LIB3234-057-P1-K1-H4
                    BLASTX
Method
NCBI GI
                    g544012
BLAST score
                    206
                    3.0e-16
E value
                    113
Match length
```

40

% identity

```
NCBI Description BASIC ENDOCHITINASE >gi_487030_pir__S37341 chitinase (EC
                  3.2.1.14) chi14 - tomato (fragment)
                  >gi 388509 emb_CAA78843_ (Z15138) chitinase [Lycopersicon
                  esculentum]
                  168410
Seq. No.
                  LIB3234-057-P1-K1-H5
Seq. -ID
                  BLASTX
Method
                  g116343
NCBI GI
                  206
BLAST score
                  3.0e-16
E value
Match length
                  101
% identity
                  41
NCBI Description BASIC ENDOCHITINASE PRECURSOR
                  168411
Seq. No.
                  LIB3234-057-P1-K1-H7
Seq. ID
Method
                  BLASTN
                  g4199934
NCBI GI
                  261
BLAST score
                  1.0e-145
E value
                  355
Match length
                  92
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
                  168412
Seq. No.
                  LIB3234-057-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  g4588001
NCBI GI
BLAST score
                  523
                  2.0e-53
E value
Match length
                  124
                  77
% identity
                  (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  168413
Seq. ID
                  LIB3234-057-P1-K1-H9
Method
                  BLASTX
                  g2135333
NCBI GI
                  268
BLAST score
                  1.0e-23
E value
Match length
                  108
% identity
                  48
                  Hep27.protein - human >gi_1079566 (U31875) Hep27 protein
NCBI Description
                  [Homo sapiens]
                  168414
Seq. No.
                  LIB3234-058-P1-K1-A10
Seq. ID
                  BLASTN
Method
                  q2264302
NCBI GI
                  204
BLAST score
                  1.0e-111
E value
Match length
                  375
                  97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

Seq. ID

NCBI GI

E value

BLAST score

Match length

Method

MAC12, complete sequence [Arabidopsis thaliana] 168415 Seq. No. Seq. ID LIB3234-058-P1-K1-A11 Method BLASTN NCBI GI q2924729 BLAST score 173 2.0e-92 E value Match length 303 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana] Seq. No. 168416 Seq. ID LIB3234-058-P1-K1-A12 Method BLASTX NCBI GI q4204277 BLAST score 538 E value 3.0e-55 Match length 109 % identity 94 NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana] Seq. No. 168417 Seq. ID LIB3234-058-P1-K1-A2 Method BLASTX NCBI GI q135858 BLAST score 263 E value 5.0e-23 Match length 52 % identity 100 NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -Arabidopsīs thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana] Seq. No. . 168418 Seq. ID LIB3234-058-P1-K1-A3 Method BLASTN NCBI GI g3426033 BLAST score 251 E value 1.0e-139 Match length 375 % identity 98 NCBI Description Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 168419

LIB3234-058-P1-K1-A4

BLASTN

143

179

g2191126

8.0e-75

% identity

```
% identity
                   96
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                   168420
Seq. ID
                   LIB3234-058-P1-K1-A5
Method
                   BLASTN
NCBI GI
                   q4539415
BLAST score
                   374
                   0.0e + 00
E value
                   374
Match length
% identity
                   72
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
NCBI Description
                  project)
Seq. No.
                   168421
Seq. ID
                   LIB3234-058-P1-K1-A6
Method
                  BLASTN
NCBI GI
                   q3176694
BLAST score
                   376
                   0.0e + 00
E value
Match length
                   380
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T14N5 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168422
Seq. ID
                  LIB3234-058-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g4027862
BLAST score
                   245
E value
                   1.0e-135
Match length
                  297
                   98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T7A14 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  168423
Seq. ID
                  LIB3234-058-P1-K1-A8
Method
                  BLASTX
                  g1107501
NCBI GI
                  388
BLAST score
                  1.0e-37
E value
                  111
Match length
                  71
% identity
NCBI Description
                   (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb Z17604, gb H76594, gb AA597972 and gb AA394824 come from
                  this gene. [Arabidopsis thaliana]
                  168424
Seq. No.
Seq. ID
                  LIB3234-058-P1-K1-B1
                  BLASTN
Method
NCBI GI
                  g2264307
BLAST score
                  49
                  2.0e-18
E value
Match length
                  101
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MED24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168425
                  LIB3234-058-P1-K1-B11 .
Seq. ID
Method
                  BLASTX
                  q1346523
NCBI GI
BLAST score
                  386
                  2.0e-37
E value
                  78
Match length
% identity
                  94
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
                  >gi 1084428 pir S49491 methionine adenosyltransferase (EC
                  2.5.1.6) - garden petunia >gi_559506_emb_CAA57696 (X82214)
                  methionine adenosyltransferase [Petunia x hybrida]
Seq. No.
                  168426
Seq. ID
                  LIB3234-058-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  q2827513
BLAST score
                  79
E value
                  2.0e-36
Match length
                  155
% identity
                  88
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16
                  (ESSAII project)
                  168427
Seq. No.
                  LIB3234-058-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244837
BLAST score
                  623
                  3.0e-65
E value
                  123
Match length
                  100
% identity
NCBI Description
                  (Z97337) proteasome chain protein [Arabidopsis thaliana]
                  >gi 2511572 emb CAA73618.1 (Y13175) multicatalytic
                  endopeptidase [Arabidopsis thaliana] >gi 3421114 (AF043535)
                  20S proteasome beta subunit PBD2 [Arabidopsis thaliana]
Seq. No.
                  168428
Seq. ID
                  LIB3234-058-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2493696
BLAST score
                  322
E value
                  7.0e-30
                  86
Match length
                  67
% identity
                  HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi 1480440 (U34204)
NCBI Description
                  ORF185; hypothetical 21.4 kD protein [Brassica oleracea]
Seq. No.
                  168429
Seq. ID
                  LIB3234-058-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  g4510392
```





```
0.0e + 00
E value
Match length
                    378
% identity
                    99
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T17D12 genomic
                    sequence, complete sequence
Seq. No.
                    168430
Seq. ID
                    LIB3234-058-P1-K1-B6
Method
                    BLASTN
NCBI GI
                    g4191760
BLAST score
                    261
E value
                    1.0e-145
Match length
                    285
% identity
                    54
NCBI Description
                    Genomic sequence for Arabidopsis thaliana BAC F17F8,
                    complete sequence [Arabidopsis thaliana]
Seq. No.
                    168431
Seq. ID
                    LIB3234-058-P1-K1-B8
Method
                    BLASTX
NCBI GI
                    q120675
BLAST score
                    454
E value
                    2.0e-45
Match length
                    104
                    84
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                    >gi_21143_emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                    alba]
Seq. No.
                    168432
Seq. ID
                   LIB3234-058-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g1402904
BLAST score
                    515
E value
                   1.0e-52
Match length
                   99
% identity
                   97
NCBI Description
                   (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                   168433
Seq. ID
                   LIB3234-058-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g4835234
BLAST score
                   407
E value
                   7.0e-40
                   82
Match length
% identity
                   100
                   (AL049862) putative cold acclimation protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   168434
                   LIB3234-058-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2459446
```

Match length

```
E value
                    2.0e-55
 Match length
                    127
 % identity
                    84
 NCBI Description
                    (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
                    thalianal
 Seq. No.
                    168435
 Seq. ID
                    LIB3234-058-P1-K1-C2
 Method
                    BLASTX
 NCBI GI
                    q3915847
 BLAST score
                    379
 E value
                    1.0e-36
 Match length
                    83
 % identity
                    89
 NCBI Description
                   40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
                    40S ribosomal protein S2 [Arabidopsis thaliana]
 Seq. No.
                    168436
 Seq. ID
                    LIB3234-058-P1-K1-C6
 Method
                   BLASTN
 NCBI GI
                   g2828180
 BLAST score
                   37
 E value
                   2.0e-11
 Match length
                   252
 % identity
                   90
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:-
                   MDK4, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168437
 Seq. ID
                   LIB3234-058-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   g4512656
BLAST score
                   142
E value
                   5.0e-74
Match length
                   325
% identity
                   85
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   168438
Seq. ID
                   LIB3234-058-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g4455323
BLAST score
                   648
E value
                   4.0e-68
Match length
                   126
% identity
                   99
NCBI Description
                  (AL035525) aminopeptidase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  168439
Seq. ID
                  LIB3234-058-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g16231
BLAST score
                  80
E value
                  1.0e-37
```

```
% identity
                     96
  NCBI Description
                     Arabidopsis CRA1 gene for 12S seed storage protein
                     >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage
                     protein CRA1 gene, exons 1-4
  Seq. No.
                     168440
  Seq. ID
                    LIB3234-058-P1-K1-D1
  Method
                    BLASTX
  NCBI GI
                    g4510397
  BLAST score
                    634
  E value
                    2.0e-66
  Match length
                    139
  % identity
                    89
  NCBI Description
                    (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
  Seq. No.
                    168441
  Seq. ID
                    LIB3234-058-P1-K1-D10
 Method
                    BLASTX
 NCBI GI
                    g3250696
 BLAST score
                    198
 E value
                    2.0e-15
 Match length
                    70
 % identity
                    26
 NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
 Seq. No.
                    168442
 Seq. ID
                    LIB3234-058-P1-K1-D11
 Method
                    BLASTX
 NCBI GI
                    g3250696
 BLAST score
                    226
 E value
                   1.0e-18
 Match length
                   92
 % identity
                   27
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
 Seq. No.
                   168443
 Seq. ID
                   LIB3234-058-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q1694976
BLAST score
                   290
E value
                   3.0e-26
Match length
                   85
% identity
                   71
NCBI Description
                   (Y09482) HMG1 [Arabidopsis thaliana]
                   >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis
                   thalianal
Seq. No.
                   168444
Seq. ID
                  LIB3234-058-P1-K1-D3
Method
                   BLASTX
NCBI GI
                  g135858
BLAST score
                  501
E value
                  7.0e-51
Match length
                  120
% identity
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
                  >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
```

```
Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf_ 1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]
```

```
Seq. No.
                   168445
Seq. ID
                   LIB3234-058-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q119350
BLAST score
                   549
E value
                   2.0e-56
Match length
                   107
% identity
                   97
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                   [Arabidopsis thaliana]
                  >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
                   (2-phospho-D-glycerate hydroylase); identical to P25696
                   [Arabidopsis thaliana]
Seq. No.
                  168446
Seq. ID
                  LIB3234-058-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g120667 .
BLAST score
                  471
E value
                  2.0e-47
Match length
                  105
% identity
                  88
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                  thaliana >gi_166706 (M64116) cystolic
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
```

dehydrogenase [Arabidopsis thaliana]

 Seq. No.
 168447

 Seq. ID
 LIB3234-058-P1-K1-D6

 Method
 BLASTN

 NCBI GI
 g3068702

NCBI GI g3068702
BLAST score 95
E value 6.0e-46
Match length 95
% identity 100
NCBI Description Arabidop

Arabidopsis thaliana putative transmembrane protein Glp (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put

thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate

Seq. No. 168448

Seq. ID LIB3234-058-P1-K1-D8

Method BLASTX NCBI GI g1352463 BLAST score 490

```
E value
                    1.0e-49
 Match length
                    109
 % identity
                    88
 NCBI Description
                   MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi 1161312
                    (U04876) myo-inositol-1-phosphate synthase \overline{\text{[Arabidopsis}]}
                    thaliana]
 Seq. No.
                    168449
 Seq. ID
                    LIB3234-058-P1-K1-D9
 Method
                    BLASTN
 NCBI GI
                    q3985957
 BLAST score
                    247
 E value
                    1.0e-136
 Match length
                    381
 % identity
                    100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MYN8, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168450
 Seq. ID
                   LIB3234-058-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g1402904
BLAST score
                   463
E value
                   8.0e-67
Match length
                   127
% identity
                   96
NCBI Description (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                   168451
Seq. ID
                   LIB3234-058-P1-K1-E12
Method
                   BLASTN
NCBI GI
                   g4006885
BLAST score
                   308
E value
                   1.0e-173
Match length
                   383
% identity
                   99
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
Seq. No.
                   168452
Seq. ID
                   LIB3234-058-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q3834314
BLAST score
                   580
E value
                   4.0e-60
Match length
                   123
% identity
                   91
NCBI Description
                   (AC005679) Similar to gene pi010 glycosyltransferase
                   gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs
                   gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   168453
Seq. ID
                  LIB3234-058-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q1695719
BLAST score
                  165
```

```
E value
                       1.0e-11
   Match length
                       77
                       57
    % identity
   NCBI Description (D89342) luminal binding protein [Arabidopsis thaliana]
                       168454
   Seq. No.
seq. ID
                       LIB3234-058-P1-K1-E4
   Method
                       BLASTX
   NCBI GI
                       q4158219
   BLAST score
                       188
   E value
                        3.0e-14
   Match length
                       58
                        66
    % identity
   NCBI Description (Y18623) amylogenin [Oryza sativa]
   Seq. No.
                       168455
   Seq. ID
                       LIB3234-058-P1-K1-E5
   Method
                       BLASTX
   NCBI GI
                       q4204299
   BLAST score
                        553
                        6.0e-57
   E value
   Match length
                       108
  % identity
                       100
                       (AC003027) lcl prt seq No definition line found
   NCBI Description
                        [Arabidopsis thaliana]
   Seq. No.
                       168456
   Seq. ID
                       LIB3234-058-P1-K1-E6
   Method
                       BLASTX
   NCBI GI
                       g2961390
   BLAST score
                        455
   E value
                       2.0e-45
   Match length
                       107
   % identity
                       (AL022141) beta-galactosidase like protein [Arabidopsis
   NCBI Description
                       thaliana]
   Seq. No.
                       168457
   Seq. ID
                       LIB3234-058-P1-K1-E8
   Method
                       BLASTX
                       g135858
   NCBI GI
   BLAST score
                       276
                       2.0e-24
   E value
                       54
   Match length
                       100
   % identity
                       TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
   NCBI Description
                       >qi 99760 pir S22201 tonoplast intrinsic protein alpha -
                       Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                        [Arabidopsis thaliana] >gi 445128 prf 1908432A tonoplast
                       intrinsic protein alpha [Arabidopsis thaliana]
   Seq. No.
                       168458
   Seq. ID
                       LIB3234-058-P1-K1-F1
   Method
                       BLASTX
   NCBI GI
                       g1718097
```

Match length

```
BLAST score
                  352
E value
                  2.0e-33
Match length
                  101
% identity
                  61
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                   (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016
                  lysosomal membrane protein DVA41 - slime mold
                   (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
Seq. No.
                  168459
Seq. ID
                  LIB3234-058-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q1345973
BLAST score
                  668
E value
                  2.0e-70
Match length
                  116
% identity
                  100
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty_acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis :
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  168460
Seq. ID
                  LIB3234-058-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  g3869073
BLAST score
                  383
E value
                  0.0e+00
Match length
                  383
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MKN22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168461
Seq. ID
                  LIB3234-058-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g4559339
BLAST score
                  494
E value
                  4.0e-50
Match length
                  127
                  78
% identity
                  (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
                  168462
Seq. No.
Seq. ID
                  LIB3234-058-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  g1931636
BLAST score
                  365
E value
                  0.0e + 00
```

```
% identity
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
Seq. No.
                  168463
                  LIB3234-058-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4314369
BLAST score
                  511
                  4.0e-52
E value
                  113
Match length
% identity
                  94
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168464
                  LIB3234-058-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  368
                  0.0e + 00
E value
Match length
                  380
% identity
                  92
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
                  168465
Seq. No.
                  LIB3234-058-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3176708
BLAST score ·
                  410
                  4.0e-40
E value
Match length
                  80
% identity
                  97
                   (AC002392) putative proline-rich protein APG [Arabidopsis
NCBI Description
                  thaliana]
                  168466
Seq. No.
Seq. ID
                  LIB3234-058-P1-K1-G10
Method
                  BLASTN
                  g4454585
NCBI GI
BLAST score
                  133
                  1.0e-68
E value
                  377
Match length
% identity
                  91
                  Arabidopsis thaliana BAC T13D4 from chromosome IV near 21.5
NCBI Description
                  cM, complete sequence
Seq. No.
                  168467
Seq. ID
                  LIB3234-058-P1-K1-G11
Method
                  BLASTN
                  q4063730
NCBI GI
                  201
BLAST score
                  1.0e-109
E value
                  355
Match length
% identity
                  89
                  Arabidopsis thaliana BAC F21J6 from chromosome V,
NCBI Description
                  containing KNAT3 and mapping near 60.5 cM, complete
```

sequence [Arabidopsis thaliana]

```
Seq. No.
                  168468
Seq. ID
                  LIB3234-058-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g4589964
BLAST score
                  613
E value
                  5.0e-64
Match length
                  127
% identity
                  87
NCBI Description (AC007169) delta 9 desaturase [Arabidopsis thaliana]
Seq. No.
                  168469
Seq. ID
                  LIB3234-058-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  q4376087
BLAST score
                  266
E value
                  1.0e-148
Match length
                  383
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  168470
                  LIB3234-058-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1809127
BLAST score
                  303
E value
                  1.0e-27
Match length
                  115
% identity
                  50
NCBI Description
                  (U77674) terminal flower 1 [Arabidopsis thaliana]
                  >gi_2208929_dbj_BAA20483_ (D86932) terminal flower1
                  [Arabidopsis thaliana] >gi_2208931_dbj_BAA20484_ (D87130)
                  terminal flower1 [Arabidopsis thaliana]
                  >gi_2208933_dbj_BAA20485_ (D87519) terminal flower1
                  [Arabidopsis thaliana]
Seq. No.
                  168471
Seq. ID
                  LIB3234-058-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3548815
BLAST score
                  662
E value
                  9.0e-70
                  122
Match length
                  99
% identity
NCBI Description
                  (AC005313) similar to axoneme-associated protein mst101
                  [Arabidopsis thaliana]
Seq. No.
                  168472
Seq. ID
                  LIB3234-058-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2583125
BLAST score
                  653
E value
                  1.0e-68
Match length
                  130
% identity
                  100
NCBI Description (AC002387) putative transketolase precursor [Arabidopsis
```

thaliana] 168473 Seq. No. LIB3234-058-P1-K1-G8 Seq. ID Method BLASTX NCBI GI q2961390 651 BLAST score 2.0e-68 E value 121 Match length % identity NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis thalianal 168474 Seq. No. Seq. ID LIB3234-058-P1-K1-G9 Method BLASTX NCBI GI q541847 BLAST score 656 4.0e-69 E value 125 Match length 98 % identity NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana 168475 Seq. No. Seq. ID LIB3234-058-P1-K1-H1 Method BLASTX NCBI GI q266989 BLAST score 459 E value 6.0e-46 Match length 109 83 % identity GTP-BINDING PROTEIN SAR1B >gi_322517_pir__\$28603 NCBI Description GTP-binding protein - Arabidopsis thaliana >gi_166734 (M95795) GTP-binding protein [Arabidopsis thaliana] Seq. No. 168476 Seq. ID LIB3234-058-P1-K1-H11 Method BLASTX NCBI GI g2129651 BLAST score 196 7.0e-41 E value Match length 92 % identity 100 myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis NCBI Description thaliana] Seq. No. 168477 Seq. ID LIB3234-058-P1-K1-H2 Method BLASTN NCBI GI q4432793 BLAST score 108 E value 1.0e-53 Match length 270 % identity Arabidopsis thaliana chromosome II BAC T19K21 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

```
168478
Seq. No. J
                  LIB3234-058-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757398
BLAST score
                  39
                  1.0e-12
E value
Match length
                  63
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MED5, complete sequence
Seq. No.
                  168479
                  LIB3234-058-P1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159712
BLAST score
                  361
E value
                  0.0e+00
Match length
                  361
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
Seq. No.
                  168480
Seq. ID
                  LIB3234-058-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                  529
                  4.0e-54
E value
Match length
                  122
% identity
                  84
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
                  168481
Seq. No.
                  LIB3234-058-P1-K1-H6
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4159707
                                                                       ;
BLAST score
                  179
                  4.0e-96
E value
Match length
                  331
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJK13, complete sequence
Seq. No.
                  168482
Seq. ID
                  LIB3234-058-P1-K1-H7
                  BLASTX
Method
NCBI GI
                  g135858
BLAST score
                  460
                  3.0e-46
E value
                  100
Match length
                  92
% identity
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                  >gi 99760 pir S22201 tonoplast intrinsic protein alpha -
                  Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
                  tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
```

Match length

304

thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]

```
Seq. No.
                    168483
                    LIB3234-058-P1-K1-H8
Seq. ID
Method
                    BLASTN
                    g4512656
NCBI GI
BLAST score
                    159
                    4.0e-84
E value
Match length
                    290
% identity
                    85
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F7D19 genomic
                    sequence, complete sequence
Seq. No.
                    168484
Seq. ID
                   LIB3234-058-P1-K1-H9
Method
                   BLASTX
NCBI GI
                    g3915961
                    376
BLAST score
E value
                    3.0e-36
Match length
                    95
                   73
% identity
                   HYPOTHETICAL 267 KD PROTEIN (ORF 2280).
NCBI Description
                   >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana
tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
                   protein [Nicotiana tabacum]
                   168485
Seq. No.
Seq. ID
                   LIB3234-059-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g4159712
BLAST score
                   184
                   4.0e-99
E value
Match length
                   364
% identity
                   88
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MWI23, complete sequence
                   168486
Seq. No.
Seq. ID
                   LIB3234-059-P1-K1-A11
Method
                   BLASTN
NCBI GI
                   g2351061
BLAST score
                   214
E value
                   1.0e-117
                   371
Match length
                   98
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MAF19, complete sequence [Arabidopsis thaliana]
                   168487
Seq. No.
Seq. ID
                   LIB3234-059-P1-K1-A12
                   BLASTN
Method
NCBI GI
                   g2477521
BLAST score
                   96
                   1.0e-46
E value
```

```
95
% identity
                  Arabidopsis thaliana chromosome I BAC F22K20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168488
                  LIB3234-059-P1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3785977
                  597
BLAST score
                  4.0e-62
E value
Match length
                  125
                  93
% identity
                   (AC005560) putative growth regulator protein [Arabidopsis
NCBI Description
                  thaliana]
                  168489
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  g2252823
BLAST score
                  366
E value
                  0.0e+00
Match length
                  382
                  99
% identity
NCBI Description Arabidopsis thaliana BAC IG005I10
Seq. No.
                  168490
Seq. ID
                  LIB3234-059-P1-K1-A5
Method
                  BLASTN
                  g2351061
NCBI GI
BLAST score
                  159
E value
                  4.0e-84
Match length
                  183
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168491
Seq. ID
                  LIB3234-059-P1-K1-A6
                  BLASTX
Method
NCBI GI
                  g2102691
BLAST score
                  235
E value
                  1.0e-19
Match length
                  90
                  58
% identity
                  (U64817) fructokinase [Lycopersicon esculentum]
NCBI Description
                  168492
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-A7
                  BLASTN
Method
NCBI GI
                  g2961370
BLAST score
                  152
E value
                  3.0e-80
                  196
Match length
                  95
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13
NCBI Description
```

(ESSAII project)

```
Seq. No.
                  168493
Seq. ID
                  LIB3234-059-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g3201632
BLAST, score
                  287
                  8.0e-26
E value
Match length
                  98
% identity
                  56
NCBI Description
                  (AC004669) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                  168494
Seq. ID
                  LIB3234-059-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  519
E value
                  5.0e-53
Match length
                  127
                  79
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  168495
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-B12
                  BLASTX
Method
NCBI GI
                  q3688189
BLAST score
                  151
E value
                  7.0e-10
                  33
Match length
                  91
% identity
                  (AL031804) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168496
Seq. ID
                  LIB3234-059-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1351837
BLAST score
                  602
                  1.0e-62
E value
                 .128
Match length
                  89
% identity
NCBI Description ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
                  BETA >gi_2144155 pir S66564 acetyl CoA carboxylase type II
                  beta-carboxyltransferase chain - rape chloroplast
                  >gi_1069998_emb_CAA90747_ (Z50868) acetyl CoA carboxylase
                  carboxyltransferase (beta subunit) [Brassica napus]
                  >gi 1589046 prf 2210244G Ac-CoA carboxylase:SUBUNIT=beta
                  [Brassica napus]
                  168497
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g2749918
BLAST score
                  313
                  1.0e-176
E value
                  370
Match length
                  95
% identity
                  Arabidopsis thaliana chromosome I BAC F3I6 genomic
NCBI Description
```

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   168498
Seq. ID
                   LIB3234-059-P1-K1-B5
Method
                   BLASTN
NCBI GI
                   g4531433
BLAST score
                   316
E value
                   1.0e-178
Match length
                   371
% identity
                   96
NCBI Description
                   Arabidopsis thaliana chromosome II P1 MFL8 genomic
                   sequence, complete sequence
Seq. No.
                   168499
Seq. ID
                   LIB3234-059-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g1890352
BLAST score
                   434
E value
                   5.0e-43
Match length
                   80
% identity
NCBI Description
                  (X91398) transcription factor L2 [Arabidopsis thaliana]
Seq. No.
                   168500
Seq. ID
                   LIB3234-059-P1-K1-B7
Method
                   BLASTN
NCBI GI
                   g2584827
BLAST score
                   342
                   0.0e+00
E value
Match length
                   373
% identity
                   98
NCBI Description Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                  . 168501
Seq. ID
                 LIB3234-059-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   q1345973
BLAST score
                   431
E value
                   1.0e-42
                   97
Match length
                   81
% identity
NCBI Description
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514 (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
Seq. No.
                   168502
Seq. ID
                   LIB3234-059-P1-K1-C10
Method
                  BLASTN
NCBI GI
                   g2264318
BLAST score
                   374
E value
                   0.0e + 00
```

```
378
Match length
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3234-059-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q3080435
BLAST score
                   659
E value
                   2.0e-69
Match length
                   126
% identity
                   99
NCBI Description
                  (AL022605) putative protein [Arabidopsis thaliana]
Seq. No.
                   168504
                   LIB3234-059-P1-K1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g516389
BLAST score
                   44
E value
                   1.0e-15
Match length
                   112
% identity
                   86
NCBI Description M.jalapa 25S ribosomal RNA
Seq. No.
                   168505
Seq. ID
                   LIB3234-059-P1-K1-C2
Method
                   BLASTN
NCBI GI
                   g4731050
BLAST score
                   47
                   3.0e-17
E value
Match length
                   59
                   95
% identity
NCBI Description
                   Drosophila melanogaster, chromosome 3L, region 79F1-80A2,
                   BAC clone BACR48E05, complete sequence
                   168506
Seq. No.
Seq. ID
                   LIB3234-059-P1-K1-C3
Method
                   BLASTX
                   q2160158
NCBI GI
BLAST score
                   275
                   2.0e-24
E value
Match length
                   95
% identity
                   63
                   (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb EF1G XENLA). ESTs gb T20564, gb T45940, gb T04527 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   168507
                  LIB3234-059-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264318
                  299
BLAST score
E value
                  1.0e-168
                  306
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

168508 Seq. No. Seq. ID LIB3234-059-P1-K1-C5 Method BLASTN NCBI GI g3212102 BLAST score 305 1.0e-171 E value Match length 350 % identity 96 Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 168509 Seq. ID LIB3234-059-P1-K1-C6 Method BLASTX NCBI GI g170354 BLAST score 540 E value 2.0e-55 Match length 114 % identity 21 NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris] Seq. No. 168510 Seq. ID LIB3234-059-P1-K1-C7 Method BLASTN NCBI GI g3449330 BLAST score 363 0.0e+00E value 383 Match length % identity 99 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana] Seq. No. 168511 Seq. ID LIB3234-059-P1-K1-C8 Method BLASTN NCBI GI g3449334 BLAST score 243 E value 1.0e-134 Match length 267 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana] Seq. No. 168512 Seq. ID LIB3234-059-P1-K1-C9 Method BLASTX NCBI GI q99688 BLAST score 628 E value 9.0e-66 Match length 126 96 % identity NCBI Description translation elongation factor eEF-1 alpha chain (gene A4) -Arabidopsis thaliana >gi_295789 emb CAA34456 (X16432)

MUP24, complete sequence [Arabidopsis thaliana]

elongation factor 1-alpha [Arabidopsis thaliana]

```
Seq. No.
                  168513
Seq. ID
                  LIB3234-059-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4204277
BLAST score .
                  619
                  1.0e-64
E value
Match length
                  117
% identity
                  98
NCBI Description
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168514
Seq. ID
                  LIB3234-059-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g4432847
                  246
BLAST score
                  1.0e-136
E value
                  302
Match length
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC F13B15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                 168515
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-D12
                  BLASTN
Method
NCBI GI
                  q2828185
BLAST score
                  142
                  5.0e-74
E value
                  385
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUD21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168516
Seq. ID
                  LIB3234-059-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2781348
BLAST score
                  623
                  3.0e-65
E value
                  128
Match length
% identity
                  93
NCBI Description (AC003113) F2401.4 [Arabidopsis thaliana]
Seq. No.
                  168517
Seq. ID
                  LIB3234-059-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                  47
E value
                  9.0e-18
                  125
Match length
                  36
% identity
NCBI Description vicilin gene B [Saguinus oedipus]
                 . 168518 .
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-D6
                  BLASTX
Method
NCBI GI
                  g2583108
```

Seq. ID

```
E value
                    3.0e-37
Match length
                    81
% identity
                    95
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.
                    168519
Seq. ID
                    LIB3234-059-P1-K1-D7
Method
                   BLASTN
NCBI GI
                    g16145
BLAST score
                    144
E value
                    3.0e-75
                   275
Match length
% identity
                    99
NCBI Description A.thaliana mRNA for ABI3 protein
Seq. No.
                   168520
Seq. ID
                   LIB3234-059-P1-K1-D8
Method
                   BLASTN
NCBI GI
                   g1279629
                   278
BLAST score
E value
                   1.0e-155
Match length
                   380
% identity -
                    93 _
NCBI Description O.lamarckiana chloroplast 16S rRNA, trnI, trnA and 23S rRNA
                   genes
                   168521
Seq. No.
Seq. ID
                   LIB3234-059-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g1345973
BLAST score
                   435
E value
                    4.0e-43
Match length
                   98
% identity
                   82
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana]
                   >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
Seq. No.
                   168522
Seq. ID
                   LIB3234-059-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g4510373
                   176
BLAST score
E value
                   8.0e-13
Match length
                   59
                   58
% identity
NCBI Description
                   (AC007017) putative harpin-induced protein [Arabidopsis
                thaliana]
                   168523
Seq. No.
```

LIB3234-059-P1-K1-E2

```
Method
                  BLASTX
NCBI GI
                  q118926
BLAST score
                  353
                  2.0e-33
E value
Match length
                  121
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi_320600_pir__E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi_227781_prf__1710351E abscisic acid responsive protein E
                  [Craterostigma plantagineum]
Seq. No.
                  168524
Seq. ID
                  LIB3234-059-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2118307
BLAST score
                  495
E value
                  3.0e-50
Match length
                  108
                  94
% identity
NCBI Description
                  cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
                  >gi 804950 emb CAA58893 (X84097) cysteine synthase
                  [Arabidopsis thaliana] >qi 1096196 prf 2111276A Ser(Ac)
                  thiol lyase [Arabidopsis thaliana]
Seq. No.
                  168525
                  LIB3234-059-P1-K1-E4
Seq. ID
Method
                  BLASTX
                  g3808062
NCBI GI
                  149
BLAST score
E value
                  1.0e-09
                  62
Match length
% identity
                  45
                  (AB019195) PV100 [Cucurbita maxima]
NCBI Description
                  168526
Seq. No.
                                                                  ....
                  LIB3234-059-P1-K1-E7
Seq. ID
                  BLASTX
Method
                  g687844
NCBI GI
                  136
BLAST score
                  4.0e-08
E value
                  91
Match length
% identity
                  (U21320) contains TPR domain-like repeats [Caenorhabditis
NCBI Description
                  elegans]
                  168527
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-E8
                  BLASTX
Method
                  q585349
NCBI GI
BLAST score
                  308
                  3.0e-28
E value
                  58
Match length.
                  100
% identity
                  CASEIN KINASE II, ALPHA CHAIN 1 (CK II)
NCBI Description
                  >gi_419752 pir S31098 casein kinase II (EC 2.7.1.-)
```

```
168528
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q4335711
                  36
BLAST score
E value
                  9.0e-11
Match length
                  88
% identity
                  Arabidopsis thaliana chromosome II BAC F9013 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  168529
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                  260
                  1.0e-144
E value
Match length
                  326
% identity
                  95
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                                 Seq. No.
                  168530
Seq. ID
                  LIB3234-059-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  g1707006
BLAST score
                  67
E value
                  3.0e-29
Match length
                  187
% identity
                  93
                  Arabidopsis thaliana chromosome II BAC T1B8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168531
Seq. ID
                  LIB3234-059-P1-K1-F12
Method
                  BLASTN
                  g3449326
NCBI GI
BLAST score
                  349
E value
                  0.0e + 00
Match length
                  369
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19M22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168532
                  LIB3234-059-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  q4589964
NCBI GI
BLAST score
                  420
E value -
                  2.0e-41
Match length
                  98
% identity
                  84
                 (AC007169) delta 9 desaturase [Arabidopsis thaliana]
NCBI Description
```

alpha-type chain (clone ATCKA1) - Arabidopsis thaliana >qi 391603 dbj BAA01090 (D10246) casein kinase II

catalytic subunit [Arabidopsis thaliana]

```
Seq. No.
                  168533
                  LIB3234-059-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  q4567246
NCBI GI
BLAST score
                  449
                  9.0e-45
E value
                  98
Match length
                  87
% identity
NCBI Description
                  (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                  168534
                  LIB3234-059-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263771
BLAST score
                  288
E value
                  6.0e-26
Match length
                  71
% identity
                  72
                  (AC006218) putative nonspecific lipid-transfer protein
NCBI Description
                  precursor [Arabidopsis thaliana]
                  >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative
                  nonspecific lipid-transfer protein precursor [Arabidopsis
                  thaliana]
Seq. No.
                  168535
                  LIB3234-059-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q135406
BLAST score
                  495
                  3.0e-50
E value
                  92
Match length
% identity
                  100
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
NCBI Description
                  alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                  168536
Seq. ID
                  LIB3234-059-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q4585997
BLAST score
                  637
E value
                  8.0e-67
Match length
                  125
% identity
                  (AC005287) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168537
Seq. ID
                  LIB3234-059-P1-K1-G10
Method
                  BLASTX
                  a4204277
NCBI GI
BLAST score
                  521
                  2.0e-53
E value
Match length
                  98
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

```
168538
Seq. No.
                   LIB3234-059-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2961375
BLAST score
                   109
                   6.0e-05
E value
                   126
Match length
                   73
% identity
                   (AL022141) NAM like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   168539
                   LIB3234-059-P1-K1-G12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2827644
BLAST score
                   199
E value
                   1.0e-108
Match length
                   363
                   89
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4
NCBI Description
                   (ESSAII project)
Seq. No.
                   168540
Seq. ID
                   LIB3234-059-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   q2914688
BLAST score
                   276
                   1.0e-154
E value
Match length
                   341
                   100
 % identity
                   Arabidopsis thaliana chromosome II BAC F24L7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168541
                   LIB3234-059-P1-K1-G5
 Seq. ID
                   BLASTX
Method
                   q4432860
NCBI GI
BLAST score
                   267
                   2.0e-23
E value
                   126
Match length
                   21
 % identity
                   (AC006300) putative glucose-induced repressor protein
 NCBI Description
                   [Arabidopsis thaliana]
                   168542
 Seq. No.
                   LIB3234-059-P1-K1-G6
 Seq. ID
 Method
                   BLASTN
                   g2952432
NCBI GI
                   102
BLAST score
                   4.0e-50
E value
                   144
Match length
                   99
 % identity
                   Arabidopsis thaliana putative ubiquitin activating enzyme
 NCBI Description
                   E1 (ECR1) mRNA, complete cds
                   168543
 Seq. No.
                   LIB3234-059-P1-K1-G7
 Seq. ID
```

```
Method
                   BLASTN
NCBI GI
                   q2760169
BLAST score
                   152
                                 4 5
                   6.0e-80
E value
Match length
                   270
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MFB13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168544
Seq. ID
                   LIB3234-059-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   q266839
BLAST score
                   539
                   2.0e-55
E value
Match length
                   109
% identity
                   99
                   PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi_478764_pir__S29240
                   multicatalytic endopeptidase complex (EC 3.4.99.46) alpha
                   chain - Arabidopsis thaliana >gi_16445_emb_CAA47298
                   (X66825) proteosome alpha subunit [Arabidopsis thaliana]
                   >gi_3421080 (AF043522) 20S proteasome subunit PAD1
[Arabidopsis thaliana] >gi_742351_prf__2009376B
                   proteasome:SUBUNIT=alpha [Arabidopsis thaliana]
Seq. No.
                   168545
                   LIB3234-059-P1-K1-G9
Seq. ID
Method
                   BLASTN
NCBI GI .
                   g3702315
BLAST score
                   137
E value
                   5.0e-71
Match length
                   316
% identity
                   98
                   Arabidopsis thaliana chromosome II BAC T3F17 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168546
Seq. ID
                   LIB3234-059-P1-K1-H1
Method
                   BLASTN
NCBI GI
                   g3449317
BLAST score
                   49
E value
                   2.0e-18
Match length
                   150
                   89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MKM21, complete sequence [Arabidopsis thaliana]
                   168547
Seq. No.
Seq. ID
                   LIB3234-059-P1-K1-H11
Method
                   BLASTX
                   g166570
NCBI GI
BLAST score
                   245
                  7.0e-21
E value
                   106
Match length
                   49
% identity
NCBI Description
                  (L04173) glycine rich protein [Arabidopsis thaliana]
```

```
168548
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g3894171
BLAST score
                  537
E value
                   4.0e-55
Match length
                   114
                   93
% identity
NCBI Description
                   (AC005312) putative glutathione s-transferase [Arabidopsis
                  thaliana]
                  168549
Seq. No.
Seq. ID
                  LIB3234-059-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g3157928
BLAST score
                  485
E value
                   5.0e-49
Match length
                   95
                  100
% identity
NCBI Description
                   (AC002131) Similar to fumarylacetoacetate hydrolase,
                  gb L41670 from Emericella nidulans. [Arabidopsis thaliana]
Seq. No.
                  168550
Seq. ID
                  LIB3234-059-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  q3659491
BLAST score
                  289
E value
                  1.0e-161
Match length
                  353
% identity
                  99
NCBI Description
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
                  168551
Seq. No.
Seq. ID
                  LIB3234-060-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  q2288979
                  389
BLAST score
                  0.0e+00
E value
                  396
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T01024 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168552
Seq. ID
                  LIB3234-060-P1-K1-A2
                  BLASTN
Method
NCBI GI
                  q3241927
BLAST score
                  362
E value
                  0.0e+00
Match length
                  395
% identity
                  61
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTE17, complete sequence [Arabidopsis thaliana]
```

168553

Seq. No.

```
Seq. ID
                  LIB3234-060-P1-K1-A3
Method
                  BLASTN
NCBI GI
                 - q3985949
                   267
BLAST score
                   1.0e-148
E value
Match length
                   392
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168554
Seq. ID
                  LIB3234-060-P1-K1-A4
Method
                  BLASTN .
NCBI GI
                   a4757406
BLAST score
                   379
E value
                   0.0e + 00
Match length
                   387
                   73
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPF21, complete sequence
Seq. No.
                   168555
Seq. ID
                  LIB3234-060-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q1864017
BLAST score
                   481
E value
                   1.0e-48
Match length
                   92
% identity
                   100
NCBI Description
                   (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   168556
Seq. ID
                   LIB3234-060-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q3953469
BLAST score
                   353
E value
                   2.0e-33
Match length
                   113
% identity
                   62
                   (AC002328) F20N2.14 [Arabidopsis thaliana]
NCBI Description
                   168557
Seq. No.
Seq. ID
                  LIB3234-060-P1-K1-B1
Method
                  BLASTN
                   g4467094
NCBI GI
BLAST score
                   235
E value
                   1.0e-129
                   308
Match length
% identity
                   54
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
NCBI Description
                   (ESSA project)
                   168558
Seq. No.
Seq. ID
                  LIB3234-060-P1-K1-B10
Method
                  BLASTX
                  g4678285
NCBI GI
```

```
E value
                    5.0e-35
                    130
Match length
                    50
% identity
                    (AL049660) putative protein [Arabidopsis thaliana]
NCBI Description
                    168559
Seq. No.
                    LIB3234-060-P1-K1-B12
Seq. ID
Method '
                    BLASTN
NCBI GI
                    q2696018
BLAST score
                    211
E value
                    1.0e-115
Match length
                    394
                    98
% identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                    168560
Seq. ID
                    LIB3234-060-P1-K1-B2
Method
                    BLASTN
NCBI GI
                    q166853
BLAST score
                    88
E value
                    2.0e-42
Match length
                    100
                    97
% identity
NCBI Description
                    Arabidopsis thaliana RNA polymerase II fifth largest
                    subunit mRNA, complete cds
Seq. No.
                    168561
Seq. ID
                    LIB3234-060-P1-K1-B3
Method
                    BLASTX
NCBI GI
                    g1871185
BLAST score
                    192
E value
                    1.0e-14
Match length
                    100
% identity
                    38
                    (U90439) seven in absentia isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    168562
                    LIB3234-060-P1-K1-B5
Seq. ID
                    BLASTX
Method
                    g133960
NCBI GI
BLAST score
                    235
E value
                    1.0e-19
                    68
Match length
                    72
% identity
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi 70876 pir R3NT4
NCBI Description
                    ribosomal protein S4 - common tobacco chloroplast >gi_11834_emb_CAA77354_ (Z00044) ribosomal protein S4 [Nicotiana tabacum] >gi_225202_prf__1211235AG ribosomal
                    protein S4 [Nicotiana tabacum]
Seq. No.
                    168563
Seq. ID
                    LIB3234-060-P1-K1-B7
Method
                    BLASTX
NCBI GI
                    g2262167
BLAST score
                    657
                    4.0e-69
E value
```

```
Match length
                   125
                   100
% identity
                   (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                   thaliana]
                   168564
Seq. No.
Seq. ID
                   LIB3234-060-P1-K1-B8
                   BLASTX
Method
                   g135858
NCBI GI
BLAST score
                   296
                   8.0e-27
E value
Match length
                   58
% identity
                   100
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                   >gi 99760 pir S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
                   tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                   [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast
                   intrinsic protein alpha [Arabidopsis Thaliana]
                   168565
Seq. No.
                   LIB3234-060-P1-K1-C1
Seq. ID
Method
                   BLASTX.
NCBI GI
                 g3128176
BLAST score
                   221
E value
                   5.0e-18
Match length
                   104
% identity
                   35
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   168566
Seq. ID
                   LIB3234-060-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   q1617268
BLAST score
                   573
                   3.0e-59
E value
                   130
Match length
% identity
                  (Z72153) acyl CoA synthetase [Brassica napus]
NCBI Description
Seq. No.
                   168567
Seq. ID
                   LIB3234-060-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   376
E value
                   3.0e-36
Match length
                   92
                   83
% identity
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   168568
Seq. ID
                   LIB3234-060-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   g3548797
BLAST score
                   140
```

8.0e-73

E value

```
Match length
                  397
% identity
                  97
                  Arabidopsis thaliana chromosome II BAC T18E12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  168569
Seq. No.
                  LIB3234-060-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2494041
BLAST score
                  231
E value
                  3.0e-19
Match length
                  57
                  74
% identity
                  DIAMINOPIMELATE EPIMERASE >qi 1653875 dbj BAA18785
NCBI Description
                   (D90917) diaminopimelate epimerase [Synechocystis sp.]
Seq. No.
                  168570
                  LIB3234-060-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  q267069
NCBI GI
                   536
BLAST score
E value
                   6.0e-55
Match length
                   99
                  100
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   168571
                  LIB3234-060-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3273743
BLAST score
                   552
E value
                   8.0e-57
Match length
                   105
% identity
                   100
                   (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                   thaliana] >gi 3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
                   168572
Seq. No.
                  LIB3234-060-P1-K1-D11
Seq. ID
Method
                  BLASTN
                   q4415905
NCBI GI
BLAST score
                   361
                   0.0e + 00
E value
                   393
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC F13K3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                  168573 -
Seq. No.
                  LIB3234-060-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  q4234768
NCBI GI
```

4- 4

€, 4

```
2.0e-16
E value
Match length
                  37
                  89
% identity
                  (AF069468) sterol-C5-desaturase [Arabidopsis thaliana]
NCBI Description
                  168574
Seq. No.
                  LIB3234-060-P1-K1-D5
Seq. ID
                  BLASTN
Method
                  g2828182
NCBI GI
BLAST score
                  394
E value
                  0.0e + 00
Match length
                  397
                  83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168575
                  LIB3234-060-P1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4432811
BLAST score
                  401
E value
                  0.0e + 00
Match length
                  401
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F16D14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168576
                  LIB3234-060-P1-K1-D7
Seq. ID
Method
                  BLASTX
                  g2129532
NCBI GI
BLAST score
                  306
                  5.0e-28
E value
Match length
                  88
% identity
                  69
                  acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -
NCBI Description
                  Arabidopsis thaliana >gi 1107507 emb CAA63746 (X93461)
                  acyl-[acyl-carrier protein] desaturase [Arabidopsis
                  thaliana]
                  168577
Seq. No.
Seq. ID
                  LIB3234-060-P1-K1-D8
                  BLASTX
Method
NCBI GI
                  g2160296
                  641
BLAST score
                  3.0e-67
E value
                  130
Match length
                  95
% identity
                  (D61395) gamma-VPE [Arabidopsis thaliana]
NCBI Description
                  168578
Seq. No.
                  LIB3234-060-P1-K1-E10
Seq. ID
                  BLASTX
Method
                  q4582468
NCBI GI
BLAST score
                  479
E value
                  2.0e-48
Match length
```

```
99
 % identity
                   (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                   C-terminal domain [Arabidopsis thaliana]
                   168579
 Seq. No.
                   LIB3234-060-P1-K1-E12
 Seq. ID
 Method
                   BLASTN.
 NCBI GI
                   g2351062
 BLAST score
                   286
                   1.0e-160
 E value
                   378
 Match length
 % identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MAH20, complete sequence [Arabidopsis thaliana]
                   168580
 Seq. No.
 Seq. ID
                   LIB3234-060-P1-K1-E4
 Method
                   BLASTX
                   g897638
 NCBI GI
 BLAST score
                   244
 E value
                   1.0e-20
 Match length
                   50
 % identity
                   92
                   (M10124) unknown protein [Nicotiana tabacum]
 NCBI Description-
                   >gi_224349_prf__1102209C ORF 3 [Nicotiana sp.]
                   168581
 Seq. No.
 Seq. ID
                   LIB3234-060-P1-K1-E5
 Method
                   BLASTX
                   g3157930
 NCBI GI
                   623
 BLAST score
                   4.0e-65
 E value
 Match length
                   117
                   99
 % identity
                    (AC002131) Strong similarity to
 NCBI Description
                   amino-cyclopropane-carboxylic acid oxidase gb L27664 from
                   Brassica napus. ESTs gb Z48548 and gb Z48549 come from
                   this gene. [Arabidopsis thaliana]
                   168582
 Seq. No.
 Seq. ID
                   LIB3234-060-P1-K1-E6
 Method
                   BLASTX
 NCBI GI
                   g3193292
 BLAST score
                   386
 E value
                   2.0e-37
 Match length
                   122
                   70
 % identity
                    (AF069298) similar to ATPases associated with various
 NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                    [Arabidopsis thaliana]
 Seq. No.
                   168583
                   LIB3234-060-P1-K1-E7
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g3228389
 BLAST score
                   321
```

0.0e + 00

E value

```
353
Match length
                  98
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  168584
Seq. No.
                  LIB3234-060-P1-K1-E8
Seq. ID
Method
                  BLASTN
                  g3241927
NCBI GI
BLAST score
                  81
                  7.0e-38
E value
Match length
                  148
% identity
                  93
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTE17, complete sequence [Arabidopsis thaliana]
                  168585
Seq. No.
                  LIB3234-060-P1-K1-F1
Seq. ID
Method
                  BLASTX
                  g584882
NCBI GI
                  763
BLAST score
E value
                  1.0e-81
Match length
                  132
% identity
                  100
                  CYCLOARTENOL SYNTHASE (2, 3-EPOXYSQUALENE--CYCLOARTENOL
NCBI Description
                  CYCLASE) >gi_452446 (U02555) cycloartenol synthase;
                   (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]
                  168586
Seq. No.
                  LIB3234-060-P1-K1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2924257
BLAST score
                  52
                  3.0e-20
E value
Match length
                  253
% identity
                  88
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                  168587
                  LIB3234-060-P1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3241916
BLAST score
                  178
E value
                  2.0e-95
Match length
                  373
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15N18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168588
Seq. ID
                  LIB3234-060-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2961390
BLAST score
                  555
E value
                  3.0e-57
Match length
                  125
% identity
                  86
```

BLAST score

```
NCBI Description
                  (AL022141) beta-galactosidase like protein [Arabidopsis
                  thaliana]
                  168589
Seq. No.
                  LIB3234-060-P1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4262209
                  231
BLAST score
                  1.0e-127
E value
Match length
                  310
% identity
                  93
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T14A4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  168590
Seq. No.
                  LIB3234-060-P1-K1-F6
Seq. ID
Method
                  BLASTX
                  q1351837
NCBI GI
                  549
BLAST score
E value
                  1.0e-56
Match length
                  117
% identity
                  86
NCBI Description
                  ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
                  BETA >gi_2144155_pir__S66564 acetyl CoA carboxylase type II
                  beta-carboxyltransferase chain - rape chloroplast
                  >gi_1069998_emb_CAA90747_ (Z50868) acetyl CoA carboxylase
                  carboxyltransferase (beta subunit) [Brassica napus]
                  >gi_1589046_prf__2210244G Ac-CoA carboxylase:SUBUNIT=beta
                  [Brassica napus]
                  168591
Seq. No.
Seq. ID
                  LIB3234-060-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  q4584531
BLAST score
                  367
E value
                  0.0e + 00
Match length
                  387
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8
                  (ESSA project)
Seq. No.
                  168592
Seq. ID
                  LIB3234-060-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  q4206762
BLAST score
                  239
E value
                  1.0e-132
Match length
                  304
                  96
% identity
NCBI Description
                  Arabidopsis thaliana cell wall-plasma membrane linker
                  protein homolog (CWLP) mRNA, complete cds
Seq. No.
                  168593
Seq. ID
                  LIB3234-060-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g3399678
```

BLAST score

```
E value
                   1.0e-161
 Match length
                   399
 % identity
                   92
                   Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,
 NCBI Description
                   complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168594
 Seq. ID
                   LIB3234-060-P1-K1-G10
Method
                   BLASTN
NCBI GI
                   g2262155
BLAST score
                   355
E value
                   0.0e + 00
Match length
                   391
% identity
                   98
                   DNA sequence of Arabidopsis thaliana BAC F5J6 from
NCBI Description
                   chromosome IV, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168595
Seq. ID
                   LIB3234-060-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q3915085
BLAST score
                   570
E value
                   6.0e-59
Match length
                   128
% identity
                   88
                   TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
NCBI Description
                   4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                   >gi_1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis
                   thaliana] >gi_1946370 (U93215) cinnamate-4-hydroxylase
                   [Arabidopsis thaliana]
Seq. No.
                   168596
Seq. ID
                   LIB3234-060-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   g2244991
BLAST score
                   39
E value
                   1.0e-12
Match length
                   190
% identity
                  89
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  168597
Seq. ID
                  LIB3234-060-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3426060
BLAST score
                  46
                  6.0e-10
E value
Match length
                  72
% identity
NCBI Description
                  (AJ007586) src2-like protein [Arabidopsis thaliana]
Seq. No.
                  168598
Seq. ID
                  LIB3234-060-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q3273743
```

% identity

```
2.0e-64
E value
Match length
                    118
                    99
% identity
                    (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                    thaliana] >gi 3786019 (AC005499) unknown protein
                    [Arabidopsis thaliana]
                    168599
Seq. No.
Seq. ID
                    LIB3234-060-P1-K1-G4
Method
                    BLASTN
NCBI GI
                    q3779020
                    130
BLAST score
                    7.0e-67
E value
Match length
                    368
% identity
                    84
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T4E14 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    168600
Seq. ID
                    LIB3234-060-P1-K1-G5
Method
                    BLASTX
NCBI GI
                    q2924779
BLAST score
                    544
                    7.0e-56
E.value
Match length
                   · 112
                    97
% identity
                    (ACO02334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
NCBI Description
                    thaliana] >gi_2981616_dbj_BAA25248_ (AB008854)
                    3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA
                    thiolase [Arabidopsis thaliana]
Seq. No.
                    168601
Seq. ID
                    LIB3234-060-P1-K1-G6
Method
                    BLASTX
NCBI GI
                    q266839
BLAST score
                    586
E value
                    8.0e-61
Match length
                    118
% identity
NCBI Description
                    PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                    COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi_478764_pir_S29240 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha
                    chain - Arabidopsis thaliana >gi_16445_emb_CAA47298
                    (X66825) proteosome alpha subunit [Arabidopsis thaliana]
                    >gi_3421080 (AF043522) 20S proteasome subunit PAD1
[Arabidopsis thaliana] >gi_742351_prf__2009376B
                    proteasome:SUBUNIT=alpha [Arabidopsis thaliana]
Seq. No.
                    168602
Seq. ID
                    LIB3234-060-P1-K1-G7
Method
                    BLASTN
NCBI GI
                    g2564048
BLAST score
                    346
                    0.0e+00
E value
                    386
Match length
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MKD15, complete sequence [Arabidopsis thaliana]
                   168603
Seq. No.
Seq. ID
                   LIB3234-060-P1-K1-H1
                  BLASTX
Method
NCBI GI
                   g2494113
BLAST score
                   684
                   2.0e-72
E value
                   130
Match length
% identity
                   98
                   (AC002376) Strong similarity to Musa pectate lyase
NCBI Description
                   (gb X92943). ESTs gb AA042458, gb ATTS4502, gb N38552 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   168604
                  LIB3234-060-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2330730
BLAST score
                  163
E value
                  3.0e-11
Match length
                  45
                  60
% identity
                  (Z98532) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  168605
Seq. ID
                  LIB3234-060-P1-K1-H11
Method
                  BLASTN
NCBI GI '
                  g4756963
BLAST score
                  354
E value
                  0.0e+00
                  378
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                  (ESSA project)
Seq. No.
                  168606
Seq. ID
                  LIB3234-060-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g3702739
BLAST score
                  133
                  9.0e-69
E value
Match length
                  193
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MXE2, complete sequence [Arabidopsis thaliana]
                  168607
Seq. No.
Seq. ID
                  LIB3234-060-P1-K1-H2
                  BLASTX
Method
NCBI GI
                  g1170373
BLAST score
                  586
                  8.0e-61
E value
                  130
Match length
                  90
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302
NCBI Description
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
```

```
cognate [Arabidopsis thaliana]
Seq. No.
                  168608
Seq. ID
                  LIB3234-060-P1-K1-H5
Method
                  BLASTX
NCBI GI
                   q4204298
BLAST score
                   331
E value
                   5.0e-31
Match length
                   81
% identity
                   85
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
                  168609
Seq. No.
Seq. ID
                  LIB3234-060-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q2342727
BLAST score
                   401
                   4.0e-39
E value
                   103
Match length
% identity
                  75
NCBI Description
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
             . ~ 168610
                  LIB3234-060-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1402914
BLAST score
                  502
E value
                   5.0e-51
Match length
                  99
                  100
% identity
NCBI Description
                  (X98318) peroxidase [Arabidopsis thaliana]
Seq. No.
                  168611
Seq. ID
                  LIB3234-060-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  q3894179
BLAST score
                  33
E value
                  6.0e-09
Match length
                  65
                  88
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13H10 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168612
Seq. ID
                  LIB3234-065-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  q4567193
BLAST score
                  43
E value
                  6.0e-15
Match length
                  173
                  72
% identity
                  Arabidopsis thaliana chromosome II BAC T26C19 genomic
NCBI Description
                  sequence, complete sequence
```

>gi 397482 emb CAA52684 (X74604) heat shock protein 70

168613

Seq. No.

BLAST score

```
Seq. ID
                  LIB3234-065-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4337178
BLAST score
                  463
                  2.0e-46
E value
Match length
                  92
% identity
                  97
                  (AC006416) T31J12.5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168614
Seq. ID ~
                  LIB3234-065-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  q3449327
BLAST score
                  190
                  1.0e-102
E value
Match length
                  307
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168615
Seq. ID
                  LIB3234-065-P1-K1-A3
Method
                  BLASTX
                  g3107905
NCBI GI
BLAST score
                  117
E value
                  8.0e-06
Match length
                  127
% identity
                  (D85101) leaf protein [Ipomoea nil]
NCBI Description
Seq. No.
                  168616
Seq. ID
                  LIB3234-065-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  q3046853
BLAST score
                  301
E value
                  1.0e-169
Match length
                  367
% identity
                  95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRA19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168617
Seq. ID
                  LIB3234-065-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  g2213606
BLAST score
                  159
E value
                  4.0e-84
Match length
                  288
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F21J9,
                  complete sequence [Arabidopsis thaliana]
                  168618
Seq. No.
Seq. ID
                  LIB3234-065-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g3449327
```

```
E value
                   3.0e-16
Match length
                   142
                   89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168619
Seq. ID
                   LIB3234-065-P1-K1-A9
Method
                  BLASTX
NCBI GI
                   q1755162
BLAST score
                   303
E value
                  1.0e-27
Match length
                  91
% identity
                  59
NCBI Description
                 (U75192) germin-like protein [Arabidopsis thaliana]
Seq. No.
                  168620
Seq. ID
                  LIB3234-065-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q4531433
BLAST score
                  243
E value
                  1.0e-134
Match length
                  344
% identity
                  94
NCBI Description
                  Arabidopsis thaliana chromosome II P1 MFL8 genomic
                  sequence, complete sequence
Seq. No.
                  168621
Seq. ID
                  LIB3234-065-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q1669668
BLAST score
                  350
E value
                  3.0e-33
Match length
                  89
% identity
                  79
NCBI Description (X97131) EF1-alpha [Forsythia x intermedia]
Seq. No.
                  168622
Seq. ID
                  LIB3234-065-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g3176659
BLAST score
                  340
E value
                  6.0e-32
Match length
                  76
% identity
                  84
NCBI Description
                  (AC004393) Strong similarity to receptor kinase gb M80238
                  from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                  168623
Seq. ID
                  LIB3234-065-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q4519193
BLAST score
                  133
E value
                  1.0e-68
Match length
                  387
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

MDC11, complete sequence

```
168624
Seq. No.
                  LIB3234-065-P1-K1-B6
Seq. ID
Method
                  BLASTX
                   g3450889
NCBI GI
BLAST score
                   80
                   6.0e-41
E value
Match length
                   123
% identity
                   80
NCBI Description
                  (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.
                  168625
                  LIB3234-065-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3241917
BLAST score
                  108
E value
                   7.0e-54
Match length
                  263
% identity
                  85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19B1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168626
Seq. ID
                  LIB3234-065-P1-K1-C1
                                                                        .....
Method
                  BLASTX
NCBI GI
                  q1255951
BLAST score
                   489
E value
                  2.0e-49
Match length
                  126
% identity
                  74
NCBI Description (X96932) PS60 [Nicotiana tabacum]
Seq. No.
                  168627
Seq. ID
                  LIB3234-065-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3831443
BLAST score
                   310 .
E value
                   2.0e-28
Match length
                   60
% identity
                  100
                   (ACO05819) putative auxin-regulated protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  168628
                  LIB3234-065-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  g2160133
NCBI GI
BLAST score
                  265
E value
                  3.0e-23
Match length
                  94
% identity
                  63
                  (AC000375) Strong similarity to Arabidopsis
NCBI Description
                  gb X91953, F19K23.3, F19K23.15. ESTs
                  gb T21984, gb ATTS0219, gb ATTS0207, gb T21984 come from this
```

gene. [Arabidopsis thaliana]

```
Seq. No.
                   168629
Seq. ID
                   LIB3234-065-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q127041
BLAST score
                   476
E valuė
                   6.0e-48
Match length
                   90
                   100
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_81647_pir__JN0131 methionine adenosyltransferase (EC
                   2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077)
                   S-adenosylmethionine synthetase [Arabidopsis thaliana]
Seq. No.
                   168630
Seq. ID
                  LIB3234-065-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  q4100059
BLAST score
                   43
E value
                   7.0e-15
Match length
                   110
% identity
                   86
NCBI Description Arabidopsis thaliana AthlecRK4 pseudogene, complete
                   sequence, receptor lectin kinase 3 (AthlecRK3) gene,
                  complete cds, and AthlecRK2 pseudogene, complete sequence
Seq. No.
                   168631
Seq. ID
                  LIB3234-065-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q4678946
BLAST score
                  532
E value
                   2.0e-54
Match length
                  104
% identity
                  99
NCBI Description
                  (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
                  168632
Seq. ID
                  LIB3234-065-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  q4544381
BLAST score
                  323
E value
                  0.0e + 00
Match length
                  384
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F16F14 genomic
                  sequence, complete sequence
Seq. No.
                  168633
Seq. ID
                  LIB3234-065-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q114335
BLAST score
                  624
E value
                  3.0e-65
Match length
                  128
% identity
                  95
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                  >gi_67973_pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
```

```
(J05570) H+-ATPase [Arabidopsis thaliana]
                  168634
Seq. No.
Seq. ID
                  LIB3234-065-P1-K1-D11
Method
                  BLASTN
NCBI GI
                   q343514
BLAST score
                   67
E value
                   3.0e-29
Match length
                   91
% identity
                   93
NCBI Description Tobacco Thr-tRNA gene
Seq. No.
                   168635
Seq. ID
                  LIB3234-065-P1-K1-D12
Method
                  BLASTN
NCBI GI
                   g4691223
BLAST score
                   149
E value
                   4.0e-78
Match length
                   382
                   95
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                   (ESSA project)
Seq. No.
                   168636
Seq. ID
                  LIB3234-065-P1-K1-D2
Method
                  BLASTX
NCBI GI
                   g114335
BLAST score
                   278
                   6.0e-25
E value
Match length
                   85
% identity
                   65
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                  >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                   type 2, plasma membrane - Arabidopsis thaliana >gi 166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
Seq. No.
                  168637
Seq. ID
                  LIB3234-065-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g3421346
BLAST score
                   513
E value
                   3.0e-52
                  115
Match length
% identity
                  90
NCBI Description
                  (AJ007723) ribosomal protein S4 [Orobanche minor]
                  168638
Seq. No.
Seq. ID
                  LIB3234-065-P1-K1-D5
                  BLASTX
Method
                  q1107501
NCBI GI
BLAST score
                   402
                  3.0e-39
E value
Match length
                  117
                  70
% identity
                   (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
NCBI Description
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
```

type 2, plasma membrane - Arabidopsis thaliana >gi 166629

```
gb Z17604, gb H76594, gb AA597972 and gb AA394824 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   168639
Seq. ID
                   LIB3234-065-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g3004551
BLAST score
                   167
E value
                   1.0e-11
                   95
Match length
% identity
                   43
NCBI Description
                  (AC003673) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   168640
                   LIB3234-065-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3183274
BLAST score
                   156
E value
                   2.0e-10
Match length
                   80
% identity
                   44
NCBI Description
                  HYPOTHETICAL 26.5 KD PROTEIN C15A10.05C IN CHROMOSOME I
                   >gi 2239182 emb CAB10102 (Z97208) hypothetical protein
                   [Schizosaccharomyces pombe]
                  168641
Seq. No.
Seq. ID
                  LIB3234-065-P1-K1-E7
Method
                  BLASTN
NCBI GI
                   g1790921
BLAST score
                   369
                   0.0e + 00
E value
Match length
                   377
                   99
% identity
NCBI Description
                  Arabidopsis thaliana recA-like protein (AtDMC1) gene,
                  complete cds
Seq. No.
                  168642
Seq. ID
                  LIB3234-065-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g1790921
BLAST score
                  281
E value
                  1.0e-157
Match length
                  342
% identity
                  98
                  Arabidopsis thaliana recA-like protein (AtDMC1) gene,
NCBI Description
                  complete cds
                  168643
Seq. No.
Seq. ID
                  LIB3234-065-P1-K1-F2
                  BLASTX
Method
NCBI GI
                  g119143
                  323
BLAST score
E value
                  3.0e-30
                  93
Match length
                  70
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi 81606 pir S06724 translation elongation factor eEF-1
```

```
>gi 1369927 emb CAA34454 (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi 1532173 (U63815) EF-l'alpha-A2 [Arabidopsis thaliana]
                  >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                  168644
Seq. ID
                  LIB3234-065-P1-K1-F4
Method
                  BLASTX
                  q3808062
NCBI GI
BLAST score
                  155
                  3.0e-10
E value
Match length
                  64
% identity
                  45
                  (AB019195) PV100 [Cucurbita maxima]
NCBI Description
Seq. No.
                  168645
Seq. ID
                  LIB3234-065-P1-K1-F5
Method
                  BLASTX
                  q132074
NCBI GI
                  604
BLAST score
                  6.0e-63
E value
Match length
                  111
% identity
                  98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                  Al precursor - Arabidopsis thaliana
                  168646
Seq. No.
Seq. ID
                  LIB3234-065-P1-K1-F8
                  BLASTX
Method
                  g3776559
NCBI GI
BLAST score
                  294
                  1.0e-26
E value
                  124
Match length
                  48
% identity
                  (AC005388) Strong similarity to gene F14J9.26 gi 3482933
NCBI Description
                  cdc2 protein kinase homolog from A. thaliana BAC
                  gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                  gene. [Arabidopsis thaliana]
                  168647
Seq. No.
Seq. ID
                  LIB3234-065-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4678368
                  492
BLAST score
E value
                  8.0e-50
                  94
Match length
                  99
% identity
                 (AJ132436) GA 2-oxidase [Arabidopsis thaliana]
NCBI Description
                  168648
Seq. No.
                  LIB3234-065-P1-K1-G11
Seq. ID
```

alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_(X16430) elongation factor 1-alpha [Arabidopsis thaliana]

```
Method
                   BLASTN
                   g4415928
NCBI GI
BLAST score
                   161
                   2.0e-85
E value
                   235
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168649
Seq. ID
                   LIB3234-065-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   q4115370
BLAST score
                   186
E value
                   1.0e-100
Match length
                   320
% identity
                  Arabidopsis thaliana chromosome II BAC F27D4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168650
Seq. ID
                   LIB3234-065-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q112681
BLAST score
                   432
                   8.0e-43
E value
Match length
                   93
% identity
                   86
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi_808936_emb_CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   168651
Seq. No.
Seq. ID
                   LIB3234-065-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   q166570
BLAST score
                   171
E value
                   4.0e-12
Match length
                   103
% identity
                   38
NCBI Description
                  (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                   168652
Seq. ID
                   LIB3234-065-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g135858
BLAST score
                   170
                   1.0e-12
E value
Match length
                   50
% identity
                   72
                  TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                  >gi 99760 pir S22201 tonoplast intrinsic protein alpha -
                 Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
                  tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
```

Seq. No.

168658

```
intrinsic protein alpha [Arabidopsis thaliana]
                   168653
 Seq. No.
 Seq. ID
                   LIB3234-065-P1-K1-H1
 Method
                   BLASTX
 NCBI GI
                   q2088654
 BLAST score
                   477
 E value
                   5.0e-48
Match length
                   109
 % identity
                   87
 NCBI Description
                   (AF002109) 60S acidic ribosomal protein PO isolog
                   [Arabidopsis thaliana]
 Seq. No.
                   168654
 Seq. ID
                   LIB3234-065-P1-K1-H10
 Method
                   BLASTX
 NCBI GI
                   q3292817
 BLAST score
                   158
 E value
                   1.0e-10
Match length
                   53
 % identity
                   64
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   168655
                   LIB3234-065-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3236248
BLAST score
                   320
E value
                   6.0e-30
Match length
                   90
% identity
                   72
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                   168656
Seq. ID
                   LIB3234-065-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   q4467131
BLAST score
                   39
                   1.0e-12
E value
Match length
                   173
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
                   (ESSA project)
Seq. No.
                   168657
Seq. ID
                   LIB3234-070-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g2160151
BLAST score
                   371
E value
                   1.0e-35
Match length
                   105
% identity
                   73
NCBI Description (AC000375) Strong similarity to Brassica aspartic protease
                   (gb X77260). [Arabidopsis thaliana]
```

[Arabidopsis thaliana] >gi_445128_prf_ 1908432A tonoplast

Method

BLASTN

```
Seq. ID
                  LIB3234-070-P1-K1-A10
Method
                  BLASTX
                  q3212869
NCBI GI
BLAST score
                  208
                  1.0e-16
E value
Match length
                  49
                  73
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168659
Seq. ID
                  LIB3234-070-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  g4753645
BLAST score
                  115
E value
                  2.0e-58
                  150
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18
NCBI Description
                  (ESSA project)
                  168660
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q629528
BLAST score
                  573
                  3.0e-59
E value
Match length
                  123
% identity
NCBI Description
                  hypothetical protein - Arabidopsis thaliana
                  >gi_1076335_pir__S51580 hypothetical protein 1 -
                  Arabidopsis thaliana >gi_499167_emb_CAA56144 (X79707) ORF
                  [Arabidopsis thaliana]
                  168661
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q1531762
BLAST score
                  191
E value
                  2.0e-14
Match length
                  50
                  74
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  168662
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4063552
BLAST score
                  608
E value
                  2.0e-63
Match length
                  123
% identity
NCBI Description
                  (AF035908) ATP synthase beta subunit [Muntingia calabura]
Seq. No.
                  168663
Seq. ID
                  LIB3234-070-P1-K1-A6
```

E value

1.0e-77

```
NCBI GI
                   q4432829
 BLAST score
                   334
 E value
                   0.0e + 00
 Match length
                   373
 % identity.
                   97
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC T1B3 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168664
 Seq. ID
                   LIB3234-070-P1-K1-A9
 Method
                   BLASTX
 NCBI GI
                   q4314363
 BLAST score
                   411
 E value
                   2.0e-40
· Match length
                   100
 % identity
                   75
 NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   168665
 Seq. ID
                   LIB3234-070-P1-K1-B10
 Method
                   BLASTX
 NCBI GI
                   q2244740
 BLAST score
                   348
 E value
                   5.0e-33
 Match length
                   120
 % identity
                   57
 NCBI Description
                   (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]
                   168666
 Seq. No.
 Seq. ID
                   LIB3234-070-P1-K1-B12
 Method
                   BLASTX
                   g1351272
 NCBI GI
 BLAST score
                   391
 E value
                   5.0e-38
Match length
                   99.
 % identity
                   78
 NCBI Description
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550
                   (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                   thaliana] >gi_742408 prf 2009415A triose phosphate
                   isomerase [Arabidopsis thaliana]
 Seq. No.
                   168667
 Seq. ID
                   LIB3234-070-P1-K1-B2
Method
                   BLASTN
 NCBI GI
                   a297420
 BLAST score
                   94
E value
                   2.0e-45
Match length
                   201
                   92
 % identity
NCBI Description
                   Nicotiana sp. promoter DNA
Seq. No.
                   168668
Seq. ID
                   LIB3234-070-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   g4512690
BLAST score
                   148
```

Seq. ID

```
Match length
                   325
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F11A3 genomic
                   sequence, complete sequence
Seq. No.
                   168669
                   LIB3234-070-P1-K1-B6
Seq. ID
                   BLASTX
Method
                   q117822
NCBI GI
BLAST score
                   594
                                        . . -
E value
                   8.0e-62
Match length
                   126
                   90
% identity
                   CYTOCHROME B6 >gi 65635 pir CBNT6
NCBI Description
                   plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                   cytochrome b6 - common tobacco chloroplast
                   >gi_11858_emb_CAA77375 (Z00044) cytochrome b6 [Nicotiana
tabacum] >gi_225226_prf__1211235BH cytochrome b6 [Nicotiana
                   168670
Seq. No.
Seq. ID
                   LIB3234-070-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   q3047074
BLAST score
                   55
                   4.0e-22
E value
Match length
                   115
% identity
                   87
NCBI Description Arabidopsis thaliana BAC F21E10
Seq. No.
                   168671
Seq. ID
                   LIB3234-070-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q1706714
BLAST score
                   358
E value
                   4.0e-34
Match length
                   117
% identity
                   64
                   ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF)
NCBI Description
                    (ELECTRON TRANSFER FLAVOPROTEIN SMALL SUBUNIT) (ETFSS)
                   >gi 1209054 (U32230) EtfS [Bradyrhizobium japonicum]
Seq. No.
                   168672
Seq. ID
                   LIB3234-070-P1-K1-C2
Method
                   BLASTX
                   g2827139
NCBI GI
BLAST score
                   654
                   7.0e-69
E value
Match length
                   123
% identity
                   98
                    (AF027172) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana] >gi 4049343 emb CAA22568 (AL034567)
                   cellulose synthase catalyt\overline{i}c subun\overline{i}t (\overline{R}SW1) (Arabidopsis
                   thaliana]
                   168673
Seq. No.
```

LIB3234-070-P1-K1-C3

```
Method
                  BLASTX
NCBI GI
                  a1655424
BLAST score
                  440
E value
                  1.0e-43
Match length
                  89
% identity
                  96
NCBI Description
                  (D83531) GDP dissociation inhibitor [Arabidopsis thaliana]
                  >gi 3212878 (AC004005) GDP dissociation inhibitor
                  [Arabidopsis thaliana]
Seq. No.
                  168674
Seq. ID
                  LIB3234-070-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q2911059
BLAST score
                  590
E value
                  2.0e-61
Match length
                  123
% identity
                  95
NCBI Description (ALO21961) putative protein [Arabidopsis thaliana]
Seq. No.
                  168675
Seq. ID
                  LIB3234-070-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  q3193305
BLAST score
                  344
E value
                  0.0e + 00
Match length
                  372
% identity
NCBI Description Arabidopsis thaliana BAC F3D13
Seq. No.
                  168676
Seq. ID
                  LIB3234-070-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q2829898
BLAST score
                  336
E value
                  1.0e-31
Match length
                  85
% identity
                  75
                 (AC002311) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168677
Seq. ID
                  LIB3234-070-P1-K1-D11
Method
                  BLASTX
                  g4557026
NCBI GI
                  173
BLAST score
                  2.0e-12
E value
Match length
                  97
% identity
NCBI Description
                  quanine nucleotide exchange factor p532 >gi 1477565
                  (U50078) p532 [Homo sapiens]
Seq. No.
                  168678
Seq. ID
                  LIB3234-070-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2244749
BLAST score
                  464
E value
                  1.0e-46
```

```
Match length
                   102
% identity
                   89
NCBI Description
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                   168679
Seq. No.
                   LIB3234-070-P1-K1-D2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4519191
BLAST score
                   34
                   1.0e-09
E value
Match length
                   70
% identity
                   87
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K9P8, complete sequence
Seq. No.
                   168680
Seq. ID
                   LIB3234-070-P1-K1-D4
Method
                   BLASTN
NCBI GI
                   q3873174
BLAST score
                   351
E value
                   0.0e + 00
Match length
                   375
% identity
                   98
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F14N23,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   168681
Seq. ID
                   LIB3234-070-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   q4757417
BLAST score
                   152
E value
                   5.0e-80
Match length
                   341
% identity
                   89
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   T30G6, complete sequence
Seq. No.
                   168682
Seq. ID
                   LIB3234-070-P1-K1-D6
Method
                  BLASTX
NCBI GI
                   g3935151
BLAST score
                   582
E value
                   2.0e-60
Match length
                   110
% identity
                   98
NCBI Description
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
Seq. No.
                   168683
Seq. ID
                  LIB3234-070-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                   592
E value
                  1.0e-61
Match length
                  118
% identity
                  97
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
```

```
168684
Seq. No.
Seq. ID
                   LIB3234-070-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g3789925
BLAST score
                   54
                   1.0e-22
E value
Match length
                   120
% identity
                   50
                   (AF086625) phosphoinositide-dependent protein kinase PDK1
NCBI Description
                    [Mus musculus]
Seq. No.
                   168685
Seq. ID
                   LIB3234-070-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   q4204263
BLAST score
                   309
E value
                   2.0e-28
Match length
                   98
% identity
                   65
NCBI Description
                   (AC005223) 40409 [Arabidopsis thaliana]
Seq. No.
                   168686
Seq. ID
                   LIB3234-070-P1-K1-E12
Method
                   BLASTN
NCBI GI
                   q4056429
BLAST score
                   165
E value
                   9.0e-88
Match length
                   265
% identity
                   74
                   Arabidopsis thaliana chromosome 1 BAC F508 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   168687
Seq. ID
                   LIB3234-070-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q2507426
BLAST score
                   569
E value
                   7.0e-59
Match length
                   125
% identity
                   92
                   ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (ALANINE--TRNA LIGASE) (ALARS) >gi_1673365_emb_CAA80380_
NCBI Description
                   (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis
                   thaliana]
Seq. No.
                   168688
Seq. ID
                   LIB3234-070-P1-K1-E4
Method
                   BLASTN
NCBI GI
                   g3548797
BLAST score
                   234
E value
                   1.0e-129
Match length
                   375
% identity
                   97
                   Arabidopsis thaliana chromosome II BAC T18E12 genomic
NCBI Description
```

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  168689
Seq. ID
                  LIB3234-070-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4191814
BLAST score
                  169
E value
                  6.0e-12
Match length
                  117
% identity
NCBI Description (AB008680) alpha' subunit of beta-conglycinin [Glycine max]
Seq. No.
                  168690
Seq. ID
                  LIB3234-070-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q2492513
BLAST score
                  149
E value
                  3.0e - 34
Match length
                  118
                  67
% identity
NCBI Description
                  CELL DIVISION PROTEIN FTSH HOMOLOG 4
                  >gi_1652085_dbj_BAA17010_ (D90902) cell division protein
                  FtsH [Synechocystis sp.]
Seq. No.
                  168691
Seq. ID
                  LIB3234-070-P1-K1-E7
Method
                  BLASTX
NCBI GI.
                  q2924784
BLAST score
                  98
E value
                  1.0e-03
Match length
                  103
% identity
NCBI Description
                  (AC002334) similar to jasmonate inducible protein
                  [Arabidopsis thaliana]
Seq. No.
                  168692
Seq. ID
                  LIB3234-070-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2583120
BLAST score
                  616
E value
                  2.0e-64
Match length
                  123
% identity
                  99
                  (AC002387) putative receptor-like protein kinase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  168693
Seq. ID
                  LIB3234-070-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q3334123
BLAST score
                  387
E value
                  2.0e-37
Match length
                  99
% identity
                  83
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of
                  mitochondrial F1-ATPase [Arabidopsis thaliana] >gi 2924787
                  (AC002334) mitochondrial F1-ATPase, gamma subunit
                  [Arabidopsis thaliana]
```

```
168694
Seq. No.
                  LIB3234-070-P1-K1-F10
Seq. ID
                  BLASTX
Method
                  g3695023
NCBI GI
                  305
BLAST score
E value
                  6.0e-28 "
                  122
Match length
% identity
                  52
                  (AF055850) unknown [Arabidopsis thaliana]
NCBI Description
                  168695
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-F3
                  BLASTX
Method
NCBI GI
                  g1864017
                  535
BLAST score
                  7.0e-55
E value
                  102
Match length
                  99
% identity
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
Seq. No.
                  168696
Seq. ID
                  LIB3234-070-P1-K1-F4
Method '
                  BLASTN
NCBI GI
                  q3184270
BLAST score
                  189
                  1.0e-102
E value
                  295
Match length
                  94
% identity
                  Arabidopsis thaliana chromosome II BAC T8K22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  168697
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g730645
BLAST score
                  469
                  4.0e-47
E value
                  107
Match length
                  89
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal
                  protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679
                  (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                  >gi 313188 emb CAA80681 (Z23162) ribosomal protein S15
                  [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
                  Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                  gb R29788, gb ATTS0365 come from this gene. [Arabidopsis
                  thaliana]
                  168698
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-F7
                  BLASTN
Method
NCBI GI
                  g2760171
BLAST score
                  345
                  0.0e+00
E value
Match length
                  369
                  98
% identity
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MPA24, complete sequence [Arabidopsis thaliana]
                    168699
Seq. No.
                    LIB3234-070-P1-K1-F8
Seq. ID
Method
                    BLASTX
NCBI GI
                    q132770
BLAST score
                    333
E value
                    3.0e-31
Match length
                    90
% identity
                    74
                    CHLOROPLAST 50S RIBOSOMAL PROTEIN L20 >gi_71275_pir__R5NT20
NCBI Description
                    ribosomal protein L20 - common tobacco chloroplast >gi_11852_emb_CAA77372_ (Z00044) ribosomal protein L20 [Nicotiana tabacum] >gi_225221_prf__1211235BC ribosomal
                    protein L20 [Nicotiana tabacum]
Seq. No.
                    168700
Seq. ID
                    LIB3234-070-P1-K1-G2
Method
                    BLASTX
NCBI GI
                    g2286069
BLAST score
                    411
E value
                    2.0e-40
Match length
                    123
% identity
                    67
NCBI Description
                    (U72155) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                    168701
Seq. ID
                    LIB3234-070-P1-K1-G3
Method
                    BLASTX
NCBI GI
                    g4586256
BLAST score
                    574
E value
                    2.0e-59
Match length
                    121
% identity
                    94
NCBI Description
                    (AL049640) probable photosystem I chain XI precursor
                    [Arabidopsis thaliana]
Seq. No.
                    168702
Seq. ID
                    LIB3234-070-P1-K1-G4
Method
                    BLASTN
NCBI GI
                    g2980787
BLAST score
                    207
E value
                    1.0e-113
Match length
                    388
% identity
                    98
NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
                    (ESSAII project)
                    168703
Seq. No.
Seq. ID
                    LIB3234-070-P1-K1-G5
Method
                    BLASTX
NCBI GI
                    g3335169
BLAST score
                    657
E value
                    3.0e-69
Match length
                    125
% identity
                    98
```

BLAST score

```
(AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
                  168704
Seq. No.
                  LIB3234-070-P1-K1-G6
Seq. ID
                  BLASTN
Method
                  q3228389
NCBI GI
                  356
BLAST score
E value
                  0.0e + 00
Match length
                  380
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  168705
Seq. ID
                  LIB3234-070-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q1170939
                  397
BLAST score
                  1.0e-38
E value
Match length
                  81
% identity
                  93
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
                  168706
Seq. No.
Seq. ID
                  LIB3234-070-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q3819164
BLAST score
                  548
E value
                  2.0e-56
Match length
                  122
% identity
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                  max]
Seq. No.
                  168707
Seq. ID
                  LIB3234-070-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4678299
BLAST score
                  54
E value
                  1.0e-53
Match length
                  112
                  98
% identity
                  (AL049655) cysteine proteinase precursor-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  168708
Seq. No.
                  LIB3234-070-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204308
```

E value

0.0e + 00

```
E value
                   7.0e-34
Match length
                   68
                   91
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   168709
Seq. ID
                   LIB3234-070-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q82051
BLAST score
                   317
E value
                   3.0e-29
Match length
                   119
% identity
                   55
                   lipid body-associated membrane protein - carrot
NCBI Description
                   >gi_259453_bbs_117620 (S47635) lipid body membrane
                   protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                   180 aa] [Daucus carota]
Seq. No.
                   168710
Seq. ID
                   LIB3234-070-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g3024871
BLAST score
                   356
E value
                   7.0e-34
Match length
                   125
% identity
                   54
                   HYPOTHETICAL 77.3 KD PROTEIN SLL0005
NCBI Description
                   >gi_1001579_dbj_BAA10206 (D64000) ABC1-like [Synechocystis
                   sp. ]
Seq. No.
                   168711
Seq. ID
                   LIB3234-070-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g3025470
BLAST score
                   341
E value
                   4.0e-32
Match length
                   127
% identity
                   49
NCBI Description
                  (U76756) endo-beta-1,4-glucanase [Pinus radiata]
Seq. No.
                  168712
Seq. ID
                  LIB3234-070-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2980772
BLAST score
                  146
                                                1
E value
                  3.0e-09
Match length
                  84
% identity
                  44
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168713
Seq. ID
                  LIB3234-070-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g4079614
BLAST score
                  322
```

```
Match length
                   370
% identity
                   96
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F21M11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168714
Seq. ID
                   LIB3234-071-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   q336274
BLAST score
                   173
E value
                   2.0e-92
Match length
                   319
% identity
                   91
NCBI Description
                   Alnus incana chloroplast 23S rRNA, 4.5S rRNA, 5S rRNA,
                   tRNA-Arg, and tRNA-Asn genes
Seq. No.
                   168715
Seq. ID
                   LIB3234-071-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q3789828
BLAST score
                   187
E value
                   4.0e-14
Match length
                   50
% identity
NCBI Description
                  (AF061412) CAULIFLOWER [Arabidopsis thaliana]
Seq. No.
                   168716
Seq. ID
                   LIB3234-071-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g3688162
BLAST score
                   178
E value
                   1.0e-19
Match length
                   56
% identity
                   95
NCBI Description
                  (AJ009672) centrin [Arabidopsis thaliana]
Seq. No.
                   168717
Seq. ID
                   LIB3234-071-P1-K1-A2
Method
                  BLASTN
NCBI GI
                   g3668073
BLAST score
                   313
E value
                   1.0e-176
Match length
                   357
                   97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T4C15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168718
Seq. ID
                  LIB3234-071-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  g4589414
BLAST score
                  179
E value
                  4.0e-96
Match length
                  298
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
```

K14B15, complete sequence

Seq. No.

```
Seq. No.
                   168719
, Seg. ID
                   LIB3234-071-P1-K1-A4
 Method
                   BLASTN
 NCBI GI
                   g16181
 BLAST score
                   81
 E value
                   1.0e-37
 Match length
                    305
 % identity
                   85
                   A.thaliana gene for tonoplast intrinsic protein
 NCBI Description
                   alpha-TIP(Ara) >gi_166622_gb_M84343_ATHATIP Arabidopsis
                   thaliana tonoplast intrinsic protein (alpha-TIP) gene,
                   complete cds
 Seq. No.
                   168720
 Seq. ID
                   LIB3234-071-P1-K1-A5
 Method
                   BLASTX
 NCBI GI
                   g1621539
 BLAST score
                   285
 E value
                   1.0e-25
 Match length
                   106
 % identity
 NCBI Description
                  (U28415) annexin-like protein [Arabidopsis thaliana]
 Seq. No.
                   168721
                   LIB3234-071-P1-K1-A8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g226120
 BLAST score
                   195
 E value
                   5.0e-15
 Match length
                   101
 % identity
                   40
 NCBI Description vicilin gene B [Saguinus oedipus]
 Seq. No.
                   168722
 Seq. ID
                   LIB3234-071-P1-K1-A9
 Method
                   BLASTN
 NCBI GI
                   q4589414
 BLAST score
                   66
 E value
                   8.0e-29
 Match length
                   158
 % identity
                   89
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                   K14B15, complete sequence
 Seq. No.
                   168723
 Seq. ID
                   LIB3234-071-P1-K1-B1
 Method
                   BLASTN
 NCBI GI
                   q4314374
 BLAST score
                   288
 E value
                   1.0e-161
 Match length
                   292
                   100
 % identity
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F10A12 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
```

```
Seq. ID
                  LIB3234-071-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q710625
BLAST score
                  246
                  1.0e-136
E value
Match length
                  281
                  96
% identity
NCBI Description Arabidopsis thaliana mRNA for ERD15 protein, complete cds
Seq. No.
                  168725
Seq. ID
                  LIB3234-071-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  q4455262
BLAST score
                  303
E value
                  1.0e-170
Match length
                  360
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                  (ESSAII project)
Seq. No.
                  168726
Seq. ID
                  LIB3234-071-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q4539378
BLAST score
                  132
E value
                  5.0e-68
Match length ~
                  328
% identity
                  77
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21
                  (ESSA project)
Seq. No.
                  168727
Seq. ID
                  LIB3234-071-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q384341
BLAST score
                  184
E value
                  1.0e-13
Match length
                  97
% identity
                  39
NCBI Description major storage protein [Theobroma cacao]
                  168728
Seq. No.
Seq. ID
                  LIB3234-071-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g3688161
BLAST score
                  105
E value
                  6.0e-52
Match length
                  124
% identity
                  100
NCBI Description Arabidopsis thaliana mRNA for centrin
                  168729
Seq. No.
Seq. ID
                  LIB3234-071-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3819164
BLAST score
                  392
E value
                  3.0e - 38
```

Seq. ID

```
Match length
                  94
% identity
                  83
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                  maxl
Seq. No.
                  168730
                  LIB3234-071-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2760170
BLAST score
                  284
E value
                  1.0e-159
Match length
                  340
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIO24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168731
Seq. ID
                  LIB3234-071-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1168256
BLAST score
                  119
E value
                  4.0e-58
Match length
                  120
% identity
                  97
NCBI Description ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR
                  (TRANSAMINASE A) >gi_693688 (U15026) aspartate
                  aminotransferase [Arabidopsis thaliana] >gi_3201622
                  (AC004669) aspartate aminotransferase [Arabidopsis
                  thaliana]
                  168732
Seq. No.
Seq. ID
                  LIB3234-071-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q118926
BLAST score
                  161
E value
                  4.0e-11
Match length
                  69
                  46
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi 167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi_227781_prf__1710351E abscisic acid responsive protein E
                  [Craterostigma plantagineum]
Seq. No.
                  168733
Seq. ID
                  LIB3234-071-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4510397
BLAST score
                  613
E value
                  5.0e-64
Match length
                  122
% identity
NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
Seq. No.
                  168734
```

LIB3234-071-P1-K1-C7

```
Method
                  BLASTX
NCBI GI
                  g3869253
BLAST score
                  229
È value
                  4.0e-19
Match length
                  104
% identity
                  51
NCBI Description
                  (U39288) ferredoxin-dependent glutamate synthase precursor
                   [Arabidopsis thaliana]
Seq. No.
                  168735
Seq. ID
                  LIB3234-071-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3334128
BLAST score
                  79
                  2.0e-52
E value
Match length
                  124
% identity
                  95
NCBI Description
                  BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE
                  PRECURSOR (BCCP) >gi 1066348 (U23155) acetyl-CoA
                  carboxylase biotin-containing subunit [Arabidopsis
                  thaliana]
Seq. No.
                  168736
                  LIB3234-071-P1-K1-D12
Seq. ID
Method
                .. BLASTX
NCBI GI
                  q267073
BLAST score
                  634
E value
                  2.0e-66
Match length
                  125
                  97
% identity
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  168737
Seq. ID
                  LIB3234-071-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q2494110
BLAST score
                  286
E value
                  1.0e-160
Match length
                  322
% identity
                  97
NCBI Description
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168738
Seq. ID
                  LIB3234-071-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  q4757413
BLAST score
                  206
E value
                  1.0e-112
Match length
                  276
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

MXO21, complete sequence

```
Seq. No.
                   168739
Seq. ID
                   LIB3234-071-P1-K1-D5
Method
                   BLASTX
NCBI GI .
                   q4581146
BLAST score
                   508
E value
                   1.0e-51
Match length
                   115
% identity
                  (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                   cytoplasmic (Arabidopsis thaliana)
Seq. No.
                   168740
Seq. ID
                   LIB3234-071-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   a548847
BLAST score
                   379
E value
                   1.0e-36
Match length
                   75
                   99
% identity
NCBI Description
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
                   >gi_1086182_pir__S39501 ribosomal protein S12 -
                   curled-leaved tobacco >gi_225248_prf 1211235CG ribosomal
                   protein S12 [Nicotiana tabacum]
Seq. No.
                   168741
Seq. ID
                   LIB3234-071-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g2642157
BLAST score
                   273
E value
                   4.0e-24
Match length
                   111
% identity
NCBI Description
                  (AC003000) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                   168742
Seq. ID
                   LIB3234-071-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   559
E value
                   1.0e-57
Match length
                   122
% identity
                   87
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   168743
Seq. ID
                   LIB3234-071-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q514324
BLAST score
                   135
E value
                   3.0ė-18
Match length
                   62
% identity
                   87
NCBI Description (L34773) RNA polymerase subunit [Arabidopsis thaliana]
```

```
[Arabidopsis thaliana] >gi 1586550 prf 2204246B RNA
                  polymerase [Arabidopsis thaliana]
Seq., No.
                  168744
Seq. ID
                  LIB3234-071-P1-K1-E4
Method
                  BLASTN
                  q3540210
NCBI GI
BLAST score
                  166
                  2.0e-88
E value
Match length
                  317
% identity
                  89
                  Arabidopsis thaliana chromosome I BAC F5A8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168745
Seq. ID
                  LIB3234-071-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2492514
BLAST score
                  361
E value
                  2.0e-34
Match length
                  92
                  77
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >gi 1483215 emb CAA68141 (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
Seq. No.
                  168746
                  LIB3234-071-P1-K1-E9
Seq. ID
Method
                  BLASTN
                  g2828278
NCBI GI
BLAST score
                  179
                  4.0e-96
E value
Match length
                  358
% identity
                  97
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
NCBI Description
                  (ESSAII project)
Seq. No.
                  168747
Seq. ID .
                  LIB3234-071-P1-K1-F10
Method
                  BLASTN
                  q2618604
NCBI GI
BLAST score
                  363
E value
                  0.0e + 00
                  383
Match length
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTG13, complete sequence [Arabidopsis thaliana]
                  168748
Seq. No.
Seq. ID
                  LIB3234-071-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g384341
BLAST score
                  173
                  2.0e-12
E value
Match length
                  101
% identity
                  38
```

>qi 2462755 (AC002292) RNA polymerase subunit (isoform B)

6 900 -

```
NCBI Description major storage protein [Theobroma cacao]
Seq. No.
                  168749
Seq. ID
                  LIB3234-071-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  g2351062
BLAST score
                  343
E value
                  0.0e+00
Match length
                  375
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168750
Seq. ID
                  LIB3234-071-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  g4757403
BLAST score
                  37
E value
                  2.0e-11
Match length
                  69
                  89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
                                   .
                  168751
Seq. No.
Seq. ID
                  LIB3234-071-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  q4406790
BLAST score
                  269
E value
                  1.0e-150
Match length
                  339
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC T1016 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  168752
Seq. No.
Seq. ID
                  LIB3234-071-P1-K1-F7
Method
                  BLASTN
                  g4678705
NCBI GI
                  295
BLAST score
E value
                  1.0e-165
                  359
Match length
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                  (ESSA project)
Seq. No.
                  168753
Seq. ID
                  LIB3234-071-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q462147
                  65
BLAST score
                  5.0e-22
E value
Match length
                  68
% identity
                  85
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)
NCBI Description
                  (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                  (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase
```

```
>gi 415923 emb CAA48940 (X69195) glucose-6-phosphate
                  isomerase [Arabidopsis thaliana]
Seq. No.
                  168754
Seq. ID
                  LIB3234-071-P1-K1-G12
Method
                  BLASTX
                  q2781354
NCBI GI
BLAST score
                  554
                  5.0e-57
E value
Match length
                  108
% identity
                  95
                 (AC003113) F2401.10 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168755
Seq. ID
                  LIB3234-071-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g3406034
BLAST score
                  46
                  8.0e-17
E value
Match length
                  175
% identity
                  88
                  BAC F18A17 from chromosome V containing TINY at 60.5 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  168756
Seq. No.
Seq. ID
                  LIB3234-071-P1-K1-H1
Method
                  BLASTN
                3. g3894179
NCBI GI
BLAST score
                  81
E value
                  1.0e-37
Match length
                  201
% identity
                  85
NCBI Description Arabidopsis thaliana chromosome II BAC F13H10 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168757
                  LIB3234-071-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133750
BLAST score
                  547
                  3.0e-56
E value
Match length
                  108
                  97
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                  >gi 320170 pir A26574 ribosomal protein S12 - soybean
                  chloroplast >gi_11572_emb_CAA28661_ (X05013) rps12 [Glycine
                  max]
                  168758
Seq. No.
Seq. ID
                  LIB3234-071-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g4753195
BLAST score
                  298
E value
                  1.0e-167
Match length
                  372
                  88
% identity
```

(EC 5.3.1.9) - Arabidopsis thaliana

Match length

```
NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5
                   cM, complete sequence
                   168759
Seq. No.
Seq. ID
                   LIB3234-071-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q2924779
BLAST score
                   363
E value
                   6.0e-35
Match length
                   91
% identity
                   80
NCBI Description
                   (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
                   thaliana] >gi_2981616_dbj_BAA25248 (AB008854)
                   3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                   >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA
                   thiolase [Arabidopsis thaliana]
Seq. No.
                   168760
Seq. ID
                   LIB3234-072-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   q4206762
BLAST score
                   215
E value
                   1.0e-117
Match length
                   282
% identity
                   93
                  Arabidopsis thaliana cell wall-plasma membrane linker
NCBI Description
                   protein homolog (CWLP) mRNA, complete cds
Seq. No.
                   168761
Seq. ID
                   LIB3234-072-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   g2760164
BLAST score
                   364
E value
                   0.0e + 00
                   380
Match length
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168762
                  LIB3234-072-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3805849
BLAST score
                  625
                  2.0e-65
E value
                  125
Match length
                  98
% identity
                  (AL031986) cytoplasmatic aconitate hydratase (citrate
NCBI Description
                  hydro-lyase) (aconitase) (EC 4.2.1.3) [Arabidopsis thaliana]
Seq. No.
                  168763
                  LIB3234-072-P1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4544435
BLAST score
                  34
E value
                  1.0e-09
```

```
% identity
                   89
NCBI Description Arabidopsis thaliana chromosome II BAC F14M13 genomic
                   sequence, complete sequence
 Seq. No.
                   168764
 Seq. ID
                   LIB3234-072-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g2842490
BLAST score
                   608
E value
                   2.0e-63
Match length
                   117
% identity
                   97
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  168765
Seq. ID
                  LIB3234-072-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g4206762
BLAST score
                  49
E value
                  2.0e-18
Match length
                  88
% identity
                  89
NCBI Description Arabidopsis thaliana cell wall-plasma membrane linker
                  protein homolog (CWLP) mRNA, complete cds
Seq. No.
                  168766
Seq. ID
                  LIB3234-072-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g4159704
BLAST score
                  223
E value
                  1.0e-122
Match length
                  361
                  97
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MCB17, complete sequence
Seq. No.
                  168767
Seq. ID
                  LIB3234-072-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2244892
BLAST score
                  272
E value
                  5.0e-24
Match length
                  68
% identity
                  76
NCBI Description
                  (Z97338) similarity to cycloartenol synthase [Arabidopsis
                  thaliana]
Seq. No.
                  168768
Seq. ID
                  LIB3234-072-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  226
E value
                  1.0e-21
Match length
                  105
% identity
                  63
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

% identity

86

cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                   168769
Seq. ID
                   LIB3234-072-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   g3659491
BLAST score
                   280
                   1.0e-156
E value
Match length
                   343
% identity
NCBI Description
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168770
Seq. ID
                  LIB3234-072-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  q1345973
BLAST score
                  421
E value
                  2.0e-41
Match length
                  95
% identity
                  81
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  168771
Seq. ID
                  LIB3234-072-P1-K1-C2
Method
                  BLASTX
                  g1345973
NCBI GI
BLAST score
                  431
E value
                  1.0e-42
Match length
                  97
% identity
                  81
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  168772
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2500378
BLAST score
                  437
E value
                  2.0e-43
Match length
                  94
```

Seq. ID

```
NCBI Description 60S RIBOSOMAL PROTEIN L37
Seq. No.
                  168773
Seq. ID
                  LIB3234-072-P1-K1-C4
Method
                  BLASTX
NCBI GI
                   g2961542
BLAST score
                   513
                   3.0e-52
E value
Match length
                   93
% identity
                   100
NCBI Description
                  (AF050463) zinc finger transcription factor [Arabidopsis
                   thaliana]
                  168774
Seq. No.
                  LIB3234-072-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062165
BLAST score
                   74
                  8.4e-01
E value
Match length
                  111
% identity
                   32
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  168775
Seq. ID
                  LIB3234-072-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q3785989
BLAST score
                  92
E value
                  5.0e-63
Match length
                  125
% identity
NCBI Description
                  (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                  168776
Seq. ID
                  LIB3234-072-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  q4756963
BLAST score
                  227
E value
                  1.0e-125
Match length
                  368
% identity
                  95
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                  (ESSA project)
Seq. No.
                  168777
Seq. ID
                  LIB3234-072-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g1785729
BLAST score
                  35
E value
                  2.0e-10
Match length
                  141
% identity
                  86
NCBI Description A.thaliana mitochondrial genome, part B
Seq. No.
                  168778
```

LIB3234-072-P1-K1-D2

```
Method
                     BLASTX
  NCBI GI
                     g2119846
  BLAST score
                     555
  E value
                     3.0e-57
  Match length
                     115
                   ∻ 91
  % identity
  NCBI Description
                    chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                     Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                     photosystem II type I chlorophyll a /b binding protein
                     [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                     II type I chlorophyll a/b binding protein [Arabidopsis
                     thaliana] >gi_3337371 (AC004481) photosystem II type I
                     chlorophyll a/b binding protein [Arabidopsis thaliana]
  Seq. No.
                     168779
  Seq. ID
                    LIB3234-072-P1-K1-D3
  Method
                    BLASTN
  NCBI GI
                     g4115930
  BLAST score
                     346
  E value
                     0.0e + 00
  Match length
                     370
  % identity
                     98
  NCBI Description Arabidopsis thaliana BAC T4B21
~ Seq. No.
                    168780
  Seq. ID
                    LIB3234-072-P1-K1-D4
  Method
                    BLASTX
  NCBI GI
                    g3024871
  BLAST score
                    244
  E value
                    9.0e-21
  Match length
                    101
  % identity
                    49
                    HYPOTHETICAL 77.3 KD PROTEIN SLL0005
  NCBI Description
                    >gi 1001579 dbj BAA10206 (D64000) ABC1-like [Synechocystis
                    sp.]
  Seq. No.
                    168781
  Seq. ID
                    LIB3234-072-P1-K1-D6
  Method
                    BLASTX
  NCBI GI
                    g4325324
  BLAST score
                    641
  E value
                    3.0e-67
  Match length
                    124
  % identity
  NCBI Description
                    (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
                    thaliana]
  Seq. No.
                    168782
  Seq. ID
                    LIB3234-072-P1-K1-D9
  Method
                    BLASTN
  NCBI GI
                    q3738313
  BLAST score
                    311
  E value -
                    1.0e-175
                    373
  Match length
                    96
  % identity
  NCBI Description Arabidopsis thaliana chromosome II BAC T29E15 genomic
```

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   168783
Seq. ID
                   LIB3234-072-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g4263722
BLAST score
                   184
E value
                   5.0e-29
Match length
                   78
% identity
                   87
NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]
Seq. No.
                   168784
Seq. ID
                   LIB3234-072-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   q3935157
BLAST score
                   182
E value
                   2.0e-25
Match length
                   72
% identity
                   86
NCBI Description
                  (AC005106) T25N20.21 [Arabidopsis thaliana]
Seq. No.
                  168785
Seq. ID
                  LIB3234-072-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g2564048 ·
BLAST score
                  233
E value
                  1.0e-128
                  325
Match length
                  95
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168786
Seq. ID
                  LIB3234-072-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  q3892698
BLAST score
                  272
E value
                  1.0e-151
                  378
Match length
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2
                  (ESSAII project)
Seq. No.
                  168787
Seq. ID
                  LIB3234-072-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2911060
BLAST score
                  161
E value
                  5.0e-11
Match length
                  78
% identity
                  30
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
                  >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  168788
Seq. ID
                  LIB3234-072-P1-K1-F12
```

BLAST score

```
Method
                  BLASTN
NCBI GI
                  q4455168
BLAST score
                  104
E value
                  3.0e-51
Match length
                  312
% identity
                  88
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
                  (ESSAII project.)
Seq. No.
                  168789
Seq. ID
                  LIB3234-072-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  q4519195
BLAST score
                  291
E value
                  1.0e-163
Match length
                  336
% identity
                  99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
Seq. No.
                  168790
Seq. ID
                  LIB3234-072-P1-K1-F3
Method
                  BLASTX ·
NCBI GI
                  q4154281
BLAST score
                  286
E value
                  1.0e-25
Match length
                  68
% identity
NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
Seq. No.
                  168791
Seq. ID
                  LIB3234-072-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1791309
BLAST score
                  467
                  6.0e-47
E value
Match length
                  102
% identity
                  93
                  (U83500) cystathionine gamma-synthase [Arabidopsis
NCBI Description
                  thaliana] >gi 2852454 dbj BAA24699 (AB010888)
                  cystathionine gamma-synthase [Arabidopsis thaliana]
Seq. No.
                  168792
Seq. ID
                 LIB3234-072-P1-K1-F5
                 BLASTX
Method
NCBI GI
                 q1113941
BLAST score
                 274
E value
                 3.0e-24
Match length
                 89
% identity
                 60
NCBI Description (U40713) Pv42p [Phaseolus vulgaris]
Seq. No.
                 168793
                 LIB3234-072-P1-K1-F6
Seq. ID
                 BLASTX
Method
NCBI GI
                 g3334128
```

```
E value
                  1.0e-54
Match length
                   125
                  97
% identity
NCBI Description
                  BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE
                  PRECURSOR (BCCP) >gi 1066348 (U23155) acetyl-CoA
                  carboxylase biotin-containing subunit [Arabidopsis
                  thaliana]
Seq. No.
                  168794
Seq. ID
                  LIB3234-072-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q3096912
BLAST score
                  450
E value
                  6.0e-45
Match length
                  95
% identity
                  98
NCBI Description
                 (AL023094) putative protein [Arabidopsis thaliana]
Seq. No.
                  168795
Seq. ID
                  LIB3234-072-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q3869088
BLAST score
                  430
E value
                  2.0e-42
Match length
                  103
% identity
                  81
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
Seq. No.
                  168796
                  LIB3234-072-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132074
                  577
BLAST score
E value
                  8.0e-60
Match length
                  106
% identity
                  99
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                  168797
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2829893
BLAST score
                  516
E value
                  1.0e-52
                  108
Match length
% identity
                  96
NCBI Description (AC002311) phosphoglucomutase [Arabidopsis thaliana]
                  168798
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g118926
BLAST score
                  252
                  1.0e-21
E value
```

Method

BLASTX

```
Match length
                  97
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi 167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi_227781_prf__1710351E abscisic acid responsive protein E
                  [Craterostigma plantagineum]
Seq. No.
                  168799
Seq. ID
                  LIB3234-072-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  350
                  3.0e - 33
E value
Match length
                  84
% identity
                  80
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                  168800
Seq. No.
                  LIB3234-072-P1-K1-G3
Seq. ID
Method
                  BLASTX
                  q4154281
NCBI GI
BLAST score
                  170
                  2.0e-12
E value
Match length
                  44
% identity
                  70
                  (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
NCBI Description
                  168801
Seq. No.
                  LIB3234-072-P1-K1-G6
Seq. ID
Method
                  BLASTN
                  q2351065
NCBI GI
BLAST score
                  300
                  1.0e-168
E value
                  352
Match length
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168802
Seq. ID
                  LIB3234-072-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q419757
BLAST score
                  522
                  2.0e-53
E value
                  125
Match length
                  83
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) precursor -
NCBI Description
                  Arabidopsis thaliana
                  168803
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-H1
```

```
NCBI GI
                  q1170606
BLAST score
                  271
                  7.0e-24
E value
Match length
                  63
% identity
                  84
                  ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi 629863 pir S45634 adenylate kinase (EC 2.7.4.3),
                  chloroplast - maize >gi 3114421 pdb 1ZAK A Chain A,
                  Adenylate Kinase From Maize In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
                  >gi 3114422 pdb 1ZAK B Chain B, Adenylate Kinase From Maize
                  In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
                  168804
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-H10
Method
                  BLASTN
                  q4538990
NCBI GI
BLAST score
                  246
                  1.0e-136
E value
Match length
                  345
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
NCBI Description
                  (ESSA project)
                  168805
Seq. No.
Seq. ID
                  LIB3234-072-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4588779
BLAST score
                  264
E value
                  4.0e-23
Match length
                  75
                  67
% identity
                  (AF117267) UDP glucose:flavonoid 3-O-glucosyl transferase
NCBI Description
                  [Malus domestica]
Seq. No.
                  168806
                  LIB3234-072-P1-K1-H2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2828182
BLAST score
                  40
                  3.0e-13
E value
                  64
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168807
Seq. ID
                  LIB3234-072-P1-K1-H3
                  BLASTX
Method
NCBI GI
                  q3983125
BLAST score
                  492
E value
                  8.0e-50
                  125
Match length
                  78
% identity
                  (AF097648) phosphate/triose-phosphate translocator
NCBI Description
                  precursor [Arabidopsis thaliana]
```

```
Seq. No.
                   168808
Seq. ID
                   LIB3234-072-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g1871174
BLAST score
                  504
                   3.0e-51
E value
Match length
                   122
% identity
                   74
NCBI Description
                 (U90439) actin isolog [Arabidopsis thaliana]
Seq. No.
                   168809
Seq. ID
                   LIB3234-072-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g2649345
BLAST score
                   369
E value
                   2.0e-35
                   120
Match length
% identity
                   58
NCBI Description
                   (AE001019) tryptophan synthase, subunit beta (trpB-1)
                   [Archaeoglobus fulgidus]
Seq. No.
                   168810
Seq. ID
                   LIB3234-072-P1-K1-H6
                           C. ava
Method
                  BLASTN
NCBI GI
                  q4753195
BLAST score
                   323
E value
                  0.0e + 00
Match length
                   379
% identity
                  89
NCBI Description
                  Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5
                  cM, complete sequence
Seq. No.
                  168811
Seq. ID
                  LIB3234-072-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1076423
BLAST score
                  186
E value
                  6.0e - 35
Match length
                  104
                  79
% identity
NCBI Description
                  transcription factor OBF5 - Arabidopsis thaliana (fragment)
                  >gi_414615_emb_CAA49525 (X69900) ocs-element binding
                  factor 5 [Arabidopsis thaliana]
                  168812
Seq. No.
                  LIB3234-072-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4038491
BLAST score
                  177
E value
                  6.0e-13
Match length
                  122
% identity
                  36
                  (AJ131705) poly(ADP-ribose) polymerase [Arabidopsis
NCBI Description
                  thaliana]
```

168813

Seq. No.

Method NCBI GI

```
Seq. ID
                   LIB3234-072-P1-K1-H9
                   BLASTN
 Method
 NCBI GI
                   g2342673
 BLAST score
                   78
E value
                   8.0e-36
                   210
Match length
                   82
 % identity
                   Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168814
Seq. ID
                   LIB3234-074-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   31
                   8.0e-09
E value
Match length
                   31
 % identity
                   50
NCBI Description Tobacco chloroplast genome DNA
 Seq. No.
                   168815
Seq. ID
                   LIB3234-074-P1-K1-A10
Method
                   BLASTN
NCBI GI
                   g4589950
BLAST score
                   118
                   4.0e-60
E value
Match length
                   130
 % identity
                   98
                   Arabidopsis thaliana chromosome II BAC T28P16 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   168816
                   LIB3234-074-P1-K1-A11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4733980
                   38
BLAST score
E value
                   .6.0e-12
Match length
                   198
% identity
                   80
                   Arabidopsis thaliana chromosome II BAC T27D6 genomic
NCBI Description
                   sequence, complete sequence
                   168817
Seq. No.
Seq. ID
                   LIB3234-074-P1-K1-A2
Method
                   BLASTN
NCBI GI
                   g4589438
BLAST score
                   373
E value
                   0.0e+00
Match length
                   385
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQJ2, complete sequence
Seq. No.
                   168818
Seq. ID
                   LIB3234-074-P1-K1-A3
```

BLASTX

q1276946

```
BLAST score
                   72
E value
                   1.0e-22
Match length
                   115
% identity
                   50
NCBI Description
                   (U47078) globulin-like protein [Daucus carota] >gi 1458098
                   (U62395) globulin-like protein [Daucus carota]
Seq. No.
                  168819
Seq. ID
                  LIB3234-074-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  340
E value
                  6.0e-32
                  73
Match length
                  90
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  168820
Seq. ID
                  LIB3234-074-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3445209
BLAST score
                  406
E value
                  9.0e-40
Match length
                  101
% identity
                  71
NCBI Description
                  (AC004786) putative serine carboxypeptidase I [Arabidopsis
                  thaliana]
Seq. No.
                  168821
Seq. ID
                  LIB3234-074-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g2182286
BLAST score
                  167
E value
                  6.0e-89
Match length
                  342
% identity
                  Sequence of BAC F20P5 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168822
Seq. ID
                  LIB3234-074-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q1170939
BLAST score
                  514
E value
                  2.0e-52
Match length
                  104
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi_429108 emb_CAA80867 (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
```

esculentuml

```
Seq. No.
                  168823
Seq. ID
                  LIB3234-074-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  158
E value
                  1.0e-10
                  64
Match length
                  47
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  168824
Seq. ID
                  LIB3234-074-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g2342727
BLAST score
                  522
E value
                  2.0e-53
Match length
                  126
% identity
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168825
                  LIB3234-074-P1-K1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3169169
BLAST score
                  59
E value
                  2.0e-24
Match length
                  132
% identity
                  91
                  Arabidopsis thaliana chromosome II BAC F21P24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  168826
Seq. No.
Seq. ID
                  ·LIB3234-074-P1-K1-B11
Method
                  BLASTN
                  g4586098
NCBI GI
BLAST score
                  355
                  0.0e+00
E value
                  355
Match length
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
NCBI Description
                   (ESSA project)
Seq. No.
                  168827
                  LIB3234-074-P1-K1-B6
Seq. ID
Method
                  BLASTN
                  q2828185
NCBI GI
                  379
BLAST score
                  0.0e+00
E value
                  379
Match length
% identity
                  59
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUD21, complete sequence [Arabidopsis thaliana]
```

Seq. No.

```
Seq. No.
                  168828
Seq. ID
                  LIB3234-074-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g125606
BLAST score
                  155
E value
                  2.0e-10
Match length
                  53
                  60
% identity
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463 pir $12248
NCBI Description
                  pyruvate kinase (EC 2.7.1.40) - potato
                  >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
                  tuberosum]
Seq. No.
                  168829
Seq. ID
                  LIB3234-074-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g3169169
BLAST score
                  63
E value
                  7.0e-27
Match length
                  160
                  89
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F21P24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  168830
Seq. No.
                  LIB3234-074-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g511598
BLAST score
                  335
E value
                  0.0e + 00
Match length
                  363
% identity
                  26
                  Arabidopsis thaliana cell wall protein (APTR-1) gene,
NCBI Description
                  complete cds
                  168831
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1350768
BLAST score
                  376
                  3.0e-36
E value
                  90
Match length
% identity
                  83
                  60S RIBOSOMAL PROTEIN L7A
NCBI Description
Seq. No.
                  168832
Seq. ID
                  LIB3234-074-P1-K1-C12
                  BLASTN
Method
NCBI GI
                  g4263813
BLAST score
                  292
                  1.0e-163
E value
                  331
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T13P21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```

Method

BLASTN

```
Seq. ID
                    LIB3234-074-P1-K1-C2
 Method
                    BLASTX
 NCBI GI
                    g1402914
 BLAST score
                    447
 E value
                    1.0e-44
 Match length
                    93
 % identity
                    96
 NCBI Description
                    (X98318) peroxidase [Arabidopsis thaliana]
 Seq. No.
                    168834
 Seq. ID
                    LIB3234-074-P1-K1-C3
 Method
                    BLASTX
 NCBI GI
                    g1943751
 BLAST score
                    644
 E value
                   1.0e-67
 Match length
                   127
 % identity
                   98
                   (U93845) Arabidopsis thaliana ER-type calcium pump
 NCBI Description
                   protein, complete sequence >gi_2078292 (U96455) ER-type
                   Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
 Seq. No.
                   168835
 Seq. ID
                   LIB3234-074-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g140285
BLAST score
                   203
E value
                   5.0e-16
Match length
                   46
% identity
                   85
NCBI Description
                   HYPOTHETICAL 19 KD PROTEIN (ORF 168)
                   >gi_2924263_emb_CAA77415_ (Z00044) Ycf3 protein [Nicotiana
                   tabacum]
Seq. No.
                   168836
Seq. ID
                   LIB3234-074-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g1402914
BLAST score
                   588
E value
                   4.0e-61
Match length
                   117
% identity
                   99
NCBI Description
                  (X98318) peroxidase [Arabidopsis thaliana]
Seq. No.
                   168837
Seq. ID
                  LIB3234-074-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  g2832611
BLAST score
                  320
E value
                  1.0e-180
Match length
                  380
% identity
                  96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
                  (ESSAII project)
Seq. No.
                  168838
Seq. ID
                  LIB3234-074-P1-K1-D10
```

E value

0.0e + 00

```
NCBI GI
                   q4220645
BLAST score
                   349
E value
                   0.0e + 00
Match length
                   376
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MYA6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168839
                   LIB3234-074-P1-K1-D11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4220645
BLAST score
                   132
E value
                   3.0e-68
Match length
                   220
% identity
                   90
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MYA6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168840
Seq. ID
                   LIB3234-074-P1-K1-D3
Method
                   BLASTN
NCBI GI
                   q3046849
BLAST score
                   239
E value
                   1.0e-132
Match length
                   365
% identity
                   92
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18L3, complete sequence [Arabidopsis thaliana].
Seq. No.
                   168841
Seq. ID
                  LIB3234-074-P1-K1-D4
Method
                  BLASTN
NCBI GI
                   g3046849
                   124
BLAST score
                   3.0e-63
E value
                   205
Match length
% identity
                   91
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168842
Seq. ID
                  LIB3234-074-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  g1931636
BLAST score
                   303
E value
                  1.0e-170
Match length
                  375
% identity
                  95
                  Arabidopsis thaliana BAC T19D16 genomic sequence
NCBI Description
Seq. No.
                  168843
Seq. ID
                  LIB3234-074-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  g4757417
                  374
BLAST score
```

```
Match length
                   378
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                   T30G6, complete sequence
Seq. No.
                   168844
Seq. ID
                   LIB3234-074-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   q4220645
BLAST score
                   345
E value
                   0.0e + 00
Match length
                   372
% identity
                   98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYA6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168845
Seq. ID
                   LIB3234-074-P1-K1-E10
Method
                   BLASTN
NCBI GI
                   g4587986
BLAST score
                   353
E value
                   0.0e + 00
Match length
                   373
% identity
                   99
NCBI Description Arabidopsis thaliana ABA-regulated gene cluster, complete
                  sequence
Seq. No.
                  168846
Seq. ID
                  LIB3234-074-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g4558521
BLAST score
                  333
E value
                  0.0e + 00
Match length
                  377
                  97
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T10024,
                  complete sequence
Seq. No.
                  168847
Seq. ID
                  LIB3234-074-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g2832643
BLAST score
                  174
E value
                  1.0e-12
Match length
                  120
% identity
                  38
NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  168848
Seq. ID
                  LIB3234-074-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g3228389
BLAST score
                  310
E value
                  1.0e-174
Match length
                  354
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,
```

complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   168849
Seq. ID
                   LIB3234-074-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   g4539290
BLAST score
                   327
                   0.0e+00
E value
Match length
                   384
% identity
                   98
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19
                   (ESSA project)
Seq. No.
                   168850
Seq. ID
                   LIB3234-074-P1-K1-E4
Method
                   BLASTN
NCBI GI
                   g4539290
BLAST score
                   197
                   1.0e-107
E value
Match length
                   237
% identity
                   96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19
                  (ESSA project)
Seq. No.
                 . 168851
Seq. ID
                   LIB3234-074-P1-K1-E5
Method
                   BLASTN
NCBI GI
                   g3046851
BLAST score
                   234
                   1.0e-129
E value
Match length
                   298
% identity
                   95
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168852
                   LIB3234-074-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510397
BLAST score
                   602
E value
                   1.0e-62
                   113
Match length
% identity
                   99
NCBI Description
                  (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
                   168853
Seq. No.
Seq. ID
                   LIB3234-074-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q544122
BLAST score
                   668
                   2.0e-70
E value
Match length
                   127
                   99
% identity
NCBI Description APOCYTOCHROME F PRECURSOR >gi 629599 pir S45661
                   plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                   cytochrome f precursor - turnip chloroplast
>gi_441282_emb_CAA54307_ (X77011) cytochrome f [Brassica
```

```
rapa]
Seq. No.
                   168854
Seq. ID
                   LIB3234-074-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   g4733991
BLAST score
                   53
                   7.0e-21
E value
Match length
                   85
% identity
                   46
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T4D8 genomic
                   sequence, complete sequence
Seq. No.
                   168855
Seq. ID
                   LIB3234-074-P1-K1-F11
Method
                   BLASTN
NCBI GI
                   g3643588
BLAST score
                   233
E value
                   1.0e-128
Match length
                   288
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168856
Seq. ID
                   LIB3234-074-P1-K1-F12
Method
                   BLASTN
NCBI GI
                   q3643588
                                                    Ę.,..
BLAST score
                   153
E value
                   1.0e-80
Match length
                   169
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                  168857
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1402878
BLAST score
                   352
E value
                  2.0e-33
Match length
                  125
                  56
% identity
                  (X98130) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168858
Seq. ID
                  LIB3234-074-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  g2459406
BLAST score
                  214
                  1.0e-117
E value
Match length
                  371
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4P9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

168859

Seq. No.

Seq. ID

```
Seq. ID
                  LIB3234-074-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q4544432
BLAST score
                   293
E value
                  2.0e-26
Match length
                  62
                  85
% identity
                  (AC006955) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  168860
Seq. ID
                  LIB3234-074-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  q3702724
BLAST score
                  102
E value
                  4.0e-50
Match length
                  153
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168861
Seq. ID
                  LIB3234-074-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  q1279569
BLAST score
                  57
E value
                  3.0e-23
Match length
                  181
% identity
                  88
NCBI Description Nicotiana acuminata chloroplast JLA region, 1-1028bp
Seq. No.
                  168862
Seq. ID
                  LIB3234-074-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  g3273742
BLAST score
                  192
E value
                  1.0e-104
Match length
                  269
% identity
                  97
                  Arabidopsis thaliana lipid transfer protein 2 precursor
NCBI Description
                  (LTP2) gene, complete cds
Seq. No.
                  168863
Seq. ID
                  LIB3234-074-P1-K1-G2
Method
                  BLASTX
NCBI GI ·
                  q548847
BLAST score
                  392
E value
                  4.0e-38
Match length
                  77
                  100
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                  >gi 1086182 pir S39501 ribosomal protein S12 ~
                  curled-leaved tobacco >gi_225248_prf__1211235CG ribosomal
                  protein S12 [Nicotiana tabacum]
Seq. No.
                  168864
```

LIB3234-074-P1-K1-G3

NCBI GI

```
Method
                  BLASTX
NCBI GI
                  q125606
BLAST score
                  199
E value
                  2.0e-15
Match length
                  61
% identity
NCBI Description
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__ S12248
                  pyruvate kinase (EC 2.7.1.40) - potato
                  >gi_22576_emb_CAA37727 (X53688) pyruvate kinase [Solanum
                  tuberosum]
                  168865
Seq. No.
Seq. ID
                  LIB3234-074-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  q2660661
BLAST score
                  132
E value
                  2.0e-68
Match length
                  172
% identity
                  79
NCBI Description
                  Arabidopsis thaliana chromosome V BAC T19K24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168866
Seq. ID
                  LIB3234-074-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  q2660661
BLAST score
                  73
                  7.0e-33
E value
Match length
                  198
% identity
                  93
NCBI Description Arabidopsis thaliana chromosome V BAC T19K24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168867
Seq. ID
                  LIB3234-074-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  280
E value
                  6.0e-25
Match length
                  90
                  59
% identity
NCBI Description
                 (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  168868
Seq. ID
                  LIB3234-074-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q166570
BLAST score
                  209
                  9.0e-17
E value
Match length
                  106
% identity
                  43
NCBI Description
                 (L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.
                  168869
Seq. ID
                  LIB3234-074-P1-K1-G9
Method
                  BLASTN
```

g1279569

Match length

```
BLAST score
                   86
E value
                   1.0e-40
Match length
                   234
% identity
                   89
NCBI Description Nicotiana acuminata chloroplast JLA region, 1-1028bp
Seq. No.
                   168870
Seq. ID
                   LIB3234-074-P1-K1-H1
Method
                   BLASTN
NCBI GI
                   q3885325
BLAST score
                   315
E value
                   1.0e-177
                   377
Match length
                   97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20P8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168871
Seq. ID
                   LIB3234-074-P1-K1-H10
Method
                   BLASTN
NCBI GI
                   g3241923
BLAST score
                   274
E value
                   1.0e-153
Match length
                  290
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168872
Seq. ID
                  LIB3234-074-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3914899
BLAST score
                  195
E value
                  1.0e-15
Match length
                  45
% identity
                  78
NCBI Description
                  40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal
                  protein S4 type I [Zea mays]
Seq. No.
                  168873
                  LIB3234-074-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4519190
BLAST score
                  289
E value
                  1.0e-161
Match length
                  364
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K6A12, complete sequence
Seq. No.
                  168874
Seq. ID
                  LIB3234-074-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q543841
BLAST score
                  472
E value
                  2.0e-47
```

NCBI GI

```
% identity
                   98
NCBI Description
                   ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__$28875
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi_4630747_gb_AAD26597.1_AC007236 2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                   168875
Seq. ID
                   LIB3234-074-P1-K1-H5
Method
                   BLASTN
NCBI GI
                   g4544405
BLAST score
                   315
E value
                   1.0e-177
Match length
                   383
% identity
                   96
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F2818 genomic
                   sequence, complete sequence
Seq. No.
                   168876
Seq. ID
                   LIB3234-074-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   q2499973
BLAST score
                   418
E value
                   3.0e-41
Match length
                   103
% identity
                   83
NCBI Description
                  PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
                   >gi_1465366_emb_CAA66701_ (X98078) photosystem II
                   [Arabidopsis thaliana]
Seq. No.
                   168877
                  LIB3234-074-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2262167
BLAST score
                   506
E value
                   2.0e-51
Match length
                   103
% identity
                   (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   168878
Seq. ID
                  LIB3234-074-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g2494110
BLAST score
                  317
E value
                  1.0e-178
Match length
                  329
% identity
                  99
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168879
Seq. ID
                  LIB3234-075-P1-K1-A1
Method
                  BLASTN
```

g2351061

E value

4.0e-90

```
BLAST score
                   83
E value
                   6.0e-39
Match length
                   121
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168880
Seq. ID
                   LIB3234-075-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g2326363
BLAST score
                   428
                   2.0e-42
E value
Match length
                   117
% identity
                   74
                   (AJ001037) DNA-directed RNA polymerase [Arabidopsis
NCBI Description
                   thaliana]
                   168881
Seq. No.
Seq. ID
                   LIB3234-075-P1-K1-A12
Method
                   BLASTN
NCBI GI
                   g12235
BLAST score
                   46
E value
                   9.0e-17
Match length
                   74
% identity
                   91
NCBI Description
                  S.cereale chloroplast ribosomal protein S15 (rpS15) gene in
                   inverted repeat I (IR-I), complete cds
Seq. No.
                   168882
Seq. ID
                  LIB3234-075-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2791606
BLAST score
                  228
E value
                  6.0e-19
Match length
                  68
% identity
                  54
NCBI Description
                  (AL021287) gatB [Mycobacterium tuberculosis]
                  168883
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4512627
BLAST score
                  180
E value
                  3.0e-40
Match length
                  101
% identity
                  92
NCBI Description
                  (AC004793) Similar to gb Z29643 protein kinase C inhibitor
                  (PKCI) from Zea mays and a member of HIT family PF_01230.
                  [Arabidopsis thaliana]
Seq. No.
                  168884
Seq. ID
                  LIB3234-075-P1-K1-A5 ·
Method
                  BLASTN
NCBI GI
                  g3128139
BLAST score
                  169
```

Match length

```
Match length
                   368
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MIK19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168885
Seq. ID
                   LIB3234-075-P1-K1-A6
Method
                   BLASTN
NCBI GI
                   g4249393
BLAST score
                   365
E value
                   0.0e+00
Match length
                   369
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9J23 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168886
Seq. ID
                   LIB3234-075-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q3335169
BLAST score
                   568
E value
                   8.0e-59
Match length
                   114
% identity
                   95
NCBI Description
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                   >gi_4455197_emb_CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                   168887
                  LIB3234-075-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220635
                   324
BLAST score
E value
                  0.0e + 00
Match length
                   360
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDB19, complete sequence [Arabidopsis thaliana]
                  168888
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-B12
Method
                  BLASTN
                  g4220635
NCBI GI
BLAST score
                  113
E value
                  8.0e-57
Match length
                  206
% identity :-
                  92
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDB19, complete sequence [Arabidopsis thaliana]
                  168889
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4522003
BLAST score
                  566
                  1.0e-58
E value
```

```
% identity
NCBI Description
                  (AC007069) putative protein kinase [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3234-075-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g2605714
BLAST score
                   356
E value
                   6.0e-34
Match length
                   108
% identity
                   71
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
NCBI Description
                   168891
Seq. No.
Seq. ID
                   LIB3234-075-P1-K1-B7
Method
                  BLASTX
NCBI GI
                   g2129727
BLAST score
                   316
E value
                   3.0e-29
Match length
                   96
% identity
                   74
NCBI Description
                  RNA-binding protein 37 - Arabidopsis thaliana >qi 1174153
                   (U44134) RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  168892
Seq. ID
                  LIB3234-075-P1-K1-B9
Method
                  BLASTN
                  g4558586
NCBI GI
BLAST score
                  255
E value
                  1.0e-141
Match length
                  360
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T518 sequence,
                  complete sequence
Seq. No.
                  168893
Seq. ID
                  LIB3234-075-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  g12219
BLAST score
                  85
E value
                  5.0e-40
Match length
                  260
% identity
                  93
NCBI Description
                  Mustard chloroplast trnk gene for tRNA-Lys(UUU)
Seq. No.
                  168894
Seq. ID
                  LIB3234-075-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  q2842474
BLAST score
                  34
E value
                  1.0e-09
Match length
                  58
% identity
                  90
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
```

(ESSAII project)

Method

BLASTX

```
Seq. No.
                   168895
Seq. ID
                   LIB3234-075-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g4490316
BLAST score
                   190
E value
                   3.0e-21
Match length
                   108
% identity
                   52
NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.
                   168896
Seq. ID
                  LIB3234-075-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                   217
E value
                  1.0e-17
Match length
                  120
% identity
                  36
NCBI Description vicilin gene B [Saguinus oedipus]
Seq. No.
                  168897
Seq. ID
                  LIB3234-075-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g4510342
BLAST score
                  186
E value
                  5:0e-14
Match length
                  110
% identity
                  46
NCBI Description
                  (AC006921) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  168898
Seq. ID
                  LIB3234-075-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1944201
BLAST score
                  160
E value
                 6.0e-11
Match length
                  55 .
% identity
                  60
NCBI Description
                  (AB002818) flavonoid 3-O-glucosyltransferase [Perilla
                  frutescens]
Seq. No.
                  168899
Seq. ID
                  LIB3234-075-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3024434
BLAST score
                  296
E value
                  7.0e-27
Match length
                  88
% identity
                  70
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
                  PROTEIN HOMOLOG 1) (TBP-1) >gi 2564337 dbj BAA22951
                  (D88663) Tat binding protein 1 [Brassica rapa]
Seq. No.
                  168900
Seq. ID
                  LIB3234-075-P1-K1-D1
```

E value

8.0e-55

```
NCBI GI
                  q3335171
BLAST score
                  547
                  3.0e-56
E value
Match length
                  116
% identity
                  90
NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
Seq. No.
                  168901
Seq. ID
                  LIB3234-075-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g2656026
BLAST score
                  346
E value
                  0.0e + 00
Match length
                  362
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  168902
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g4006827
BLAST score
                  539
                . 2.0e-55
E value
Match length
                  116
% identity
                  93
NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]
                  168903
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2851581
BLAST score
                  517
E value
                  8.0e-53
Match length
                  106
% identity
                  96
                  DNA-DIRECTED RNA POLYMERASE BETA CHAIN
NCBI Description
                  >gi 2196464 emb CAA74024 (Y13690) DNA-dependent RNA
                  polymerase subunit beta [Arabidopsis thaliana]
Seq. No.
                  168904
Seq. ID
                  LIB3234-075-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g4159701
BLAST score
                  42
E value
                  2.0e-14
Match length
                  124
                  94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K22G18, complete sequence
Seq. No.
                  168905
Seq. ID
                  LIB3234-075-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1864017
BLAST score
                  534
```

Match length

```
104
Match length
% identity
                   98
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   168906
Seq. ID
                   LIB3234-075-P1-K1-D7
Method
                   BLASTX
NCBI GI
                  g3335169
BLAST score
                   488
E value
                   2.0e-49
Match length
                   117
                   76
% identity
NCBI Description
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                   >gi_4455197 emb CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
                  168907
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4164473
BLAST score
                  175
                  1.0e-12
E value
Match length
                   40
                  78
% identity
NCBI Description
                   (AF061157) negatively light-regulated protein [Vernicia
                  fordii]
                  168908
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2129767
BLAST score
                  485
                  4.0e-49
E value
                  105
Match length
                  89
% identity
NCBI Description
                  vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
                  precursor - Arabidopsis thaliana >gi 1805364 dbj BAA09615
                  (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
                  168909
Seq. ID
                  LIB3234-075-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g3510341
BLAST score
                  228
E value
                  1.0e-125
Match length
                  362
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFC16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168910
                  LIB3234-075-P1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4199934
BLAST score
                  124
                  3.0e-63
E value
```

NCBI Description

```
95
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   168911
Seq. ID
                   LIB3234-075-P1-K1-E3
                  BLASTN
Method
NCBI GI
                  g2351066
                   37
BLAST score
E value
                   2.0e-11
Match length
                   138
% identity
                   88
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOP9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168912
Seq. ID
                  LIB3234-075-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3980388
BLAST score
                   288
E value
                   6.0e-26
Match length
                   61
                  95
% identity
                   (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                  thaliana
                  168913
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g2351066
BLAST score
                  254
E value
                  1.0e-141
Match length
                  315
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOP9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168914
Seq. ID
                  LIB3234-075-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g4159712
BLAST score
                  87
E value
                  2.0e-41
Match length
                  126
% identity
                  93
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MWI23, complete sequence
                  168915
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g132675
BLAST score
                  351
                  2<sup>-</sup>.0e-33
E value
                  82
Match length
                  88
% identity
```

CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi 71222 pir R5NT14

```
[Nicotiana tabacum] >gi 225233 prf 1211235BQ ribosomal
                  protein L14 [Nicotiana tabacum]
                  168916
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-F11
Method
                  BLASTN
                  g4589411
NCBI GI
                  55
BLAST score
                  2.0e-22
E value
Match length
                  63
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F5H8, complete sequence
                  168917
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-F3
                  BLASTX
Method
NCBI GI
                  g4455159
BLAST score
                  301
                  2.0e-27
E value
Match length
                  118
% identity
                  61
                  (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                  168918
Seq. No.
                  LIB3234-075-P1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1695719
                  531
BLAST score
                  2.0e-54
E value
                  125
Match length
% identity
                  86
                  (D89342) luminal binding protein [Arabidopsis thaliana]
NCBI Description
                  168919
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3128172
BLAST score
                  491
                  1.0e-49
E value
Match length
                  108
                  92
% identity
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  168920
Seq. No.
Seq. ID
                  LIB3234-075-P1-K1-F7
Method
                  BLASTN
                  g4159712
NCBI GI
BLAST score
                  361
E value
                  0.0e+00
Match length
                  361
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
```

ribosomal protein L14 - common tobacco chloroplast >gi_11864_emb_CAA77379_ (Z00044) ribosomal protein L14

MWI23, complete sequence

Seq. No.

```
Seq. No.
                   168921
Seg. ID
                   LIB3234-075-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g2924258
BLAST score
                   474
                   9.0e-48
E value
Match length
                   119
% identity
                   84
NCBI Description
                  (200044) RNA polymerase beta'' subunit [Nicotiana tabacum]
Seq. No.
                   168922
Seq. ID
                   LIB3234-075-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   g3702724
BLAST score
                   334
E value
                   0.0e+00
Match length
                   362
% identity
                   98
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168923
Seq. ID
                   LIB3234-075-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q2062169
BLAST score
                   507
E value
                   1.0e-51
Match length
                   119
% identity
                   73
                   (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   168924
                   LIB3234-075-P1-K1-H3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3128136
BLAST score
                   349
E value
                   0.0e+00
Match length
                   365
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K1F13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168925
Seq. ID
                   LIB3234-075-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q1345967
BLAST score
                   68
E value
                   5.0e-29
Match length
                   93
% identity
                   72
NCBI Description
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                   (VERSION 2) >gi_322649_pir__A44227 omega-3 fatty acid desaturase (EC 1.14.99.-) - rape >gi_167148 (L01418)
                   linoleic acid desaturase [Brassica napus]
```

```
Seq. ID
                   LIB3234-076-P1-K1-A1
Method
                  BLASTX '
NCBI GI
                   g2246456
BLAST score
                   563
                   3.0e-58
E value
                   106
Match length
                   97
% identity
                  (U71400) S-adenosyl-methionine-sterol-C-methyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  168927
Seq. ID
                  LIB3234-076-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2244906
BLAST score
                  146
E value
                  1.0e-16
Match length
                  92
% identity
                  54
NCBI Description
                  (Z97339) indole-3-acetate beta-glucosyltransferase
                  [Arabidopsis thaliana]
Seq. No.
                  168928
Seq. ID
                  LIB3234-076-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  g2335191
BLAST score
                  36
                  9.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description
                  Arabidopsis thaliana bHLH protein (Atmyc-146) gene,
                  complete cds
Seq. No.
                  168929
Seq. ID
                  LIB3234-076-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2244906
BLAST score
                  336
E value
                  1.0e-31.
Match length
                  94
% identity
NCBI Description
                  (Z97339) indole-3-acetate beta-glucosyltransferase
                  [Arabidopsis thaliana]
Seq. No.
                  168930
Seq. ID
                  LIB3234-076-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g1839188
BLAST score
                  168
E value
                  7.0e-12
Match length
                  94
% identity
                  57
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
Seq. No.
                  168931
                  LIB3234-076-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
```

q4835233

BLAST score

```
BLAST score
                  535
E value
                  6.0e-55
Match length
                  108
% identity
                  100
NCBI Description
                  (AL049862) putative protein 1 photosystem II
                  oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                  168932
Seq. ID
                  LIB3234-076-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g541847
BLAST score
                  616
E value
                  2.0e-64
                  114
Match length
                  98
% identity
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
Seq. No.
                  168933
Seq. ID
                  LIB3234-076-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g2914688
BLAST score
                  184
E value
                  4.0e-99
Match length
                  360
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F24L7 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168934
Seq. ID
                  LIB3234-076-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  555
E value
                  3.0e-57
Match length
                  118
% identity
                  88
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  168935
Seq. ID
                  LIB3234-076-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g16428
BLAST score
                  180
                  1.0e-96
E value
Match length
                  368
                  98
% identity
NCBI Description
                  A.thaliana posF21 gene
Seq. No.
                  168936
                  LIB3234-076-P1-K1-B9
Seq. ID
                  BLASTN
Method
                  g3449332
NCBI GI
```

BLASTN

```
0.0e + 00
E value
Match length
                    355
% identity
                    99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MSF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                    168937
Seq. ID
                    LIB3234-076-P1-K1-C1
Method
                    BLASTN
NCBI GI
                    g2924257
BLAST score
                    61
                    1.0e-25
E value
Match length
                    85
% identity
                    93
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                    168938
Seq. ID
                    LIB3234-076-P1-K1-C10
Method
                    BLASTX
NCBI GI
                    q464987
BLAST score
                    524
                    1.0e-53
E value
Match length
                    96:
                   .100
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN 🚕
NCBI Description
                    LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                    >gi_421858_pir__S32672 ubiquitin--protein ligase (EC
6.3.2.19) UBC10 - Arabidopsis thaliana
                    >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin
                    conjugating enzyme [Arabidopsis thaliana]
Seq. No.
                    168939
Seq. ID
                   LIB3234-076-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   g11576
BLAST score
                    132
                    2.0e-68
E value
Match length
                    164
                    95
% identity
NCBI Description
                   Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
                   NADH dehydrogenase and ORF
Seq. No.
                   168940
Seq. ID
                   LIB3234-076-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q4587550
BLAST score
                   237
E value
                   6.0e-20
Match length
                   90
                   56
% identity
NCBI Description
                    (AC006577) EST gb_R64848 comes from this gene. [Arabidopsis
                   thaliana]
                   168941
Seq. No.
Seq. ID
                   LIB3234-076-P1-K1-C2
```

% identity

100

```
NCBI GI
                   q3738313
BLAST score
                   50
                   4.0e-19
E value
Match length
                   145
% identity
                   83
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T29E15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168942
Seq. ID
                   LIB3234-076-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   q2499945
BLAST score
                   523
E value
                   2.0e-53
Match length
                   105
% identity
                   100
                   URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) /
                   orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                   Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)
                   pyrE-F [Arabidopsis thaliana]
Seq. No.
                   168943
                   LIB3234-076-P1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g128877
BLAST score
                   343
E value
                   2.0e-32
Match length
                   100
% identity
                   73
                   NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4L, CHLOROPLAST
NCBI Description
                   >gi 66167 pir DENTNL NADH dehydrogenase (ubiquinone) (EC
                   1.6.5.3) chain 4L - common tobacco chloroplast
                   >gi 1223668 emb CAA77396 (Z00044) NADH dehydrogenase ND4L
                   subunit [Nicotiana tabacum] >gi 225256 prf 1211235CQ NADH
                   dehydrogenase 4L-like ORF 101 [Nicotiana tabacum]
Seq. No.
                   168944
                   LIB3234-076-P1-K1-C6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2924257
BLAST score
                   37
E value
                   2.0e-11
Match length
                   89
                   91
% identity
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                   168945
Seq. ID
                  LIB3234-076-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   g2252823
BLAST score
                  178
E value
                   8.0e-96
Match length
                  178
```

% identity

93

```
NCBI Description Arabidopsis thaliana BAC IG005I10
 Seq. No.
                     168946
 Seq. ID
                     LIB3234-076-P1-K1-C8
Method
                     BLASTN
NCBI GI
                     g2252823
BLAST score
                     51
E value
                     6.0e-20
Match length
                     83
% identity
                     90
NCBI Description
                    Arabidopsis thaliana BAC IG005I10
Seq. No.
                     168947
Seq. ID
                    LIB3234-076-P1-K1-C9
Method
                    BLASTX
NCBI GI
                     g1864017
BLAST score
                     548
E value
                    2.0e-56
Match length
                    104
% identity
                    100
NCBI Description
                    (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                    168948
Seq. ID
                    LIB3234-076-P1-K1-D1
Method ~
                    BLASTX
NCBI GI
                    q114532
BLAST score
                    548
E value
                    2.0e-56
Match length
                    122
% identity
                    89
                    ATP SYNTHASE ALPHA CHAIN >gi_67824_pir_PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain -
NCBI Description
                    common tobacco chloroplast >gi_11769_emb_CAA23471 (V00162)
                    alpha subunit of ATPase [Nicotiana tabacum]
                    >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit
[Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha
                    [Nicotiana tabacum]
Seq. No.
                    168949
                    LIB3234-076-P1-K1-D3
Seq. ID
Method
                    BLASTN
NCBI GI
                    q3327867
BLAST score
                    367
E value
                    0.0e + 00
Match length
                    367
% identity
NCBI Description
                    Arabidopsis thaliana CIP7 mRNA for COP1-Interacting Protein
                    7, complete cds
Seq. No.
                    168950
Seq. ID
                    LIB3234-076-P1-K1-D5
Method
                    BLASTX
NCBI GI
                    q2288887
BLAST score
                    585
E value
                    8.0e-61
Match length
                    117
```

_ *

```
(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
NCBI Description
                    thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]
                    >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                    [Arabidopsis thaliana]
Seq. No.
                    168951
Seq. ID
                    LIB3234-076-P1-K1-D7
Method
                    BLASTX
NCBI GI
                    g1592679
BLAST score
                    261
E value
                    9.0e-23
Match length
                    71
                    77
% identity
NCBI Description
                   (X91915) LEA D113 homologue typel [Arabidopsis thaliana]
Seq. No.
                    168952
                   LIB3234-076-P1-K1-D8
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4090884
BLAST score
                    511
E value
                    4.0e-52
Match length
                    97
                   100
% identity
NCBI Description
                   (AF025333) vesicle-associated membrane protein 7B;
                   synaptobrevin 7B [Arabidopsis thaliana]
Seq. No.
                   168953
Seq. ID
                   LIB3234-076-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   q4760411
BLAST score
                   340
                   0.0e+00
E value
Match length
                   365
% identity
                   98
NCBI Description
                   Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
                   complete sequence
Seq. No.
                   168954
Seq. ID
                   LIB3234-076-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   q1705463
BLAST score
                   471
E value
                   2.0e-47
Match length
                   104
% identity
                   BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547 pir
NCBI Description
                   biotin sythase - Arabidopsis thaliana >\overline{gi}_10453\overline{1}6 (\overline{U2}4147)
                   biotin sythase [Arabidopsis thaliana] >gi 1403662 (U31806)
                   BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413)
                   biotin synthase [Arabidopsis thaliana] >gi_2288983
                   (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
                  ->gi 1589016 prf 2209438A biotin synthase [Arabidopsis
                   thaliana]
Seq. No.
                   168955
Seq. ID
```

LIB3234-076-P1-K1-E10

Seq. No.

```
Method
                   BLASTN
NCBI GI
                   q2828185
BLAST score
                   262
E value
                   1.0e-145
Match length
                   353
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUD21, complete sequence [Arabidopsis thaliana]
                   168956
Seq. No.
Seq. ID
                   LIB3234-076-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   70
E value
                   4.0e-31
Match length
                   134
% identity
                   89
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                   168957
Seq. ID
                   LIB3234-076-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q4559372
BLAST score
                   241
E value
                   2.0e-20
Match length
                   61
% identity
                   77
                   (AC006585) putative CONSTANS protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4646235_gb_AAD26898.1 AC007266 6 (AC007266) putative
                   CONSTANS protein [Arabidopsis thaliana]
Seq. No.
                   168958
Seq. ID
                   LIB3234-076-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g1169515
BLAST score
                   220
E value
                   3.0e-18
                   70
Match length
                   70
% identity
                   EM-LIKE PROTEIN GEA1 >gi 2119768 pir S34819 embryonic
NCBI Description
                   abundant protein Eml - Arabidopsīs thaliana
                   >gi_298070_emb_CAA77509_ (Z11158) Em protein [Arabidopsis
thaliana] >gi_298072_emb_CAA77979_ (Z11921) Em protein
                   homologue [Arabidopsis thaliana] >gi 3068708 (AF049236) Em1
                   protein [Arabidopsis thaliana]
Seq. No.
                   168959
Seq. ID
                   LIB3234-076-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q4558547
BLAST score
                   281
E value
                   4.0e-25
Match length
                   121
% identity
NCBI Description
                   (AC007138) hypothetical protein [Arabidopsis thaliana]
```

BLASTX

```
Seq. ID
                   LIB3234-076-P1-K1-E7
Method
                   BLASTX
NCBI GI
                 g3176874
BLAST score
                   406
E value
                   8.0e-40
Match length
                   116
% identity
                   63
NCBI Description
                   (AF065639) cucumisin-like serine protease [Arabidopsis
                   thaliana]
Seq. No.
                   168961
Seq. ID
                   LIB3234-076-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   g3789706
BLAST score
                   163
E value
                   1.0e-86
Match length
                   325
% identity
                   88
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   168962
Seq. ID
                  LIB3234-076-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1628583 ·
BLAST score
                   625
E value
                  2.0e-65
Match length
                  120
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  168963
Seq. ID
                  LIB3234-076-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g2264309
BLAST score
                  360
E value
                  0.0e+00
Match length
                  360
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJJ3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  168964
Seq. ID
                  LIB3234-076-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2924258
BLAST score
                  563
E value
                  3.0e-58
Match length
                  120
% identity
NCBI Description
                  (200044) RNA polymerase beta'' subunit [Nicotiana tabacum]
Seq. No.
                  168965
Seq. ID
                  LIB3234-076-P1-K1-F2
```

BLASTN

```
NCBI GI
                  q3892057
BLAST score
                  585
                  9.0e-61
E value
Match length
                  122
                  49
% identity
                  (AC002330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  168966
Seq. ID
                  LIB3234-076-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  g120675
BLAST score
                  458
                  7.0e-46
E value
Match length
                  105
% identity
                  84
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                  >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                  alba]
                  168967
Seq. No.
Seq. ID
                  LIB3234-076-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3860242
BLAST score
                  298
E value
                  1.0e-167 ;
                  374
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome I BAC T13M11 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  168968
Seq. ID
                  LIB3234-076-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q4455336
BLAST score
                  422
E value
                  1.0e-41
Match length
                  77
                  100
% identity
NCBI Description
                  (AL035525) pectinesterase-like protein [Arabidopsis
                  thaliana]
                  168969
Seq. No.
Seq. ID
                  LIB3234-076-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g4455321
                                                   5,00
BLAST score
                  45
E value
                  3.0e-16
Match length
                  85
                  89
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
                  (ESSAII project)
Seq. No.
                  168970
Seq. ID
                  LIB3234-076-P1-K1-G10
```

```
NCBI GI
                    q3298532
 BLAST score
                    340
                    0.0e+00
 E value
 Match length
                    360
                    99
 % identity
 NCBI Description Arabidopsis thaliana chromosome II BAC T26B15 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168971
                   LIB3234-076-P1-K1-G11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2980771
 BLAST score
                    435
 E value
                   3.0e-43
 Match length
                   101
 % identity
                   86
 NCBI Description
                    (AL022198) chloroplast omega-6 fatty acid desaturase (fad6)
                    [Arabidopsis thaliana]
 Seq. No.
                   168972
                   LIB3234-076-P1-K1-G2
 Seq. ID
Method
                   BLASTN .
NCBI GI
                   q4468103
BLAST score
                   333
E value
                   0.0e + 00
Match length
                   362
 % identity
                   98
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
                   (ESSA project)
Seq. No.
                   168973
Seq. ID
                   LIB3234-076-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   q3298532
BLAST score
                   48
E value
                   5.0e-18
Match length
                   86
% identity
                   94
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T26B15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   168974
Seq. ID
                   LIB3234-076-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g2244750
BLAST score
                   494
E value
                   4.0e-50
Match length
                   110
% identity
                   87.
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
Seq. No.
```

168975

LIB3234-076-P1-K1-G6

Method BLASTX NCBI GI q1169601

Seq. ID

```
BLAST score
                    389
E value
                    9.0e-38
Match length
                    98
% identity
                    80
NCBI Description
                    OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
                    >gi_493068 (U09503) chloroplast omega-6 fatty acid
                    desaturase [Arabidopsis thaliana]
Seq. No.
                    168976
Seq. ID
                    LIB3234-076-P1-K1-H1
Method
                    BLASTX
NCBI GI
                    q3355308
BLAST score
                    258
E value
                    2.0e-22
Match length
                    50
% identity
                    100
NCBI Description
                   (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
Seq. No.
                    168977
Seq. ID
                    LIB3234-076-P1-K1-H10
Method
                    BLASTN
NCBI GI
                    g2262135
BLAST score
                    117
E value
                    3.0e-59
Match length
                    216
% identity
                    93
                   Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
NCBI Description
                    cM, complete sequence
Seq. No.
                    168978
Seq. ID
                    LIB3234-076-P1-K1-H12
Method
                   BLASTX
NCBI GI
                    g3367596
BLAST score
                    188
                    4.0e-23
E value
Match length
                    83
% identity
                    68
NCBI Description
                   (AL031135) putative protein [Arabidopsis thaliana]
Seq. No.
                   168979
Seq. ID
                   LIB3234-076-P1-K1-H3
Method
                   {\tt BLASTX}
NCBI GI
                   g1345973
BLAST score
                    677
E value
                   1.0e-71
Match length
                   122
                   100
% identity
NCBI Description
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                   >gi_541882_pir_JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                   omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                   [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                   microsomal omega-3 fatty acid desaturase (Arabidopsis
                   thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
```

E value

2.0e-47

```
Seq. No.
                   168980
 Seq. ID
                   LIB3234-076-P1-K1-H4
 Method
                   BLASTN
 NCBI GI
                   g2760169
 BLAST score
                   151
 E value
                   1.0e-79
 Match length
                   167
 % identity
                   98
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFB13, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   168981
 Seq. ID
                   LIB3234-076-P1-K1-H5
 Method
                   BLASTN
 NCBI GI
                   g2262135
 BLAST score
                   151
 E value
                   1.0e-79
Match length
                   214
 % identity
                   93
NCBI Description
                   Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                   cM, complete sequence
Seq. No.
                   168982
Seq. ID
                   LIB3234-076-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q99837
BLAST score
                   195
E value
                   4.0e-15
Match length
                   97
% identity
                   48
NCBI Description
                   2S storage protein - wild cabbage >gi_17878_emb_CAA46783_
                   (X65970) 2S storage protein [Brassica oleracea]
                   >gi_17880_emb_CAA46172_ (X65038) 2S storage protein
                   [Brassica oleracea]
Seq. No.
                   168983
Seq. ID
                   LIB3234-077-P1-K1-A1
Method .
                   BLASTX
NCBI GI
                   g120667
BLAST score
                   181
E value
                   8.0e-14
Match length
                   55
% identity
                   69
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                   thaliana >gi 166706 (M64116) cystolic
                   glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                   thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                   dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   168984
Seq. ID
                  LIB3234-077-P1-K1-A10
Method
                   BLASTX
NCBI GI
                  q3249096
BLAST score
                   471
```

```
Match length
                   108
 % identity
                   (AC003114) Match to mRNA for importin alpha-like protein 4
NCBI Description
                   (impa4) gb_Y14616 from A. thaliana. ESTs gb N96440,
                   gb_N37503, gb_N37498 and gb_T42198 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   168985
Seq. ID
                   LIB3234-077-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   q4679028
BLAST score
                   58
E value
                   7.0e-26
Match length
                   130
% identity
                   47
NCBI Description
                  (AF077207) HSPC021 [Homo sapiens]
Seq. No.
                   168986
Seq. ID
                   LIB3234-077-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g4490737
BLAST score
                   333
E value
                   4.0e-31
Match length
                   127
% identity
                   56
NCBI Description
                  (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   168987
Seq. ID
                   LIB3234-077-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g3980396
BLAST score
                   501
                   7.0e-51
E value
Match length
                   95
% identity
                   99
NCBI Description
                   (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
                   thaliana]
Seq. No.
                   168988
Seq. ID
                   LIB3234-077-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g231442
BLAST score
                   63
E value
                   4.0e-37
Match length
                   126
% identity
                   59
NCBI Description
                  HYPOTHETICAL 260 KD PROTEIN (ORF 2216) >gi_336938 (M81884)
                  ORF2216 [Epifagus virginiana] >gi_336942 (\overline{M}81884) ORF2216
                   [Epifagus virginiana]
Seq. No.
                  168989
Seq. ID
                  LIB3234-077-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q2829918
BLAST score
                  601
E value
                  1.0e-62
Match length
                  120
```

.

BLAST score

```
% identity
                   98
NCBI Description
                   (AC002291) similar to "tub" protein gp U82468 2072162
                   [Arabidopsis thaliana]
                  168990
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-A8
                  BLASTX
Method
NCBI GI
                  g3915961
BLAST score
                  592
E value
                  1.0e-61
Match length
                  124
                  90
% identity
                  HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
NCBI Description
                  >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana
                  tabacum] >gi 2924285 emb CAA77438 (Z00044) hypothetical
                  protein [Nicotiana tabacum]
Seq. No.
                  168991
Seq. ID
                  LIB3234-077-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g3915961
BLAST score
                  400
E value
                  4.0e-39
Match length
                  106
                  75
% identity
                  HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
NCBI Description
                  >gi 2924274 emb CAA77427 (Z00044) Ycf2 protein [Nicotiana
                  tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
                  protein [Nicotiana tabacum]
Seq. No.
                  168992
Seq. ID
                  LIB3234-077-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g3885325
BLAST score
                  324
E value
                  0.0e + 00
                  336
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T20P8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  168993
Seq. No.
                  LIB3234-077-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1486472
BLAST score
                  406
E value
                  1.0e-39
Match length
                  94
                  85
% identity
                  (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                  tuberosum]
                  168994
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-B2
                  BLASTX
Method
                  g4678311
NCBI GI
```

```
3.0e-47
E value
                   90
Match length
                   99
% identity
NCBI Description
                   (AL049655) aquaporin/MIP-like protein [Arabidopsis
                   thaliana]
                   168995
Seq. No.
Seq. ID
                   LIB3234-077-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g3808062
BLAST score
                   155
                   2.0e-10
E value
Match length
                   64
% identity
                   45
NCBI Description
                  (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                   168996
                   LIB3234-077-P1-K1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4199934
BLAST score
                   275
E value
                   1.0e-153
                   279
Match length
                   100
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  168997
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-C11
Method
                  BLASTN
NCBI GI
                   g4757403
BLAST score
                   252
E value
                   1.0e-139
Match length
                   382
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
                  168998
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3445209
BLAST score
                  526
                  8.0e-54
E value
                  129
Match length
% identity
NCBI Description
                  (AC004786) putative serine carboxypeptidase I [Arabidopsis
                  thaliana]
                  168999
Seq. No.
Seq. ID
                  LIB3234-077-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3953466
                  585
BLAST score
E value
                  1.0e-60
Match length
                  131
% identity
                  87
```

```
NCBI Description (AC002328) F20N2.11 [Arabidopsis thaliana]
Seq. No.
                    169000
Seq. ID
                    LIB3234-077-P1-K1-C5
Method
                    BLASTN
NCBI GI
                    g2760165
BLAST score
                    144
E value
                   .3.0e-75
Match length
                    335
% identity
                    95
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                    169001
Seq. ID
                    LIB3234-077-P1-K1-C6
                    BLASTX
Method
NCBI GI
                    g4587529
BLAST score
                    369
E value
                    8.0e-36
Match length
                   78
% identity
                    90
NCBI Description
                    (AC007060) Strong similarity to F19I3.2 gi 3033375 putative
                   berberine bridge enzyme from Arabidopsis thaliana BAC
                   gb AC004238. EST gb_H76902 comes from this gene
Seq. No.
                   169002
Seq. ID
                   LIB3234-077-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g544424
BLAST score
                   267
E value
                   2.0e-23
Match length
                   86
% identity
                   62
                   GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__$30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                   169003
Seq. ID
                   LIB3234-077-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q3395432
BLAST score
                   260
E value
                   1.0e-22
Match length
                   89
% identity
                   56
NCBI Description
                   (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   169004
Seq. ID
                   LIB3234-077-P1-K1-C9
Method<sup>*</sup>
                   BLASTN
NCBI GI
                   g2656026
BLAST score
                   250
E value
                   1.0e-138
```

```
293
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDF20
Seq. No.
                   169005
Seq. ID
                   LIB3234-077-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   q4204277
BLAST score
                   654
E value
                   8.0e-69
Match length
                   121
                   100
% identity
NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   169006
Seq. ID
                   LIB3234-077-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g544424
BLAST score
                   160
E value
                   2.0e-20
Match length
                   74
                   77
% identity
NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__$30147
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                   169007
Seq. ID
                   LIB3234-077-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g4006881
BLAST score
                   447
E value
                   2.0e-44
Match length
                   115
                   80
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                   169008
Seq. No.
Seq. ID
                   LIB3234-077-P1-K1-D3
                   BLASTX
Method
NCBI GI
                   q4006881
BLAST score
                   361
E value
                   2.0e-34
Match length
                   109
                   72
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   169009
Seq. ID
                   LIB3234-077-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   g2832611
BLAST score
                   379
E value
                  0.0e+00
```

```
Match length
                   391
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
                   (ESSAII project)
Seq. No.
                   169010
                   LIB3234-077-P1-K1-D7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3461834
BLAST score
                   268
E value
                   1.0e-149
                   358
Match length
                   97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9I4 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169011
Seq. ID
                   LIB3234-077-P1-K1-D8
Method
                   BLASTX
NCBI GI
                  g4309732
BLAST score
                  156
E value
                   2.0e-10
Match length
                  110
% identity
                   42
NCBI Description
                  (AC006439) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   169012
Seq. ID
                  LIB3234-077-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g12279
BLAST score
                  35
E value
                  4.0e-10
Match length
                  43
% identity
NCBI Description
                  Spinach chloroplast genes for the D2 and 44 kd reaction
                  centre, chlorophyll a-binding protein and for tRNA-Ser
                   (UGA)
Seq. No.
                  169013
Seq. ID
                  LIB3234-077-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q4063536
BLAST score
                  604
E value
                  5.0e-63
Match length
                  120
% identity
                  (AF035900) ATP synthase beta subunit [Capparis spinosa]
NCBI Description
Seq. No.
                  169014
Seq. ID
                  LIB3234-077-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g4586098
BLAST score
                  224
E value
                  1.0e-123
Match length
                  349
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
```

Seq. ID

(ESSA project) Seq. No. 169015 Seq. ID LIB3234-077-P1-K1-E3 Method BLASTX NCBI GI g3128188 BLAST score 550 E value 1.0e-56 Match length 109 % identity 94 NCBI Description (AC004521) putative beta-glucosidase [Arabidopsis thaliana] Seq. No. 169016 Seq. ID LIB3234-077-P1-K1-E7 Method BLASTN NCBI GI g4586241 BLAST score 378 E value 0.0e+00Match length 394 % identity 99 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project) Seq. No. 169017 Seq. ID LIB3234-077-P1-K1-E8 Method BLASTN NCBI GI g4510338 BLAST score 391 E value 0.0e+00Match length 395 % identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence Seq. No. 169018 Seq. ID LIB3234-077-P1-K1-E9 Method BLASTX NCBI GI g3080442 BLAST score 705 E value 8.0e-75 Match length 128 % identity NCBI Description (AL022605) putative protein [Arabidopsis thaliana] Seq. No. 169019 Seq. ID LIB3234-077-P1-K1-F10 Method BLASTX NCBI GI g2342690 BLAST score 243 E value 1.0e-20 Match length % identity (AC000106) Similar to Homo copine I (gb_U83246). NCBI Description [Arabidopsis thaliana] Seq. No. 169020

LIB3234-077-P1-K1-F11

```
Method
                    BLASTX
NCBI GI
                    g135858
BLAST score
                    292
E value
                   2.0e-26
Match length
                   57
                   100
% identity
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                   >gi 99760 pir S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
                   tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                    [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast
                   intrinsic protein alpha [Arabidopsis Thaliana]
Seq. No.
                   169021
Seq. ID
                   LIB3234-077-P1-K1-F12
Method
                   BLASTN
NCBI GI
                   g4582411
BLAST score
                   110
E value
                   7.0e-55
Match length
                   130
% identity
                   96
                   Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,
NCBI Description
                   complete sequence
Seq. No.
                   169022
Seq. ID
                   LIB3234-077-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   g2828180
                   234
BLAST score
E value
                   1.0e-129
Match length
                   392
% identity
                   98
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MDK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169023
Seq. ID
                   LIB3234-077-P1-K1-F4
Method
                   BLASTN
NCBI GI
                   g4589437
BLAST score
                   38
E value
                   3.0e-12
Match length
                   182
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MPN9, complete sequence
Seq. No.
                   169024
Seq. ID
                   LIB3234-077-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   q16181
BLAST score
                   120
E value
                   4.0e-61
Match length
                   128
% identity
                   A.thaliana gene for tonoplast intrinsic protein
NCBI Description
```

alpha-TIP(Ara) >gi_166622_gb_M84343 ATHATIP Arabidopsis

```
complete cds
 Seq. No.
                   169025
 Seq. ID
                   LIB3234-077-P1-K1-F8
 Method
                   BLASTX
 NCBI GI
                   g1110531
 BLAST score
                   171
 E value
                   3.0e-12
 Match length
                   124
 % identity
                   37
 NCBI Description
                   (U40570) autoantigen Ku86 [Mesocricetus auratus]
 Seq. No.
                   169026
 Seq. ID
                   LIB3234-077-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g2252841
BLAST score
                   492
E value
                   8.0e-50
Match length
                   125
% identity
                   75
NCBI Description
                  (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                   169027
Seq. ID
                   LIB3234-077-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   72
E value
                   8.0e-24
Match length
                   106
% identity
                   64
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   169028
Seq. ID
                  LIB3234-077-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g1619602
BLAST score
                   383
E value
                   5.0e-37
Match length
                   91
% identity
                   79
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  169029
Seq. ID
                 : LIB3234-077-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2129577
BLAST score
                  429
E value
                  2.0e-42
Match length
                  83
% identity
                  99
NCBI Description
                  DnaJ homolog protein - Arabidopsis thaliana >gi_727357
                  (U22340) DnaJ homolog [Arabidopsis thaliana]
Seq. No.
                  169030
```

thaliana tonoplast intrinsic protein (alpha-TIP) gene,

BLASTX

```
Seq. ID
                   LIB3234-077-P1-K1-G4
 Method
                   BLASTN
NCBI GI
                   g2924505
 BLAST score
                   301
E value
                   1.0e-169
Match length
                   393
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13
                   (ESSAII project)
Seq. No.
                   169031
Seq. ID
                   LIB3234-077-P1-K1-G5
Method
                   BLASTN
NCBI GI
                   g4455339
BLAST score
                   125
E value
                   7.0e-64
Match length
                   199
% identity
                   98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
                   (ESSAII project)
Seq. No.
                   169032
Seq. ID
                   LIB3234-077-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g4115921
BLAST score
                   413
E value
                   1.0e-40
Match length
                   121
% identity
                   62
NCBI Description
                   (AF118222) F3H7.4 gene product [Arabidopsis thaliana]
                  >gi_4539434_emb_CAB40022.1_ (AL049523) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                  169033
Seq. ID
                  LIB3234-077-P1-K1-G9
Method
                  BLASTX
                  q2970654
NCBI GI
BLAST score
                  239
E value
                  4.0e-20
Match length
                  95
% identity
                  57
NCBI Description
                  (AF052058) ferritin subunit cowpea2 precursor [Vigna
                  unguiculata]
Seq. No.
                  169034
                  LIB3234-077-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4337195
BLAST score
                  159
E value
                  9.0e-11
Match length
                  44
% identity
NCBI Description
                  (AC006403) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  169035
Seq. ID
                  LIB3234-077-P1-K1-H11
```

```
NCBI GI
                    q3915866
 BLAST score
                    187
 E value ..
                    5.0e-14
 Match length
                    58
 % identity
                    76
                    GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
NCBI Description
                    >gi_2995455_emb_CAA62901 (X91787) tRNA-glutamine
                    synthetase [Lupinus luteus]
Seq. No.
                    169036
Seq. ID
                    LIB3234-077-P1-K1-H3
Method
                    BLASTN
NCBI GI
                    q3860242
BLAST score
                    330
                    0.0e+00
E value
Match length
                    389
                    96
% identity
NCBI Description
                   Arabidopsis thaliana chromosome I BAC T13M11 genomic
                    sequence, complete sequence
Seq. No.
                   169037
Seq. ID
                   LIB3234-077-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g2160146
BLAST score
                   417
E value
                   5.0e-41
Match length
                   99
% identity
                   85
NCBI Description
                   (AC000375) Strong similarity to Arabidopsis gb_X91953,F21M12.3,F21M12.1. EST gb_H36326 comes from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   169038
Sea. ID
                   LIB3234-077-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q4581166
BLAST score
                   144
E value
                   4.0e-09
Match length
                   55
% identity
NCBI Description
                   (AC006220) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   169039
Seq. ID
                   LIB3234-077-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   355
E value
                   5.0e-34
Match length
                   88
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   169040
Seq. ID
                   LIB3234-078-P1-K1-A11
Method
```

BLASTN

NCBI GI

```
NCBI GI
                   g2980787
BLAST score
                   216
E value
                   1.0e-118
Match length
                   350
% identity
                   50
                   Arabidopsis thaliana DNA chromosome 4, Pl clone M7J2
NCBI Description
                   (ESSAII project) -
Seq. No.
                   169041
Seq. ID
                   LIB3234-078-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g4581120
BLAST score
                   437
E value
                   2.0e-43
Match length
                   78
% identity
                   100
NCBI Description
                  (AC005825) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   169042
Seq. ID
                   LIB3234-078-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g267073
BLAST score
                   271
E value
                   5.0e-26
Match length
                   100
% identity
                   65
NCBI Description
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir_ JQ1587 tubulin
                  beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                   169043
Seq. ID
                  LIB3234-078-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  g3789706
BLAST score
                  179
E value
                  3.0e-96
Match length
                  294
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  169044
                  LIB3234-078-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4008006
BLAST score
                  493
E value
                  5.0e-50
Match length
                  121
% identity
NCBI Description
                  (AF084034) receptor-like protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  169045
Seq. ID
                  LIB3234-078-P1-K1-A6
Method
                  BLASTN
```

g3763944

```
BLAST score
                    64
 E value
                    1.0e-27
 Match length
                    144
 % identity
                    90
 NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23
                    (ESSAII project)
 Seq. No.
                    169046
 Seq. ID
                    LIB3234-078-P1-K1-A7
 Method
                    BLASTX
 NCBI GI
                    g1345973
BLAST score
                    229
 E value
                    2.0e-19
Match length
                    46
 % identity
                    93
                   OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
 NCBI Description
                   >gi_541882_pir_JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                    omega-3 fatty acid desaturase [Arabidopsis thaliana]
                    >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                    [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                   microsomal omega-3 fatty acid desaturase [Arabidopsis
                   thaliana] >gi_3420053 (AC004680) omega-3 fatty acid
                   desaturase [Arabidopsis thaliana]
Seq. No.
                   169047
Seq. ID
                   LIB3234-078-P1-K1-A9
Method
                   BLASTN
NCBI GI
                   g16375
BLAST score
                   34
                   4.0e-10
E value
Match length
                   106
% identity
                   83
NCBI Description
                   A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding
                   protein
Seq. No.
                   169048
Seq. ID
                   LIB3234-078-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   490
E value
                   1.0e-49
Match length
                   104
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
Seq. No.
                   169049
                   LIB3234-078-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832707
BLAST score
                   427
E value
                   3.0e-42
Match length
                   88
% identity
                   99
```

```
NCBI Description
                   (ALO21713) translation initiation factor eIF-2 gamma
                   chain-like protein [Arabidopsis thaliana]
                   169050
 Seq. No.
Seq. ID
                   LIB3234-078-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g4337188
BLAST score
                   284
E value
                   2.0e-25
Match length
                   82
% identity
                   76
                  (AC006403) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   169051
Seq. ID
                   LIB3234-078-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   g4415928
BLAST score
                   335
E value
                   0.0e + 00
Match length
                   400
                   100
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F13A10 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169052
Seq. ID
                   LIB3234-078-P1-K1-B5
Method
                   BLASTN
NCBI GI
                   g2264302
BLAST score
                   387
E value
                   0.0e+00
Match length
                   387
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAC12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169053
Seq. ID
                   LIB3234-078-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g1350680
BLAST score
                   527
E value
                   6.0e-54
Match length
                   109
% identity
                   94
NCBI Description
                  60S RIBOSOMAL PROTEIN L1
Seq. No.
                  169054
Seq. ID
                  LIB3234-078-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  g16375
BLAST score
                  74
E value
                  9.0e-34
Match length
                  182
% identity
                  85
NCBI Description
                  A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding
                  protein
Seq. No.
                  169055
```

```
Seq. ID
                    LIB3234-078-P1-K1-B8
Method
                    BLASTX
NCBI GI
                    g123541
BLAST score
                    400
                    5.0e-39
E value
Match length
                    76
                    99
% identity
                    17.4 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.4)
NCBI Description
                    >gi_81639_pir__JQ0351 heat shock protein 17 - Arabidopsis
thaliana >gi_16340_emb_CAA35182_ (X17293) heat shock
                    protein (\overrightarrow{AA} \overline{1} - 15\overline{6}) [\overline{A}rabidops\overline{i}s thaliana]
                    169056
Seq. No.
Seq. ID
                    LIB3234-078-P1-K1-B9
Method
                    BLASTN
NCBI GI
                    g16339
BLAST score
                    151
E value
                    1.0e-79
Match length
                    207
% identity
                    94
                    Arabidopsis HSP17.4 gene for 17.4kDa heat shock protein
NCBI Description
                    169057
Seq. No.
Seq. ID
                    LIB3234-078-P1-K1-C1
Method
                    BLASTN
NCBI GI
                    g4589432
BLAST score
                    264
                    1.0e-147
E value
Match length
                    366
% identity
NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                    MMJ24, complete sequence
Seq. No.
                    169058
                    LIB3234-078-P1-K1-C12
Seq. ID
Method
                    BLASTN
NCBI GI
                    g2656030
BLAST score
                    380
                    0.0e+00
E value
Match length
                    380
% identity
                    100
NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MUL8
Seq. No.
                    169059
Seq. ID
                    LIB3234-078-P1-K1-C2
Method
                    BLASTN
NCBI GI
                    q4220468
BLAST score
                    330
                    0.0e + 00
E value
Match length
                    374
% identity
NCBI Description
                    Arabidopsis thaliana chromosome II BAC T8011 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
                    169060
Seq. No.
Seq. ID
                    LIB3234-078-P1-K1-C3
```

```
Method
                   BLASTN
NCBI GI
                   g4589428
BLAST score
                   226
E value
                   1.0e-124
Match length
                   351
                   100
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFH8, complete sequence
                   169061
Seq. No.
Seq. ID
                   LIB3234-078-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   g4589428
BLAST score
                   91
                   9.0e-44
E value
Match length
                   227
                   85
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFH8, complete sequence
Seq. No.
                   169062
Seq. ID
                   LIB3234-078-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q1009712
BLAST score
                   351
E value
                   2.0e-33
Match length
                   100
                   67
% identity
NCBI Description
                  (U27698) calreticulin [Arabidopsis thaliana]
                  169063
Seq. No.
Seq. ID
                  LIB3234-078-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q4314363
BLAST score
                   659
E value
                  2.0e-69
Match length
                  130
% identity
NCBI Description
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  169064
Seq. ID
                  LIB3234-078-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3450842
BLAST score
                  436
E value
                  3.0e-43
Match length
                  94
% identity
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  169065
                  LIB3234-078-P1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2245126
BLAST score
                  245
E value
                  1.0e-135
```

```
Match length
                    353
 % identity
                   100
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
 Seq. No.
                   169066
 Seq. ID
                   LIB3234-078-P1-K1-D10
 Method
                   BLASTN
 NCBI GI
                   g2245031
 BLAST score
                   243
 E value
                   1.0e-134
 Match length
                   378
 % identity
                   96
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
 Seq. No.
                   169067
 Seq. ID
                   LIB3234-078-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g520478
BLAST score
                   444
E value
                   3.0e-44
Match length
                   89
% identity
                   100
NCBI Description
                  (U09137) pyruvate dehydrogenase E1 beta subunit
                   [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate
                   dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   169068
Seq. ID
                   LIB3234-078-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q113026
BLAST score
                   518
E value
                   7.0e-53
Match length
                   113
% identity
                   88
NCBI Description
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                  >gi 68211 pir WZRPI isocitrate lyase (EC 4.1.3.1) - rape
                  >gi_255220_bbs_112862 isocitrate lyase, threo-D
                  S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
                  napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
                  isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A
                  isocitrate lyase [Brassica napus]
Seq. No.
                  169069
Seq. ID
                  LIB3234-078-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g1402904
BLAST score
                  486
E value
                  3.0e-49
Match length
                  96
% identity
                  97
NCBI Description (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                  169070
Seq. ID
                  LIB3234-078-P1-K1-D5
Method
                  BLASTN
```

BLASTX

```
NCBI GI
                     g2894557
 BLAST score
                     392
 E value
                     0.0e + 00
 Match length
                     392
 % identity
                     100
 NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, BAC clone T805
                     (ESSAII project)
 Seq. No.
                    169071
 Seq. ID
                    LIB3234-078-P1-K1-D6
 Method
                    BLASTX
 NCBI GI
                    g1361982
 BLAST score
                    546
 E value
                     4.0e-56
 Match length
                    103
 % identity
                    100

    NCBI Description

                    4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis
                    thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase
                    [Arabidopsis thaliana]
 Seq. No.
                    169072
 Seq. ID
                    LIB3234-078-P1-K1-D7
 Method
                    BLASTX
NCBI GI
                    g400923
 BLAST score
                    451
 E value
                    5.0e-45
Match length
                    89
 % identity
                    98
                    RAS-RELATED PROTEIN RAB7 >gi_485497_pir__S33531 GTP-binding protein rab - garden pea >gi_20756_emb_CAA46600_ (X65650)
 NCBI Description
                    RAS-related GTP-binding protein [Pisum sativum]
Seq. No.
                    169073
Seq. ID
                    LIB3234-078-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g2738248
BLAST score
                    587
E value
                    6.0e-61
Match length
                    118
% identity
                    92
NCBI Description
                    (U97200) cobalamin-independent methionine synthase
                    [Arabidopsis thaliana]
Seq. No.
                    169074
Seq. ID
                    LIB3234-078-P1-K1-E11
Method
                    BLASTX
NCBI GI
                    g99735
BLAST score
                    603
E value
                    7.0e-63
Match length
                    114
% identity
                   100
NCBI Description
                   L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                   Arabidopsis thaliana (fragment)
Seq. No.
                   169075
Seq. ID
                   LIB3234-078-P1-K1-E12
```

```
NCBI GI
                   g2065173
 BLAST score
                   150
 E value
                   5.0e-15
 Match length
                   85
 % identity
                   52
 NCBI Description (Y11174) similarities with RP1 and EB1 [Homo sapiens]
 Seq. No.
                   169076
                   LIB3234-078-P1-K1-E3
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g2828180
 BLAST score
                   162
 E value
                   6.0e-86
 Match length
                   265
 % identity
                   95
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MDK4, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   169077
                   LIB3234-078-P1-K1-E6
 Seq. ID
Method
                   BLASTN
NCBI GI
                   q4756963
BLAST score
                   347
E value
                   0.0e + 00
Match length
                   372
% identity
                   98
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                   169078
Seq. ID
                   LIB3234-078-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q4589964
BLAST score
                   287
E value
                   5.0e-26
Match length
                   84
% identity
                   73
NCBI Description
                  (AC007169) delta 9 desaturase [Arabidopsis thaliana]
Seq. No.
                  169079
Seq. ID
                  LIB3234-078-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  619
E value
                  1.0e-64
Match length
                  117
% identity
                  100
NCBI Description
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  169080
Seq. ID
                  LIB3234-078-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q266693
BLAST score
                  457
E value
                  1.0e-45
```

```
Match length
                    123
  % identity
                    76
  NCBI Description
                    OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis
                    thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin
                    [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1
                    (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
  Seq. No.
                    .169081
  Seq. ID
                    LIB3234-078-P1-K1-F11
 Method
                    BLASTX
 NCBI GI
                    q99735
 BLAST score
                    563
 E value
                    4.0e-58
 Match length
                    114
 % identity
                    94
 NCBI Description
                   L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                    Arabidopsis thaliana (fragment)
 Seq. No.
                    169082
 Seq. ID
                    LIB3234-078-P1-K1-F12
 Method
                    BLASTN
 NCBI GI
                    q4544365
 BLAST score
                    322
 E value
                    0:0e+00
 Match length:
                 # 384
 % identity
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F26H6 genomic
                   sequence, complete sequence
 Seq. No.
                   169083
 Seq. ID
                   LIB3234-078-P1-K1-F2
 Method
                   BLASTX
 NCBI GI
                   g3023848
BLAST score
                   533
E value
                   1.0e-54
Match length
                   113
% identity
                   34
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                  >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis
                   thalianal
Seq. No.
                   169084
Seq. ID
                  LIB3234-078-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4218002
BLAST score
                  459
E value
                  6.0e-46
Match length
                  93
% identity
                  100
NCBI Description
                  (AC006135) putative UTP-glucose glucosyltransferase
                  [Arabidopsis thaliana]
Seq. No.
                  169085
Seq. ID
                  LIB3234-078-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3420042
```

Match length

```
BLAST score
                   371
E value
                   0.0e+00
Match length
                   391
 % identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T13E15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169086
Seq. ID
                   LIB3234-078-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   q2924651
BLAST score
                   208
E value
                   1.0e-113
Match length
                   216
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                   169087
Seq. ID
                   LIB3234-078-P1-K1-F7
Method
                   BLASTN
NCBI GI
                   g2924651
BLAST score
                   171
E value
                   2.0e-91
Match length
                   185
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  169088
Seq. ID
                  LIB3234-078-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2262167
BLAST score
                  598
E value
                  3.0e-62
Match length
                  114
% identity
                  100
NCBI Description
                  (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
                  thaliana]
Seq. No.
                  169089
Seq. ID
                  LIB3234-078-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g2058311
BLAST score
                  405
E value
                  1.0e-39
Match length
                  98
% identity
                  78
NCBI Description
                  (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]
Seq. No.
                  169090
Seq. ID
                  LIB3234-078-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q126079
BLAST score
                  163
E value
                  3.0e-11
```

```
% identity
 NCBI Description
                   LATE EMBRYOGENESIS ABUNDANT PROTEIN 76 (LEA 76)
                   >gi_81683_pir__S04130 embryonic abundant protein (clone
                   pLEA76) - rape >gi_17829_emb_CAA33406_ (X15348) LEA76
                   peptide (AA 1-280) [Brassica napus]
                   >gi 226789 prf 1605299A Lea76 gene [Brassica napus]
 Seq. No.
                   169091
 Seq. ID
                   LIB3234-078-P1-K1-G12
 Method
                   BLASTX
 NCBI GI
                   q1161171
 BLAST score
                   156
 E value
                   2.0e-10
 Match length
                   121.
 % identity
                   18
 NCBI Description
                  (L42465) late embryogenesis abundant protein [Picea glauca]
 Seq. No.
                   169092
 Seq. ID
                   LIB3234-078-P1-K1-G2
 Method
                   BLASTX
 NCBI GI
                   q3025470
 BLAST score
                   376
E value
                   3.0e-36
Match length
                   126
% identity
                   54
NCBI Description (U76756) endo-beta-1,4-glucanase [Pinus radiata]
Seq. No.
                   169093
Seq. ID
                   LIB3234-078-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g927575
BLAST score
                   63
E value
                   1.0e-11
Match length
                   78
% identity
                   55
NCBI Description
                  (U12926) alpha galactosidase [Glycine max]
Seq. No.
                  169094
Seq. ID
                  LIB3234-078-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1864017
BLAST score
                  559
E value
                  1.0e-57
Match length
                  106
% identity
                  100
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  169095
Seq. ID
                  LIB3234-078-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2645971
BLAST score
                  509
E value
                  8.0e-52
Match length
                  110
% identity
                  83
NCBI Description
                  (AF034255) reversibly glycosylated polypeptide-3
```

[Arabidopsis thaliana]

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Seq. No.
                     169096
   Seq. ID
                     LIB3234-078-P1-K1-G8
  Method
                     BLASTX
  NCBI GI
                     g112682
  BLAST score
                     571
  E value
                     4.0e-59
  Match length
                     122
  % identity
                     88
  NCBI Description
                     12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir___S08510
                     cruciferin precursor (CRB) - Arabidopsis thaliana
                     >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                     thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                     storage protein [Arabidopsis thaliana]
  Seq. No.
                     169097
  Seq. ID
                    LIB3234-078-P1-K1-G9
  Method
                    BLASTN
  NCBI GI
                    g3128142
  BLAST score
                    311
  E value
                    1.0e-175
  Match length
                    356
  % identity
                    96
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                    MQN23, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    169098
  Seq. ID
                    LIB3234-078-P1-K1-H1
 Method
                    BLASTX
 NCBI GI
                    g2244905
 BLAST score
                    517
 E value
                    9.0e-53
 Match length
                    128
 % identity
                    77
 NCBI Description
                   (Z97339) indole-3-acetate beta-glucosyltransferase
                    [Arabidopsis thaliana]
Seq. No.
                   169099
 Seq. ID
                   LIB3234-078-P1-K1-H10
 Method
                   BLASTN
 NCBI GI
                   q1707006
 BLAST score
                   183
 E value
                   1.0e-98
 Match length
                   256
 % identity
                   93
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC T1B8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   169100
 Seq. ID
                   LIB3234-078-P1-K1-H11
 Method
                   BLASTN
 NCBI GI
                   g3659491
 BLAST score
                   93
 E value
                   2.0e-45
Match length
                   101
% identity
                   99
NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
```

```
1, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    169101
  Seq. ID
                    LIB3234-078-P1-K1-H2
  Method
                    BLASTX
  NCBI GI
                    g2244905
  BLAST score
                    382
  E value
                    5.0e-37
  Match length
                    110
  % identity
  NCBI Description
                    (Z97339) indole-3-acetate beta-glucosyltransferase
                    [Arabidopsis thaliana]
  Seq. No.
                    169102
  Seq. ID
                    LIB3234-078-P1-K1-H5
 Method
                    BLASTN
 NCBI GI
                    g1707006
 BLAST score
                    143
 E value
                    9.0e-75
 Match length
                    235
 % identity
                    94
 NCBI Description Arabidopsis thaliana chromosome II BAC T1B8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   169103
 Seq. ID
                   LIB3234-078-P1-K1-H6
 Method
                   BLASTX
NCBI GI
                   g633890
 BLAST score
                   250
 E value
                   2.0e-21
 Match length
                   88
 % identity
                   62
 NCBI Description
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                   vulgare]
 Seq. No.
                   169104
 Seq. ID
                   LIB3234-079-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   q3334123
BLAST score
                   645
E value
                   9.0e-68
Match length
                   132
% identity
                   99
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of
                  mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787
                   (AC002334) mitochondrial F1-ATPase, gamma subunit
                   [Arabidopsis thaliana]
Seq. No.
                  169105
Seq. ID
                  LIB3234-079-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g2129753
BLAST score
                  662
E value
                  1.0e-69
Match length
                  132
% identity
                  96
```